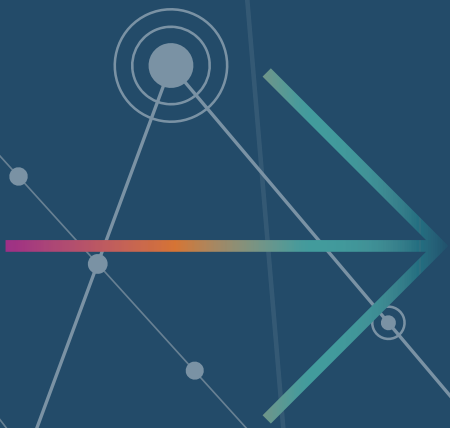
UK Human Functional Genomics Initiative

Inaugural Scientific Symposium

University of Exeter
Monday 16th June 2025

Contents



#fgx2025

1. Foreword

It is my great pleasure to welcome you to the beautiful Streatham Campus at the University of Exeter for the inaugural UK Human Functional Genomics Initiative Scientific Symposium.

This event marks the beginning of what we hope will become a flagship annual gathering for the UK functional genomics community. Our aim is to create a vibrant and inclusive forum for researchers across career stages to meet, share ideas, forge collaborations, and learn about the latest research in this rapidly moving field.

The UK Human Functional Genomics Initiative launched in September 2024 and aims to bring together scientists, clinicians and industry partners to explore the genomic basis of human health and disease. Our goal is to characterise the functional consequences of disease-associated genetic variation so that we can understand pathogenic mechanisms and ultimately develop new treatments.

Our ethos is grounded in the principles of open and reproducible science. We are committed to building a collaborative culture in which tools, protocols, data and resources are shared, and where researchers across the UK can participate, contribute, and benefit. Today marks the launch of our first wave of collaborative funding opportunities - designed to support ambitious, interdisciplinary projects that leverage the Initiative's infrastructure and expertise.

I really hope you can all stay for the networking drinks at the end of the day - an ideal chance to continue the conversation and start building the connections that will shape the future of functional genomics in the UK.

Thank you for joining us today. I look forward to seeing you again next year!

Jonathan Mill

Director, UK Human Functional Genomics Initiative
Professor of Epigenomics, University of Exeter Medical School

2. Agenda

09:30 – 10:30	**Registration, coffee, pastries and networking**
10:30 – 12:10	**Session 1:**
10:30 – 10:45	Jonathan Mill, Director of the UK Human Functional Genomics Initiative, University of Exeter
10:45 – 11:00	Wendy Bickmore, Institute of Genetics and Cancer, University of Edinburgh
11:00 – 11:10	Nicola McCarthy, Milner Therapeutics Institute, University of Cambridge
11:10 – 11:30	Delphine Larrieu, Altos Labs, Cambridge institute of Science
11:30 – 11:45	Sara Wells, Mary Lyons Centre, MRC Harwell Institute
11:45 – 12:15	Lea Starita, Department of Genome Sciences, University of Washington
12:15 – 13:30	**Lunch, posters & networking**
13:30 – 15:00	**Session 2:**
13:30 – 13:40	Sponsored talk
13:40 – 14:00	Ioannis Sarropoulos, Cambridge Stem Cell Institute, University of Cambridge
14:00 – 14:30	Roser Vento-Torno, Wellcome Sanger Institute
14:30 – 15:00	Martin Kircher, Institute of Human Genetics of the University Medical Center Schleswig-Holstein, University of Lübeck
15:00 – 15:30	**Break with refreshments**
15:30 – 17:00	**Session 3:**
15:30 – 15:40	Sponsored talk
15:40 – 15:45	Tony Burdett, BioFAIR
15:45 – 16:05	Matthew Child, Imperial College London
16:05 – 16:20	Mina Ryten, Dementia Research Institute, University of Cambridge
16:20 – 16:50	Ralda Nehme, Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard
16:50 – 17:00	**Closing remarks & poster winner announced**
17:00 – 18:00	**Drinks Reception**

