CAMBIO: NRPDTP Inaugural CASE Conference, John Innes Centre, 29th June 2026

norwich research park
Doctoral Training Partnership

UNIVERSITY OF CAMBRIDGE · Babraham Institute · NIAB · wellcome sanger institute · UKRI Biotechnology and Biological Sciences Research Council

PROGRAMME		
10.00-10.30	*Arrival at John Innes Centre Conference Centre, registration and refreshments*	
10.30-10.35	**WELCOME: Prof Anne Graham, NRPDTP; Prof Ross Waller, Cambridge Bioscience**	
10.30-11.30	**Case Studies: Joint Student Host Partner/ Supervisor Presentations including Q&A panel**	
10.30-10.50	Case Study 1 NRPDTP: Engineering the yeast cytochrome bc1	Finlay McGhie (Y1), Urvashi Thacker (Syngenta) & David Swainsbury (JIC)
10.50-11.10	Case study 2 NRPDTP: Applying next generation genetic approaches for trait discovery in the commercial vegetable industry.	Charles Dickinson (Y4), Rodrigo Echegoyen-Nava (Elsoms Seeds) & Ant Hall (EI- TBC)
11.10-11.40	**Workshop Discussion: Successful Engagement with and Transition to Industry**	Dr Fiona Leigh (academic sup & CTP-SAI program manager at NIAB) Dr Ursula Gompels (Virothera Ltd) Dr Rasa Elmentaite (Ensocell Therapeutics)
11.40-12.30	**SMALLER GROUP WORKSHOPS**	
Valuable Unexpected Skills and Learnings Dr Stephen Rawsthorne; TMAF *Student Facilitators: Maegan Green & John McGinty (cohort 2024, Cambridge Biosciences)*	**Communication and Industry Stakeholder Engagement** Dr Liliya Serazetdinova EI & Cansu Bayindirli AIP *Student Facilitators (NRPDTP): Charles Dickinson (cohort 2022, EI), Bernice Waweru (cohort 2022, JIC), Issy Frost (Cohort 2023, JIC)*	
12.30-13.45	**NETWORKING LUNCH AND POSTERS**	
13.45-14.45	**Keynote Presentation: Translating Biology into Medicines: An Industry View from a CRO**	**Dr Steven Harborne, Sygnature Discovery**
14.45-15.05	**BREAK & REFRESHMENTS**	
	STUDENT TALKS	
15.05-15.20 **15.20-15.35** **15.35-15.50** **15.50-16.05** **16.05-16.20**	Kara Boyd (NRPDTP) Mehmethan Aris (NRPDTP) Milena Malcharek (Cambridge Biosciences) Krissy Wang (Cambridge Biosciences) Christianah Oseni (BBSRC CTP – Harper Adams University)	
16.20-16.30	**Closing Statements** **END**	

Keynote Speaker Biography

Dr Steven Harborne, Sygnature Discovery

Dr Steven Harborne is a Senior Principal Scientist with over a decade of experience in membrane protein science, spanning academia and industrial drug discovery.

He earned his undergraduate and Master's degrees in Biochemistry from the University of Sheffield, followed by a PhD at the University of Cambridge, where his research focused on the functional and structural biology of human mitochondrial membrane proteins. He subsequently joined the Astbury Centre for Structural and Molecular Biology at the University of Leeds as a post-doctoral research associate, continuing his work on membrane protein structural biology and contributing to the development of computational tools to enable and accelerate research in this technically challenging area.

In 2019, Dr Harborne joined Sygnature Discovery Protein and Structure (formerly Peak Proteins), where he has played a central role in building and scaling industrial capabilities for the production of membrane proteins as drug discovery targets. Over the past seven years, he has led the development of approaches and teams addressing some of the most demanding challenges in the field.

Dr Harborne now leads a growing team of membrane protein specialists, supporting multidisciplinary discovery programmes. His work sits at the interface of structural biology, protein engineering, and translational science, with a particular focus on turning difficult and previously intractable targets into tractable opportunities within drug discovery pipelines.

