norwich research park
Doctoral Training Partnership

NRPDTP Summer Conference 2026
Healthy Humans, Animals & Plants
Thursday 18th June, John Innes Centre, Norwich

Biotechnology and Biological Sciences Research Council

NRPDTP Summer Conference supported by UKRI-BBSRC

norwich research park
Doctoral Training Partnership

NRPDTP Summer Conference 2026
Healthy Humans, Animals and Plants
Thursday 18th June 2026

08.45 –09.15	**Registration & Poster Set-up**
09.15 – 09.25	NRPDTP Director & Conference Student Committee Welcome
CHAIR:	**Samuel Matthew Shackleton-Chavez, UEA**
09.25 – 09.58	Combining genomics and plant grafting allows the detection of mobile RNAs in plants Dr Marco Catoni, University of Birmingham Introduced by Samuel Matthew Shackleton-Chavez
09.58 – 10.31	The molecular mechanisms underlying reproduction and their real-world implications Prof. Simone Immler, University of East Anglia Introduced by Samuel Matthew Shackleton-Chavez
10.31– 10.41	Summer Conference Bingo Introduction Summer conference committee member Issy Frost
10.41– 11.15	**Refreshment Break and Poster Presentations**
CHAIRS:	**Mehmethan Aris, UEA & Angus Bucknell, TSL**
11.15 – 11.48	From Bench to Batch: Navigating Precision Fermentation Dr Camila Cotrim. Introduced by Mehmethan Aris
11.48 – 12.21	Regulating bacterial infection: how plants control entry and immune signalling Dr Pierre Buscaill, University of Bristol Introduced by Angus Bucknell
12.21 – 12.54	Resistance or Death? Searching for my research question Dr Hee-Kyung Ahn, University of Edinburgh Introduced by Angus Bucknell
12.54 –14.05	**Lunch and Poster Presentations**

CHAIR:	**John Williams, UEA**
14.05 –14.40	**PANEL OF EXTERNAL SPEAKERS Q&A**
	STUDENT TALK Y2 8 MIN EACH
14.41 – 14.49	Garlic Oils as a Redox-Active Trigger for Budbreak? Student Speaker Ahmed Nada
14.49 –15.20	**Refreshment Break and submission of bingo cards and poster votes**
CHAIR:	**Isabella Frost, JIC**
	STUDENT TALKS Y3/Y4 15 MIN EACH
15.20 – 15:35	Pushing the boundary: How the adaxial-abaxial boundary coordinates leaf growth direction Student Speaker Kestrel Maio
15.35 – 15.50	Ageing alters changes to liver fatty acid metabolism in response to infection Student Speaker Alyssa Polski-Delve
15.50 – 16.05	Battling Biofilms: Investigating the role of MaoP in Enterobacteriaceae biofilm formation Student Speaker Joshua Horton
16.05 – 16.20	Functional Impact of Short Tandem DNA Repeat Instability Student Speaker Łukasz Sitko
16.20 - 16.35	Production of the building block molecule 3-hydroxypropionic acid from seaweed waste Student Speaker Ndeye Bineta Dia
16.35 –16.55	Closing Remarks and Presentation of Prizes
17.00 –18.00	**End of Conference Refreshments & Networking**

External Speakers

Dr Marco Catoni, University of Birmingham

In plants, RNA molecules can act as intercellular signals, with evidence of transport for both messenger RNA (mRNA) and small RNA (sRNA) over long distances. Such RNA molecules that move from the cell in which they originated are termed mobile RNA, and are fundamental to control distant communication by affecting epigenetic regulation in distant tissues. In grafted plants, when different genotypes are joined together, the movement of RNAs between distant tissues can be revealed by approaches that exploit natural polymorphisms between the genomes involved. However, current methods suffer from a high level of technological noise, and the lack of standardised approaches makes it challenging for researchers to robustly identify mobile RNA molecules. Here, we introduce an automated pipeline, mobileRNA, which combines a multi-genome approach based on simultaneous alignment of RNA sequencing data to merged reference genomes with advanced statistical procedures. Using simulated grafting combinations and real datasets, we show that mobileRNA can identify putative mobile RNAs with unprecedented accuracy, in absence of post-alignment filtering steps.