3. The UK Human Functional Genomics Initiative

About the UK Human Functional Genomics Initiative

The UK Human Functional Genomics Initiative is a nationwide effort to unlock the mechanisms of disease by understanding the functional consequences of disease-associated genetic variation. Through a collaborative network that spans academia and industry, the Initiative leverages advanced technologies and data science to accelerate biomedical discovery and improve human health. At its core, the Initiative is committed to open science, shared resources, and enabling reproducible research that benefits the entire genomics community. Funded initially by £28.5M from the MRC and BBSRC, the initiative plans to grow with new clusters and research areas.

Coordination Hub

Based at the University of Exeter, the Coordination Hub provides strategic oversight and operational leadership for the Initiative. It manages data coordination, training opportunities, and funding streams, while actively fostering collaboration and knowledge exchange across the UK's functional genomics landscape. The Hub works closely with the Initiative's research clusters, the Data Coordination Centre, and the Functional Genomics Screening Laboratory to drive engagement and innovation across the sector.

University of Exeter

3. The UK Human Functional Genomics Initiative

Neurodevelopmental Cluster

Led by Oscar Marin and Deepak Srivastava at KCL, this cluster seeks to deepen our understanding of how genetic variation influences brain development and contributes to neurodevelopmental conditions such as epilepsy, schizophrenia, intellectual disability, autism, and ADHD. While genetic studies have linked certain variants to these disorders, many questions remain about how these genes affect brain structure and function.

To address this, the cluster will develop advanced lab-grown brain models known as cortical organoids. These organoids mimic the human cerebral cortex and allow researchers to study how specific cell types respond to genetic mutations. Using genome editing techniques, researchers will manipulate genes linked to disorders and analyse organoid development using single-cell genomics, imaging, electrophysiology, and computational tools. This approach will reveal how genetic variants alter cellular functions, gene regulation, and neural activity, providing insights into the molecular pathways that contribute to neurodevelopmental disorders.

Molecular Mechanisms Cluster

Led by Kenneth Baillie in Edinburgh, this cluster focuses on identifying the molecular events that link genetic variation to disease—bridging a major gap in our understanding of human biology. Although thousands of disease-associated variants have been identified over the past two decades, many of their mechanisms remain unknown.

By analysing single cells from surplus tissue donated by patients undergoing surgery or medical procedures, the cluster will generate a comprehensive dataset of molecular signals across diverse tissues—including brain, skin, blood, and lung. These cells will be exposed to experimental stimuli, revealing the biological changes associated with disease. The team will also develop new artificial intelligence tools to extract more detailed insights from each sample.

This approach has already proven successful: the cluster previously identified a genetic variant linked to Covid-19 severity, traced its molecular impact in immune cells, and helped lead to the development of a globally used therapeutic.

KING'S College LONDON

THE UNIVERSITY of EDINBURGH

Musculoskeletal Cluster

Led by Dominic Furniss in Oxford, this cluster is tackling some of the most common—and disabling—health conditions by exploring the genetics of bones, joints, cartilage, and soft tissues. Diseases such as osteoarthritis and carpal tunnel syndrome are widespread, yet remain under-researched despite their profound impact on quality of life.

By analysing tissue discarded during surgery, the cluster investigates how genetic variation affects the cellular and extracellular matrix biology that underpins musculoskeletal health. The aim is to connect genetic findings with functional consequences and use this knowledge to identify new therapeutic targets.

A second arm of the research involves building robotic "bioreactors"—devices that mimic the physical forces experienced by musculoskeletal tissues in the body. These systems allow researchers to study how mechanical stress interacts with disease genes, providing a new dimension to functional genomic analysis. The cluster is also committed to equipping the broader research community with tools, data, and training to accelerate discovery in this underdeveloped field.

UNIVERSITY OF OXFORD

Protein Post-Translational Modification Cluster

Led by Matthew Child at Imperial, this cluster uses data from the 100,000 Genomes Project to investigate how specific genetic changes—particularly missense variants—affect protein function, with a focus on improving diagnosis for rare diseases. Many of these genetic changes alter the building blocks of proteins, yet their impact on protein activity remains unclear.