ABSTRACT

Dr Steven Harborne: Translating Biology into Medicines: An Industry View from a CRO

Careers in scientific research increasingly extend beyond academia, yet the structure and realities of industrial drug discovery are often poorly understood by students and early-career researchers. In this keynote, Dr Steven Harborne will offer an industry perspective on modern drug discovery, drawing on his experience at a contract research organisation (CRO) supporting early-stage pharmaceutical research.

The talk will begin with a brief overview of Dr Harborne's own career path from academic research in membrane protein structural biology to a leadership role in industry, setting the context for how scientists can transition into roles outside academia. He will introduce the role of CROs within the drug discovery ecosystem, using Sygnature Discovery as an example to illustrate how multidisciplinary teams collaborate with pharmaceutical and biotechnology partners to advance challenging biological targets.

The presentation will highlight membrane proteins (particularly G protein-coupled receptors; GPCRs) as a critical and historically difficult class of drug targets, and discuss how advances in protein production, structural biology, and cryo-electron microscopy are reshaping what is now possible. Broader trends in early-stage drug discovery will also be explored, including the evolving roles of small molecules, biologics, antibody–drug conjugates, and targeted protein degraders.

The talk will conclude with an industrial case study drawn from an internal GPCR programme, illustrating how scalable protein production and structure elucidation can support drug discovery at pace while maintaining scientific quality. Through this example, the keynote will provide insight into how modern discovery teams balance speed, robustness, and innovation, and what this means for scientists considering a career in industry.

STUDENT POSTERS		
Name	**Organisation**	**Title**
Advait Aithal	University of East Anglia	From Photoactivation to Photodegradation: LASSO, a Long-Wavelength Platform for Light-Activated Selective Switch-Off of Proteins
Ahmed Nada	University of East Anglia	Garlic Oils as a Redox-Active Trigger for Budbreak?
Alessandra Learmount	University of Cambridge	Feeding a Changing World: Root Architecture and Rhizosphere Microbiome Insights in the Underutilised Cereal Crop Eragrostis tef.
Alice McCallister	John Innes Centre	Enhancing genetic resistance to downy mildew in pea
Amelie Davies	University of Cambridge	Understanding the spatial determinants of targeted protein degradation
Ash Norcott	Quadram Institute	Characterisation and In Vitro Human Colon Fermentation of Fucoidan Extracted from Ascophyllum nodosum.
Brandon Thompson	Cranfield University	Creating bruise resistant cv Maris Piper potatoes.
Christianah Oseni	Harper Adams University	Optimising Transient Carbohydrate Partitioning in Wheat to Improve Climate Resilience
Euan Cawston	The Sainsbury Laboratory	Who regulates the regulator? Coordination of signalling by pathogenicity mitogen activated protein kinase 1 during developmental transitions in Magnaporthe oryzae.

Issy Frost	John Innes Centre	Biocontrol activity of Pseudomonas spp. against Pseudomonas syringae pv. actinidiae is linked to novel natural product clusters.
Joe Payne	University of Cambridge	Spore mimetics: Bioengineering Gram-negative bacteria for enhanced desiccation tolerance
Kara Boyd	John Innes Centre	Kara Boyd: Downy but not out – identifying resistance to downy mildew in pea
Luke Dee	University of Cambridge	Genomic and Immunological Analyses of a Novel Immunotherapeutic for HSV-2
Maegan Green	University of Cambridge	Capturing Genetic Diversity Without Compromising Adaptation In Wheat Breeding
Matthew Marshall	University of Cambridge	Sex and Trait Anxiety interactions predict loss of control over cocaine intake and relapse after abstinence
Mehmethan Arış	University of East Anglia	FIDA-Based Quantification of Small Molecule Binding to Membrane Proteins in Solution
Miles Curl	John Innes Centre	Exploring the role of NAM-2 in delaying drought-induced senescence in wheat
Nathaniel Wright	University of Cambridge	Grasping affordances in Large Language Models (LLMs)
Sanjayani Ramanan	John Innes Centre	Pseudomonas Biocontrol of Strawberry rots: elucidating mechanisms of bioactivity
Yicong (Krissy) Wang	University of Cambridge	Selective Antibody Engineering for Point-of-Care Neutrophil Quantification

STUDENT SPEAKERS

ABSTRACTS

Kara Boyd (NRPDTP)

Two peas in a pod? Identification of allelic resistances to downy mildew in pea.