In Marco Catoni's laboratory they are combining molecular biology, genomics and computational approaches to study genome plasticity and epigenetics in model and crop plants. This includes but it is not limited to the study of transgenerational epigenetic memory, priming, transposable elements regulation and mobilisation, dynamics of extrachromosomal DNA and viral elements, mobile nucleic acid molecules and horizontal gene transfer between plants and other organisms

Simone Immler, Professor of Genetics and Reproduction, University of East Anglia

Reproduction is a central process of life in all eukaryotes, and yet the molecular processes occurring from the germline to the early zygote are still poorly understood. Our research focuses on the epigenetic and genetic mechanisms linking germ cells and offspring fitness, with a focus on male reproduction and fertility and how I will present recent insights into the causes and consequences of genetic diversity among gametes in shaping the next generations. We study how environmental conditions affect epigenetic mechanisms, namely small RNAs, and how these in turn control the activity of transposable elements in the germ cells. If these epi9genetic) changes are heritable they offer substrate for selection, and we study how selection on gametes affects the transmission of specific alleles. I will also show how our research has led to the formation of a spinout medtech company in male fertility.

Simone Immler is Professor of Genetics and Reproduction at the University of East Anglia, UK. She earned her MSc from the University of Basel, Switzerland and her PhD from the University of Sheffield, UK. She spent time as a Research Fellow and Associate Professor at Uppsala University, Sweden, before returning to the UK. She was awarded both a Starting Grant and a Consolidator Grant from the European Research Council and a Wallenberg Academy Fellowship. She is the co-founder and scientific director of Virilitas Labs, a spinout company developing diagnostics and services around male fertility.

Dr Camila Cotrim, Head of Bioprocessing, Better Dairy

The transition of recombinant protein production from bench-scale academic discovery to commercial-scale manufacturing is rarely a linear path. In a fast-paced biotechnology startup, bridging this gap requires moving beyond isolated biological discoveries to master the intersection of whole-process engineering, economic viability, and operational agility.

This presentation pulls back the curtain on the real-world realities of scaling a precision fermentation platform. Drawing from recent bioprocessing campaigns, we explore the core technical challenges of transitioning a process through changing infrastructure constraints to de-risking downstream recovery via depth filtration and ultrafiltration/diafiltration (UF/DF) optimisation.

Beyond the laboratory bench, we will discuss the critical "mindset shift" required to translate academic research skills into industrial leadership. Attendees will gain insight into how cross-functional communication, robust data accountability, and a focus on process economics drive commercial timelines, offering a practical roadmap for early-career scientists looking to make a high-impact transition into the climate-tech and food-tech startup ecosystems.

Camila Cotrim is the Head of Bioprocessing at Better Dairy, bridging the gap between bench-scale biochemistry and commercial precision fermentation. With an international track record and 15+ peer-reviewed publications, she leads tech transfer and whole-process optimisation, aligning upstream and downstream workflows with manufacturing economics to drive major organisational milestones.

Dr Pierre Buscaill, Lecturer, University of Bristol

Plants live surrounded by microbes, yet only a fraction of encounters result in disease.

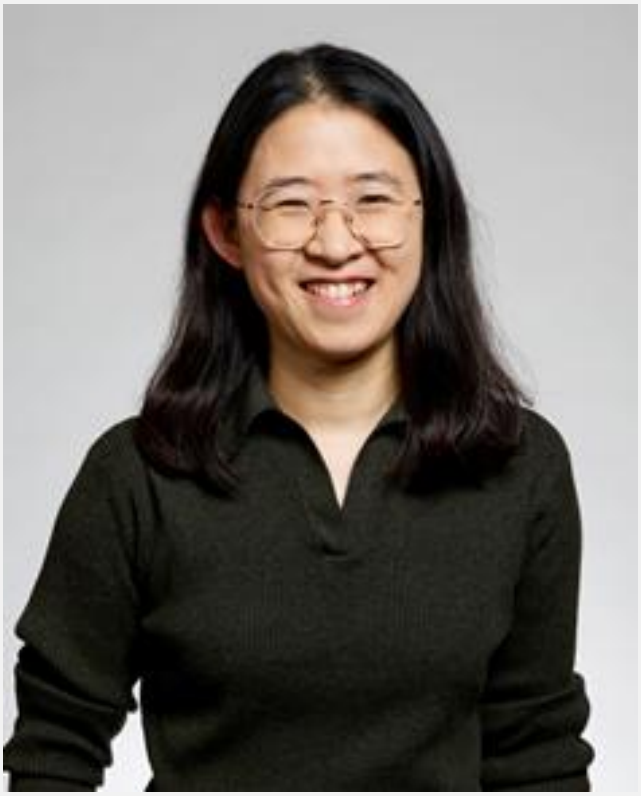
Understanding how plants regulate these interactions is a central question for plant biotechnology and agriculture.