By modelling how these changes influence post-translational modifications—chemical alterations that regulate protein behaviour—the cluster will prioritise variants for experimental validation. Using automated high-throughput technologies, hundreds of variants will be tested in living cells. The cluster works closely with the European Bioinformatics Institute and the ProtVar resource to share its findings, supporting the wider research community in interpreting complex variants.

This cross-disciplinary work draws on expertise from computational genomics, proteomics, cell biology, and more. Ultimately, it aims to bridge the gap between genetic discovery and clinical diagnosis, providing insights that can directly inform patient care.

IMPERIAL

3. The UK Human Functional Genomics Initiative

Functional Genomics Screening Laboratory

Located at the Milner Therapeutics Institute at the University of Cambridge, the Functional Genomics Screening Laboratory (FGSL) is a cornerstone of the UK Functional Genomics Initiative. Designed as both a research space and collaborative hub, the FGSL enables high-throughput exploration of how genes influence complex biological traits and disease mechanisms.

Using cutting-edge technologies such as arrayed CRISPR screening, the FGSL initially focuses on non-oncology diseases —including those affecting the immune, cardiovascular, and respiratory systems —with scope to expand into additional areas. The lab operates in close partnership with academic researchers, industry leaders such as AstraZeneca, and the wider UK scientific community.

By offering technical expertise, screening capacity, and open access to UK researchers, the FGSL will play a transformative role in advancing functional genomics and driving innovation in therapeutic discovery.

Functional Genomics Data Coordination Centre

The Data Coordination Centre, based in Exeter, will play a central role in enabling scientists to find, use, and share the data generated across the Initiative. Working with the clusters and partners including EMBL-EBI and BioFAIR, we are developing a scalable data sharing platform that supports federated analysis and integrates datasets across multiple modalities. From the outset, the Initiative will adopt FAIR principles and embraces open and reproducible research. Core data standards will ensure compatibility, and all resources including raw data, metadata, protocols, analysis code, and pipelines will be openly available.

MILNER THERAPEUTICS INSTITUTE

AstraZeneca

University of Exeter

4. Guest Speakers

Wendy Bickmore

Title: Exploring function in the dark genome

Professor Wendy Bickmore is Director of the MRC Human Genetics Unit at the University of Edinburgh. Her undergraduate degree is in Biochemistry from the University of Oxford, and she then completed a PhD in molecular biology at the University of Edinburgh.

Following a postdoc in human genetics, Wendy started her independent research group as a fellow of the Lister Institute for Preventive Medicine. She is fascinated by the three-dimensional organization of the human genome in cells and how that influences genome function in health and disease. Her current research explores how the non-coding genome regulates gene expression including how distant enhancers communicate with their target gene promoters.

Wendy is a Fellow of the Royal Society, the Royal Society of Edinburgh and of the Academy of Medical Sciences and is a member of the European Molecular Biology Organization and an international member of the National Academy of Sciences. She was awarded a CBE for services to science and to women in science.

Nicola McCarthy

Title: An introduction to the Functional Genomics Screening Laboratory

Dr Nicola McCarthy is Head of Research at the Milner Therapeutics Institute and oversees the MRC-AZ-University of Cambridge Joint Functional Genomics Screening Laboratory (FGSL). Nicola has a degree in Anatomical Studies and a PhD focused on apoptosis and cancer. She has a wealth of experience from a career in academic, science publishing and industry roles.

4. Guest Speakers

Delphine Larrieu

Title: Harnessing the power of whole genome arrayed screening to discover new mechanisms and targets in rare genetic conditions.

Dr. Delphine Larrieu is currently a Principal Investigator at Altos Labs in Cambridge where she contributes to the mission of restoring cell health and resilience in ageing.