Pea (*Pisum sativum*) is an increasingly economically important crop due to the rising demand for plant-based protein, and its ability to biologically fix nitrogen reduces the need for synthetic nitrogen fertilisers and promotes sustainable agriculture. However, at present, peas are an unattractive option to growers because their susceptibility to abiotic and biotic stresses causes yield instability. One of the most prevalent diseases in the UK and Europe is downy mildew, caused by the oomycete pathogen *Peronospora viciae* f. sp. *pisi* (*Pvp*). Currently, no resistance has been characterised to *Pvp*. Here, we have identified two resistances to *Pvp* in two wild accessions: one discovered through a *k*-mer-based GWAS and found in JI0015, and another rare resistance identified through bulked segregant analysis found in JI0085. The QTL sizes were reduced through a haplotyping approach and fine mapping, and candidate genes were identified by analysing the correlation between gene presence and resistance. We have shown through virus-induced gene silencing that the JI0015 resistance is caused by one of two NLRs with 97% nucleotide identity. Both the JI0015 and the JI0085 resistances are located on chromosome 2. Phylogenetic and syntenic analysis suggests that they are derived from a single ancestral NLR cluster and that they are likely alleles. Additionally, each resistance has a distinct isolate recognition pattern, demonstrating that they are able to detect different *Pvp* effectors and therefore stacking both resistances into one cultivar may provide a more durable resistance. Marker genotyping showed that neither resistance is present in tested elite cultivars or European breeding material, showing they are novel and have not yet been deployed in breeding programs and will therefore be useful to breeders. To conclude, we have discovered two allelic resistances to downy mildew in pea which are able to recognise different isolates of *Pvp*. We have reduced the number of candidate genes to two or three for each resistance and have shown that neither have yet been deployed in European breeding programs.

Mehmethan Arış (NRPDTP)

Expression and Purification of Intact UCP2 in Higher Eukaryotic Systems.

Uncoupling protein 2 (UCP2) is a mitochondrial carrier found in a variety of mammalian tissues and has pathophysiological roles in diabetes and cancer. The protein is a homologue of UCP1, which catalyses proton leak in the mitochondria of brown adipose tissue to generate heat for thermoregulation. Though unlike UCP1, a role for UCP2 in proton leak is not clear, and some evidence suggests that it may exchange 4-carbon metabolites in a conventional solute transport function. UCP2 is poorly understood, which relates to the technical challenges associated with its study. The protein has low abundance in tissues, is unstable when isolated, and is susceptible to generating incorrectly folded material in common recombinant protein production systems (e.g., *E. coli*). Hence, new production methods are needed to help clarify its function, role in pathologies and potential to be targeted.

Through our CASE partner, Sygnature Discovery, we have utilised modern higher eukaryotic protein expression systems to generate intact UCP2 for subsequent purification and functional assessment. Our studies have focused on both insect and mammalian cell systems, with initial construct and expression screening conducted to assess the suitability of various affinity purification tags and conditions. We found that all cell types were able to express recombinant UCP2, however, only insect cells produced UCP2 in a form that was almost fully extractable in mild detergent, indicative of an appropriately folded protein. In further tests, we found that the specific insect cell line used was important for achieving optimal expression levels, whereas other parameters were less critical (e.g. multiplicity of infection or glutamine addition). We also observed that UCP2 exhibited reduced solubility in mild detergents and under temperature challenge conditions, confirming its limited stability. Our purification trials showed that UCP2 could be enriched using an appropriate affinity resin, which we are continuing to optimise to enable subsequent functional characterisation of the protein.

Milena Malcharek (Cambridge Biosciences)

Characterisation of Peptide Agonists' Binding at Amylin and Calcitonin Receptors

Amylin (AMY) is a pancreas–derived peptide hormone that acts on centrally located receptors to induce satiation, making amylin receptors (AMYRs) promising targets for novel anti–obesity medications. AMYRs are heterodimers formed by the class B1 G protein–coupled receptor (GPCR) calcitonin receptor (CTR) and one of the three receptor activity–modifying proteins (RAMP1–3). Currently, our knowledge of how the different RAMP isoforms influence ligand affinity and kinetics of ligand/receptor interactions remains scarce. Furthermore, most published studies have only tested a handful of peptides in binding assays, with AMY2R frequently omitted. Measuring the binding of a wide range of agonists at both CTR and all three AMYRs will enable the elucidation of structure–activity relationships, thus helping with drug discovery and development.