In this talk, I will explore how plants control microbial access through key entry points, including stomatal pores and wound sites, and how they sense molecular signals associated with microbes and tissue damage. I will introduce work from my lab at Bristol on three connected themes: how bacterial pathogens exploit wounds to access plant tissue; how the signalling molecule cyclic GMP contributes to plant immunity; and how plants and microbes compete to process the molecular signals that trigger immune responses.

I will also reflect on how my research path has progressively shifted toward these earliest stages of plant-microbe interaction, from studying intracellular immune responses during my PhD, to exploring early pathogen perception during postdoctoral work, and now to investigating how pathogens physically access plant tissues.

Pierre Buscaill is a Lecturer in Plant Science at the University of Bristol. He completed a PhD at the National Institute for Research and Agronomy (INRA) Toulouse, followed by a postdoctoral position at the University of Oxford. His lab focuses on how plants control pathogen entry and regulate immune activation.

Dr Hee-Kyung Ahn, University of Edinburgh, Institute of Molecular Plant Sciences (IMPS)



All living organisms on Earth face unique challenges to respond to various stresses, both biotic and abiotic, while maintaining key cellular processes to stay alive. These responses often depend on protein-protein interactions in cells. While 1-to-1 protein-protein interactions have been studied extensively, we are beginning to understand the importance of higher-order protein-protein interactions, that enable assembly of protein complexes. Some protein complexes are essential for survival and needs to be assembled constantly. One example is the protein folding chaperonin CCT (Chaperonin Containing T-Complex Polypeptide) that folds cytoskeletal proteins. In others, induced assembly of protein complexes are required to respond in time against biotic or abiotic stresses. Examples are intracellular immune receptors that respond to pathogenic proteins in plants. We have now identified different variations of immune receptor complex formation. In this presentation, I will discuss what led me to study plants and protein complex assembly, with examples from my past and current research.

Hee-Kyung was born in Seoul, Korea and completed her BSc and PhD at Yonsei University. She then moved to Norwich to join The Sainsbury Laboratory as postdoctoral scientist. Her current group at IMPS is interested in how proteins assemble into protein complexes in response to environmental stimuli. Hee-Kyung is passionate about science communication, and has published a popular science book about plants in Korean.

Student Speakers

Ahmed Nada, UEA, 2nd Year

Garlic Oils as a Redox-Active Trigger for Budbreak?

In the winter months, perennial fruits (e.g. grapes, apples, cherries) require a prolonged period of winter chill to optimise their timely emergence from dormancy in the spring. The chill period stimulates the gradual accumulation of low levels of oxidative stress which is responsible for the redox mediated stimulation of budbreak. In recent years, climate change has proven to be detrimental for timely budbreak. As a result, hydrogen cyanamide (HC) is often used to artificially stimulate budbreak. A promising alternative to HC lies in garlic, as evidenced by preliminary field experimentation. It is believed that the plant regulatory activity exhibited by garlic is due to its rich content of diallyl polysulfides (DAS), which have been studied in different organisms in the past, and they have been found to cause oxidative stress within them. Could this be translatable within plants? To investigate, exploratory plant models have been employed and the development of analytical tools for use in field trials are underway.

Ahmed is a second-year PhD researcher at the University of East Anglia (UEA), working within the School of Chemistry, Pharmacy, and Pharmacology under the supervision of Dr. Christopher Hamilton. His research bridges agricultural and synthetic chemistry, building on a background in natural product and pharmaceutical chemistry.

Ahmed is currently exploring how garlic-derived oils influence budbreak, using a combination of laboratory experiments and fieldwork to better understand plant responses and support improved agricultural strategies.