After completing her PhD at the University Grenoble Alpes in France, Delphine moved to the University of Cambridge in 2011 for her postdoctoral research in Steve Jackson Laboratory. She obtained personal funding from EMBO and from the Medical Research Council (MRC) that allowed her to develop an independent line of research, focusing on understanding nuclear envelope function and its links with disease, more specifically premature ageing.

In 2017, Delphine was awarded a Wellcome Trust Sir Henry Dale fellowship, to launch her own lab at the Cambridge Institute for Medical Research to pursue her research in the field of nuclear envelope. During this period, she developed pioneering approaches based on the principle of synthetic rescue and relying on cutting-edge whole genome genetic screening approaches. Her work identified novel, unexpected targets and cellular pathways that can reverse several age-related nuclear envelope phenotypes in cells from progeria patients.

Driven by her discoveries, Delphine co-founded Adrestia Therapeutics, a synthetic rescue company dedicated to restoring cellular balance in genetic diseases. The company's vision, directly inspired by her research, recently culminated in its acquisition by Insmed.

In 2022, she was appointed Assistant Professor at the Department of Pharmacology, University of Cambridge. Here, her efforts concentrated on characterising and expanding the number of targets that could be exploited therapeutically to extend health and lifespan in progeria syndromes as well as in ageing. Her journey continues at Altos Labs Cambridge, which she joined in 2024, bringing her expertise to the forefront of cellular rejuvenation.

Sara Wells

Title: An introduction to the MRC National Mouse Genetics Network

Dr Sara Wells is the Director of the Mary Lyon Centre at MRC Harwell and the MRC Centre for Macaques at Porton Down and is the Chief Biological Research Facility officer for the Francis Crick Institute. Sara received her undergraduate degree in genetics at the University of Sheffield and a PhD in genetics and neuroendocrinology at MRC's National Institute for Medical Research.

Sara is the Director of the hub of the National Mouse Genetics Network and the president of LASA (Laboratory Animal Science Association, UK). Sara is interested in developing ways of increasing the relevance of animal models in preclinical studies whilst refining their use.

Lea Starita

Title: Understanding the functional effects of coding variation at scale

Dr Lea Starita is an Associate Professor of Genome Sciences at the University of Washington and co-director of the Advanced Technology Lab at the Brotman Baty Institute for Precision Medicine. She develops massively parallel methods to measure the effects of genetic variation on protein function. Using this approach, she hopes to help solve the problem of variants of uncertain significance by scoring the pathogenic potential of genetic variants before they are found in the clinic.

Ioannis Sarrapoulos

Title: Mapping the human thymus one cell at a time: a Human Cell Atlas perspective

Dr Ioannis Sarropoulos is an EMBO-funded postdoctoral researcher in the group of Professor Sarah Teichmann at the Cambridge Stem Cell Institute and a Research Fellow at Darwin College of the University of Cambridge. During his PhD at Heidelberg University in Germany, for which he was recognized with an International Birnstiel Award and a Ruprecht Karl Prize, he employed comparative genomics and multiomics methods to investigate the development and evolution of mammalian organs. His current work combines single-cell multiomics, spatial transcriptomics, and machine learning models to study T cell development in the human thymus.

Roser Vento-Tormo

Title: Gene regulation of human cell systems

Dr Roser Vento-Tormo's research interest is to understand the influence of cellular microenvironments on individual cellular identities and responses, in the context of development and immunity. Her team employs single-cell and spatial transcriptomics methods to deconstruct the cell signals in human organs and tissues, and utilise this information to inform the reconstruction of novel in vitro models.

Essential for this work is the novel computational tools her team develops to build cell–cell interactions networks from transcriptomics data. Her team has used these computational and genomics tools to generate atlases of the human reproductive tissues leading to transformative advances in the area of women's health.

Roser's work has been funded by many recognised international agencies (ERC, Wellcome-LEAP, CZI), and she has been awarded multiple prizes, including the Early Career Research Award from the Biochemistry Society (2021) and the Michelson & Science Prize Finalist (2023).

4. Guest Speakers

Martin Kircher

Title: Interpreting variant function across the human genome

Dr Martin Kircher works in the fields of Functional Genomics and Machine Learning. He studied Computational Molecular Biology at Saarland University in Germany (B.Sc/M.Sc. hon). During his PhD in Computer Sciences at the Max Planck Institute for Evolutionary Anthropology, Department of Evolutionary Genetics (Drs Janet Kelso & Svante Pääbo), Martin worked on the Neandertal and Denisova genome projects, resulting in unique insights into human history and adaptation. Between 2012 and early 2017, he held a Senior Research Fellow position with Dr Jay Shendure in the Department of Genome Sciences at the University of Washington, Seattle, USA. From 2012 to 2015, he was also part of the University of Washington's Center for Mendelian Genomics and actively involved in several disease studies.

In 2013, Martin developed (and since maintains) a framework for objectively combining diverse annotations to a single measure of variant deleteriousness, called Combined Annotation Dependent Depletion (CADD). In another line of research, he joined a team to show that an epigenetic signal of cell-type origin is captured in cell-free DNA fragments (liquid biopsies). During the time in Seattle, he also got interested in better understanding regulatory variation and the development of Massively Parallel Reporter Assays (MPRAs). Since 2017, he continues these lines of research in his own lab at the Berlin Institute of Health (BIH) at Charité in Germany. In January 2022, he was appointed the Professor of Regulatory Genomics at the Institute of Human Genetics of the University Medical Center Schleswig-Holstein by the University of Lübeck and maintains a dual affiliation as BIH research group leader.

Matthew Child

Title: Protein feature-targeted mutagenesis to interrogate rare disease mechanisms

Dr Matthew Child studied for a PhD in molecular parasitology with Prof. Mike Blackman at the National Institute for Medical Research, London, UK. After his PhD, he worked as a post-doc in the chemical biology laboratory of Prof. Matt Bogyo at Stanford University, California. Matthew's group is based at Imperial College London, where he is an Associate Professor within the department of Life Sciences.

Matthew's team seek to understand how individual amino acids contribute to protein function in live cells, in rare disease, and during infections by old and emergent pathogens. A technology-led approach allows them to do this at scale for allosteric sites, covalently druggable residues, sites of post-translational modification, and disease-associated missense variants.

Mina Ryten

Title: The Long View: Functional Genomics and Therapeutic Discovery Through Long-Read RNA-Seq

Professor Mina Ryten is a clinical geneticist and neuroscientist, currently serving as Director of the UK Dementia Research Institute (UK DRI) at the University of Cambridge. Appointed in January 2024, she also holds the Van Geest Professorship and leads a multidisciplinary lab focused on understanding molecular mechanisms driving neurodegeneration.

Mina's research harnesses human brain transcriptomic data to decode how genetic variation influences neurological diseases, particularly Lewy body disorders. Her work has advanced the use of single cell and long-read RNA sequencing to map disease pathways and identify potential therapeutic targets.

Before her move to Cambridge, Mina led her own research group at University College London and served as an Honorary Consultant in Clinical Genetics at Great Ormond Street Hospital.

Her dual expertise in clinical care and functional genomics has enabled her to bridge the gap between patient experience and scientific discovery.

Ralda Nehme

Title: Unravelling complexity using genetically diverse human cellular models

Dr. Ralda Nehme is a Principal Investigator at the Stanley Center for Psychiatric Research at the Broad Institute of MIT and Harvard, where she also dire cts the stem cell program. Her lab investigates the genetic, cellular, and molecular mechanisms driving neurodevelopmental and psychiatric disorders, with a focus on how human genetic variation shapes cellular phenotypes. Combining human pluripotent stem cell models, genome editing technologies, high-content imaging, electrophysiology, and multiomic approaches, the Nehme lab aspires to build scalable and quantitative experimental approaches for dissecting disease-relevant biology.

Ralda earned her B.S. from the American University of Beirut and completed her Ph.D. at Dartmouth College, studying neuronal development in C. elegans. She conducted postdoctoral research at Harvard University, where she developed robust methods for generating human stem cell–derived neural cells and became engaged in modeling psychiatric disease.