Originally trained as a pharmacist at Alexandria University, Ahmed brings a multidisciplinary perspective to his research. Outside the lab, he plays an active role in the academic

community as Chair of both the University's Postgraduate Committee and the Faculty of Science Postgraduate Researcher Committee.

Kestrel Maio, John Innes Centre, 3rd Year

Pushing the boundary- How the adaxial-abaxial boundary coordinates leaf growth direction

The Arabidopsis thaliana leaf is characteristically flat and ovate. Two domains are required to inform this shape: the adaxial and abaxial domains, which face towards and away from the meristem, respectively. These domains are mutually antagonistic. At the point where they meet, a boundary forms, which directs the development of the leaf blade. My project explores whether ectopic boundary formation, through shifts in adaxial-abaxial identity, induces tissue outgrowth from the leaf surface. This raises two hypotheses: a) that inducing an ectopic adaxial/abaxial sector would result in the development of a boundary, and b) that the formation of this boundary would redirect cell growth outward from the plane of the leaf. The hat3athb4 double mutant is used as a model to explore these hypotheses. This mutant, which lacks two HD-ZIPII transcription factors regulating adaxial identity (HAT3 and ATHB4), develops tissue outgrowths from the adaxial surface. This project aims to determine whether these outgrowths result from mosaic loss of adaxial identity coupled with gain of abaxial identity, and how these identity changes interact with known boundary and margin genes, using a mixture of confocal microscopy, optical projection tomography and computational modelling in GFtbox (MATLAB).

Kestrel is a 3rd year student at the John Innes Centre researching Leaf Morphogenesis under the supervision of Dr Richard Smith. Kestrel is part of the research group: Using mathematical and computer simulation techniques to investigate questions in plant development. Kestrel

holds previous degrees with a MSc in Plant Genetics and Crop improvement, and a BSc in Biological Sciences.

Alyssa Polski-Delve, UEA, 3rd Year

Ageing alters changes to liver fatty acid metabolism in response to infection

During infection, haematopoietic stem and progenitor cells (HSPCs) have increased energy demands to facilitate expansion and differentiation. These demands are met by upregulation of fatty acid (FA) uptake, metabolism, and use in oxidative phosphorylation. Ageing is a well-known risk factor for serious infections, where chronic low-grade inflammation and immunosenescence impact HSPC and overall immune function. This study examines alterations in FA metabolism during infection in aged mice and the impact this has on immune function.

Aged mice (18-24 month) were administered lipopolysaccharide (LPS) for 2, 6 and 16 hours. Liquid-chromatography mass spectrometry performed on serum indicated that long-chain FAs do not increase in response to LPS. In young mice, serum long-chain FAs are known to increase during infection.

The liver is the principal site of lipid metabolism. In young mice LPS induces down-regulation of FA metabolism in the liver. Here we show, using bulk RNA-seq of aged LPS mouse liver tissue and KEGG pathway analysis, that FA metabolic processes are not downregulated during early infection, unlike young. We found PPARa, the master regulator of FA metabolism in the liver, to be significantly downregulated in aged livers both with and without LPS, indicating dysregulated FA homeostasis during ageing. Aged mice were treated for 7 days with fenofibrate (a PPARa agonist), then LPS for 16 hours. Analysis of HSPC and downstream progenitor expansion via flow cytometry indicated a stronger, more sustainable response to infection when fenofibrate was given.

Overall, we have found that the lipid response to infection is altered during ageing, which may affect the ability of HSPCs to expand. We have identified PPARa as a key factor dysregulated

in aged livers, and have shown that agonism with fenofibrate positively impacts the HSPC response to infection in aged mice.

Alyssa is student at the Norwich Medical School in Metabolic Health, supervised by Prof. Stuart Rushworth.

Joshua Horton, the Quadram Institute, 3rd Year

Battling Biofilms: Investigating the role of maoP in Enterobacteriaceae biofilm formation

Biofilm formation is a key process in the life cycle of many important bacteria, where organisms form multicellular aggregates, often stuck to a surface. Despite substantial research into the complex and tightly regulated pathways involved in biofilm formation, we do not have a full understanding of how biofilm formation is regulated. Modifying biofilm formation is an important goal in preventing infection and in biotechnology, but the knowledge base to enable this remains incomplete.