5. Our Sponsors

BioFAIR is a five year £34M UK government-funded initiative to create a federated biocommons infrastructure for life sciences. Conceptualised by ELIXIR UK and launched in 2024, BioFAIR aims to drive a shift towards FAIR data principles, enhance coordination, and promote efficient, collaborative research through better access to data and increased reuse. We also seek to strengthen research data management skills nationwide.

BioFAIR focuses on delivering four core capabilities: a data commons, method commons, knowledge centre, and people hub. These capabilities, combined and supported through the BioFAIR portal, will form a "concierge service" to help researchers navigate existing tools and infrastructure.

In 2025, BioFAIR will launch two calls:

- The BioFAIR Fellowship Programme, supporting research data analysis and data management experts, across career stages, to become ambassadors for FAIR research data management, and support the development and adoption of reproducible, open workflows.
- Pathfinder Projects, where BioFAIR will support research groups seeking to address domain-specific, complex, or emerging challenges in FAIR implementation.

The Pathfinder Project programme will fund teams experimenting with innovative approaches to data sharing, interoperability, and reuse. The goal is to apply existing FAIR tools, knowledge, and expertise from across the UK life sciences community to develop practical, real-world solutions and inform the future of BioFAIR.We invite all researchers, infrastructure teams, and data specialists to engage with BioFAIR and contribute to building a more connected, FAIR-enabled life sciences community across the UK.

BioFAIR is a joint Biotechnology and Biological Sciences Research Council (BBSRC) and Medical Research Council (MRC) project. It has received funding through the UKRI Infrastructure Fund and UKRI Digital Research Infrastructure Programme.
Learn more at **www.biofair.uk**

Tony Burdett, Director

Title: Driving Culture Change in Research Data Management in the UK Life Sciences

Twist Bioscience is a leading, rapidly growing synthetic biology company that has developed a disruptive DNA synthesis platform to industrialize the engineering of biology.
The core of Twist's platform is a proprietary technology that pioneers a new method of manufacturing synthetic DNA by "writing" DNA on a silicon chip.

They leverage their unique technology platform to manufacture a broad range of synthetic DNA-based products, including synthetic genes, tools for NGS sample preparation, and antibody libraries for drug discovery and development. Additionally, Twist believe their platform will enable new opportunities including discovery partnerships for biologic drugs.

Oxford Nanopore has developed a new generation of DNA/RNA sequencing technology. It is the only platform offering real-time analysis, scalable from pocket to population level, capable of analysing native DNA or RNA, and sequencing any fragment length from short to ultra-long reads.
It is used across a wide range of biological and applied research areas, including human genomics, cancer, microbiology, plant science, environmental research, healthcare, agriculture, food, surveillance, and education.

As shown by the research community, Oxford Nanopore sequencing can access regions of the genome that are unreachable with legacy short-read technologies, enabling more comprehensive genome analysis and advancing our understanding of health and disease.

Julian Jude, Director of Emerging Applications & Genetic Medicine

Title: 500 bps in 5 Minutes: Multiplexing Gene Fragments with Twist Bioscience

Dan Dancer, Senior Account Manager

Title: ONT - enabling a multiomic view of the genome and transcriptome

5. Our Sponsors

At Illumina, our mission is to improve human health by unlocking the power of the genome. Our sequencing by synthesis chemistry is used to generate high-accuracy DNA and RNA sequence data in studies around the globe. The innovative products that we provide are helping drive advancements in a multiomic understanding of cellular functions, combining transcriptomics, epigenetics, and proteomics. Multiomics profiling studies enable a more comprehensive understanding of development, cellular response, and disease, fueling the discovery of novel drug targets and biomarkers. The progress our customers have made and what lies ahead inspire us to push the boundaries of what is possible so we can create the next generation of genomics solutions.