MaoP is a protein originally proposed to be involved in chromosomal organisation, although other work has also identified MaoP as an RNA-binding protein. We have recently shown it to be important in biofilm formation by the key foodborne pathogens *Escherichia coli* and *Salmonella* Typhimurium.

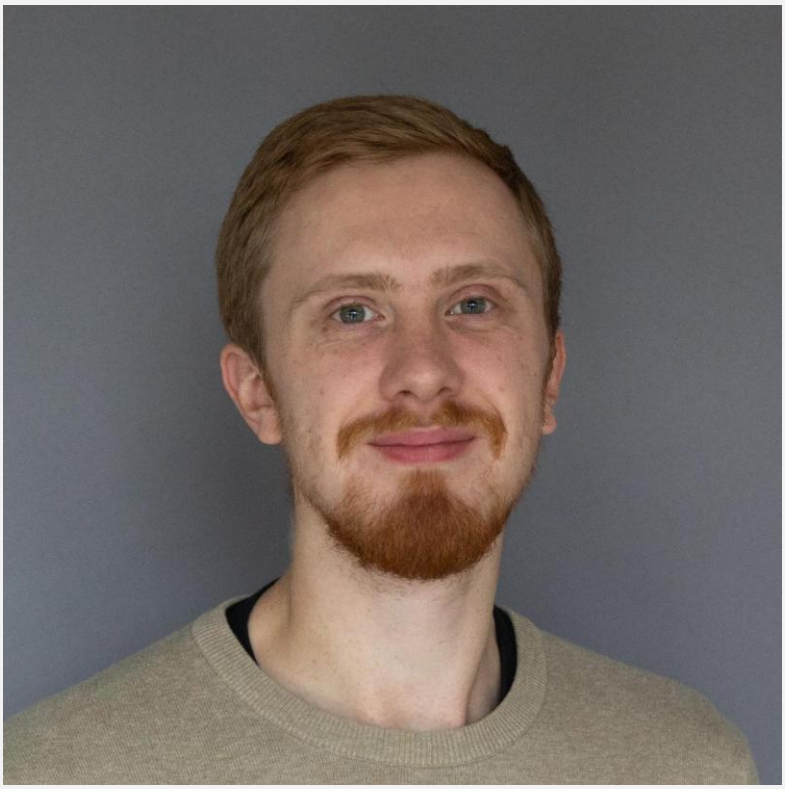
This project aims to characterise how *maoP* impacts biofilm formation in Enterobacteriaceae, using *Salmonella* Typhimurium as a model. We show that deletion of *maoP* reduces production of key biofilm components curli and cellulose, which is due to reduced transcription of the master biofilm regulator *csgD*. Using a biofilm evolution model, we isolated *maoP* deletion mutants that have recovered biofilm formation. We found that such isolates have mutations resulting in an increased expression of *csgD*. Others have mutations in pathways that are involved in adhesion. Future work aims to understand how *maoP* impacts on *csgD* expression.

Joshua is a 3rd year PhD student in Prof. Mark Webber's group at the Quadram Institute. The Webber group investigates how various species of bacteria respond to stress, using molecular genetics and genomics. Joshua’s research looks into the biofilm formation process, which many species use to protect themselves from a stressful external environment.

Łukasz Sitko, the Earlham Institute, 3rd Year

Functional Impact of Short Tandem DNA Repeat Instability

Short tandem repeats (STRs) exhibit mutation rates orders of magnitude higher than single nucleotide variants, and instability at these loci underlies nearly 50 human neurodegenerative and neuromuscular diseases. Repeat-length variation within coding and regulatory regions has been linked to phenotypic diversity across species, including circadian clock periodicity, skeletal morphogenesis, antimicrobial resistance, and transcriptional regulation. In particular, CAG/CTG expansions represent a major class of pathogenic mutation, yet how replication fork dynamics and DNA secondary structure jointly determine tract-length outcomes at the cellular level remains an open question.



This project investigates STR instability in engineered CAG repeat tracts in S. cerevisiae, with the aim of dissecting how replication slippage and non-B DNA secondary structures contribute to length heterogeneity. To this end, I developed two methodological advances: a PCR-free cloning strategy enabling iterative, controlled expansion and precise chromosomal integration of defined CAG repeat tracts, overcoming a fundamental challenge in repetitive DNA synthesis; and a computational pipeline exploiting ONT duplex reads with per-base quality filtering for single-molecule tract length distribution quantification — addressing a longstanding challenge in both clinical and forensic STR analysis.

To investigate the structural context of repeat instability, I employed FiberSeq — a single-molecule chromatin accessibility assay based on Hia5 m6A adenine methylation — and observed a pronounced absence of methylation signal across the CAG repeat region. This depletion is consistent with either stable nucleosome occupancy or DNA secondary

structures occluding Hia5 access, both of which could suppress replication-coupled expansion by restricting error-prone replication and repair machinery. These results identify local chromatin architecture and secondary structure as candidate determinants of repeat stability, with broader implications for understanding the molecular basis of CAG expansion diseases.

Lukasz Sitko is a NRPDTP PhD student in the Nieduszynski Group at the Earlham Institute. His work focuses on short tandem repeats (STRs) instability, combining molecular genetics with Oxford Nanopore sequencing approaches to investigate how repeat sequence, chromatin architecture, and replication dynamics jointly determine tract-length outcomes.

Prior to his PhD, Lukasz obtained a BSc in Medical Sciences from the University of South Wales and an MSc in Biological Sciences from the Ulsan National Institute of Science and Technology (UNIST), South Korea, during which he conducted research on DNA repair pathways at the Institute for Basic Science (IBS). He joined the Nieduszynski Group in October 2023.

Ndeye Bineta Dia, UEA, 3rd Year

Production of the building block molecule 3-hydroxypropionic acid from seaweed waste

Microorganisms, leveraging organic resources such as agricultural products and waste, present promising opportunities for sustainable production, provided that efficient processes are established and optimized. This study proposes a greener method for producing 3-hydroxypropionic acid (3-HP) using seaweeds.

3-HP is a building block molecule of significant interest serving in the manufacture of various materials. To reduce the environmental impact of its production, its synthesis from algal waste stands as an interesting alternative.

Seaweeds can be exploited to produce various commercially valuable constituents, but none of the current applications utilizes dimethylsulfuniopropionate (DMSP), which can be present up to millimolar amounts per gram of dry cell weight. Thus, producing 3-HP from DMSP-rich algal waste supports the transition to a circular economy, where resources are utilized more efficiently, waste is minimized, and added value is maximized. We firstly identified Ulva fenestrata (previously lactuca) as the highest DMSP producer, then determined the most cost-effective method to extract it, and finally developed a cellular tool that enables the conversion of DMSP into 3-HP while eliminating its undesirable co-product dimethyl sulfate (DMS) from the cultivation media.

Our findings indicate that the 3-HP producing enzyme, expressed in E. coli using the pET16 vector, yielded 24 % 3-HP relative to the initial DMSP concentration. In contrast, Labrys with

the pLMB509 vector achieved a higher yield of 80 %, directly excreting 3-HP into the medium. These results show that, once optimized, this approach could significantly enhance the sustainability of 3-HP production processes.

Ndeye Bineta is a CASE NRPDTP PhD student in Jonathan Todd's research group based at QIB and working in partnership with Central Pharma Biotechnica.

Ndeye Bineta's research focuses on developing sustainable biotechnological solutions from marine biomass and microbial systems.

Ndeye Bineta's main project investigates the microbial production of the platform chemical 3-hydroxypropionic acid from seaweed-derived waste, using molecular microbiology, fermentation, GC and NMR.

In collaboration with Central Pharma Biotechnica, Ndeye Bineta investigates the prebiotic effects of Ascophyllum nodosum fibres. This work includes fibre fractionation and in-vitro epithelial models, where they use TEER measurements to assess gut barrier integrity, ELISA assays to quantify immune and metabolic markers, and flow cytometry to characterise cell viability and activation at the single-cell level.

Alongside these projects, Ndeye Bineta explores sulfur cycling in wastewater treatment plants and specialise in Stable Isotope Probing (SIP), particularly using sulfur-based compounds.

Ndeye Bineta holds engineering degrees in Food Science and Process Engineering (Ecole Supérieure Polytechnique, Dakar) and in Biotechnology and Bioprocess Engineering (AgroParisTech, Paris).