10x Genomics was founded on the vision that this century will bring advances in biomedicine and transform the way we understand and treat disease. We deliver powerful, reliable tools that fuel scientific discoveries and drive exponential progress to master biology to advance human health.

Our end-to-end single cell and spatial solutions include instruments, consumables, and intuitive software, letting you unravel highly intricate biological systems, while bringing into focus the details that matter most.

Mohammad Ali, Senior Technical Specialist

Title: Key technology updates from Illumina

Nicola Cahill, Senior Science and Technology Advisor

Title: Unlocking the Power of Single-Cell & Spatial Analysis with New 10x Genomics tools

QUANTUM SI

Quantum-Si is redefining proteomic analysis by making single molecule protein analysis fast, simple, and accessible to every lab, everywhere.

Powered by our core technology, Next-Gen Protein Sequencing⊠, Quantum-Si's single-molecule platform enables kinetic measurements, revealing not just which proteins are present, but how they behave and interact within biological systems. By removing the complexity of traditional workflows like gels, Western blots, or specialized core facilities, Quantum-Si brings powerful, quantitative proteomic capabilities directly to the benchtop. It's a new approach to protein analysis, one that provides both identification and quantitative understanding in a single platform with unparalleled resolution.

With Quantum-Si, researchers gain deeper clarity into the molecular mechanisms that shape life, and the human condition. This advancement supports a new era of functional proteomics, accelerating discoveries across research, therapeutic development, and beyond.

Olink

Olink offers an unmatched high-multiplex technique to identify actionable biomarkers, with a strong focus on the human plasma proteome. Using minimal sample volume we provide quantifiable results with high-throughput, exceptional sensitivity and specificity, with coverage across a broad dynamic range. Our mission is to accelerate proteomics together with the scientific community across multiple disease areas to enable new discoveries and better understand complex real-time human biology. We are committed to develop our offering and are continuously expanding our protein coverage or a growing number of biological processes and pathways.

University *of* Exeter

Genomics is a key strength in the Department of Clinical and Biomedical Sciences at the University of Exeter. We have tripled the number of academics in our Medical School over the last 10 years and there are now groups working on epigenetics, rare disease genomics, complex traits, RNA biology and monogenic diabetes. The University has invested in a £27M building to house the Genomics teams and secured funding for state-of-the-art genomics facilities such as Illumina NovaSeq 6000, Oxford Nanopore PromethION sequencers and 10X Genomics platforms. NIHR recently funded a £15M Biomedical Research Centre in Exeter with Genetics & Genomics as a core theme. This funding supports internal research projects, plus fellowships and clinical academics to translate academic research and scientific discoveries into benefits for patients. As a department, we are keen to continue our growth and translate our genomics research into impact through collaboration with academic and industry partners.

6. Get involved

Scan the QR Code to interact with us

Vote for your favourite poster
Please do visit the posters on display today in the Forum MarketPlace and vote for your favourite posters using the QR code. There will be prizes for the top-ranked posters.

Register for our funding webinar
Find out how to apply for our funding opportunities which will be open to academics from UK HEIs.

The webinar will be recorded and made available on the UK Human Functional Genomics Initiative website **ukfunctionalgenomics.com**

Venue information
All talks will be in the Alumni Auditorium in the Forum at the University of Exeter.

Refreshments and lunch will be in the Forum.

Please visit our sponsor stands in the Forum MarketPlace.

We have a selection of break out spaces available at the Forum for delegates.

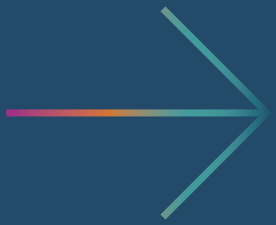
Level 0: Seminar rooms 1,2 & 3 – Seated space to sit down and eat
Level 0: Seminar room 4 – Luggage

Level 0: Seminar rooms 5 and 6 – Space for online meetings

Level M: Rooms 7 & 8 – Quiet space (no meetings or calls please)

Level M: Room 9 – Prayer room

With thanks to
our sponsors



UK Human Functional Genomics Initiative

2025RS015