Student Posters

Student	Org	Sch	Title
Aleksandra Teriosina	QIB	BIO	Glycogen metabolism in the human gut symbiont Ruminococcus gnavus
Alice Bradford	UEA	PHA	A pathway-centric framework for understanding VSMC diversity in ageing and disease
Alyssa Polski-Delve	UEA	MED	Ageing alters changes to hepatic fatty acid metabolism in response to infection
Angus Bucknell	TSL	BIO	AI-driven protein design to understand effector function within the Magnaporthe oryzae rice pathosystem
Charlotte Lousia Delf Utting	EI	BIO	Functional Analysis of RNA Binding Proteins in Haematopoiesis with long-read single-cell Perturb-seq
Deus Dedit Kamya	QIB	BIO	Understanding the molecular mechanisms of phage resistance and phage-driven capsule variation in Klebsiella.
Elin Smith	QIB	MED	Acid-Mediated Suppression of Listeria monocytogenes by Bifidobacterium spp. in Co-Culture
Ella Penny	JIC	MTH	Modelling Wheat Development Using a Dynamical Systems Approach

Emma Chareyre	JIC	BIO	Understanding how Streptomyces venezuelae coordinates DNA damage and cell division
Euan Cawston	TSL	BIO	Who regulates the regulator? Coordination of signalling by pathogenicity mitogen activated protein kinase 1 during developmental transitions in Magnaporthe oryzae.
Fabio Dos Santos Barbosa	TSL	BIO	Determining the Sln1-mediated turgor-sensor complex and phosphohistidine landscape in the blast fungus Magnaporthe oryzae
Harry Gordon	UEA	BIO	Whole-genome sequencing from mammalian snow prints
Harry Steward	UEA	BIO	Polar Growth and Asymmetric Cell Division In Labrenzia Aggregata
Heloise Vinette	QIB	BIO	The role of neuropilins in regulating blood-brain-barrier function and integrity
Isabella Frost	JIC	BIO	Pseudomonas biocontrol of kiwifruit canker: elucidating novel mechanisms of bioactivity
Jade Van Wijk	EI	BIO	AirSeq as a tool for cereal rust surveillance
Jessica Moon	JIC	BIO	Coordination of chloroplast transcription initiation and elongation by the PEP subunit PAP11

Joshua Horton	QIB	MED	Battling Biofilms: Investigating the role of maoP in Enterobacteriaceae biofilm formation
Katie Millar	UEA	BIO	Host-microbe symbioses in an agricultural pest, the Mediterranean fruit fly
Kestrel Maio	JIC	BIO	Pushing the boundary- How the adaxial-abaxial boundary coordinates leaf growth direction
Lukasz Sitko	EI	BIO	Functional Impact of Short Tandem DNA Repeat Instability
Lydia Pouncey	UEA	BIO	Deciphering novel gene regulatory networks governing avian embryonic hematopoiesis through single-cell multi-omics
Maisie Evans	UEA	BIO	Investigating the IRE1 Pathway as a Novel Regulator of Ageing
Marianthi Firoglani Moschi	QIB	BIO	Catechol sulfate in humans: Is catechol-3-O-sulfate formed by hepatic or intestinal cells?
Mehmethan Aris	UEA	MED	FIDA-Based Quantification of Small Molecule Binding to Membrane Proteins in Solution
Miaomiao Gao	UEA	CHE	ISC [2Fe–2S] cluster biogenesis machinery in E. coli: cluster assembly on IscU and its IscR-mediated regulation
Ndeye Bineta Dia	QIB	BIO	Production of the building-block molecule 3-hydroxypropionate from seaweed waste

Nicholas Martin	QIB	BIO	A systematic review of ETEC to inform the rational design of bacteriophage cocktails
Rachel Chiu	UEA	CHE	Measuring electron transfer across MtrC using electrochemical scanning tunnelling microscopy
Samuel Bruty	JIC	BIO	Mendelian Mishaps: How breeding has impacted pea microbiomes and disease
Samuel Matthew Shackleton-Chavez	UEA	BIO	A Novel Polymerase III Promoter for Gene Editing in the Mediterranean Fruit Fly
Sanjayani Ramanan	JIC	BIO	Pseudomonas biocontrol of berry rot: elucidating mechanism of bioactivity