Since CTR is capable of trafficking to the cell surface on its own and can bind to most AMYR agonists, the NanoBiT split luciferase system was used to reconstitute bona fide AMYRs: co–transfection with LgBiT–CTR and SmBiT–RAMP1/2/3 ensured that only CTR/RAMP heterodimers possessed a functional luminescent tag. First, the binding parameters of Cy5–labelled salmon calcitonin (Cy5–sCT) were established in a BRET–based saturation assay; subsequently, the displacement of Cy5–sCT by increasing concentrations of non–fluorescent ligands was used to calculate their affinities and on–/off–rates. Additionally, the binding profiles of pramlintide Ala scan peptides revealed residues likely to form key interactions with the receptor complex. Further research will focus on modelling the ligand/receptor interactions in silico, as well as examine downstream signalling pathways.

Krissy Wang (Cambridge Biosciences)

Selective Antibody Engineering for Point-of-Care Neutrophil Quantification

Chemotherapy-induced neutropenia increases susceptibility to life-threatening neutropenic sepsis, yet rapid near-patient neutrophil assessment remains unavailable outside laboratories. A lateral flow assay (LFA) format could transform patient triage, but requires binders with robust isoform selectivity against highly homologous surface markers that co-exist across multiple cell types in whole blood.

We present a structure-guided computational–experimental pipeline for selectivity-first antibody engineering. A surface comparison framework identifies target-preferential epitopes by integrating residue-level physicochemical and structural divergence between near-identical receptor isoforms. These epitopes condition CDR loop design via an in-house generative ML model, with multi-stage in silico triage enforcing selectivity before experimental screening. Candidates are validated for binding and isoform discrimination using a rapid cell-free kinetic platform, then assessed for diagnostic deployability in partnership with the industrial collaborator, 52North.

This integrated approach provides a generalizable framework for selectivity-first binder engineering — directly addressing a central bottleneck in point-of-care diagnostic development where target and off-target share near-identical molecular surfaces.

Christianah Oseni (BBSRC CTP – Harper Adams University)

Optimising Transient Carbohydrate Partitioning in Wheat to Improve Climate Resilience

Climate change is increasing the frequency and severity of drought, heat, and cold stress events, posing a major threat to global wheat production. Transient carbohydrate storage in leaves plays a critical role in maintaining energy balance and supporting metabolism when photosynthesis is limited. While wheat primarily accumulates sucrose, natural variation exists in the partitioning of carbon between sucrose, fructose, and starch. In addition, fructose accumulation has been associated with abiotic stress responses through roles in osmotic adjustment, energy buffering, and post-stress recovery.

Preliminary evidence shows considerable natural variation in transient leaf fructose content among Watkin landrace accessions, but the reproducibility and functional roles of this phenotype remain unclear. To validate this phenotype, two pairs of contrasting high- and low-transient fructose Watkins accessions were selected, alongside the spring wheat cultivar Paragon as a reference. Plants were grown under both controlled glasshouse conditions and in a polytunnel environment (representing winter field-like conditions). Leaf tissue was harvested at the end of the photoperiod and analysed for fructose, sucrose, and starch content using enzymatic assays. Carbohydrate profiling demonstrated that fructose accumulation is strongly influenced by both genotype and environment. While one pair showed limited and inconsistent differences across environments, a second pair displayed a clear and reproducible carbohydrate partitioning phenotype under glasshouse conditions. This phenotype was characterised by increased fructose accumulation accompanied by reduced starch allocation, while sucrose levels remained unchanged, indicating a shift in carbon partitioning rather than a change in total carbohydrate production.

These findings identify a robust pair of contrasting wheat accessions and an experimental environment suitable for investigating the genetic control of transient carbohydrate partitioning. Ongoing work will use mapping populations derived from these accessions to identify loci associated with fructose accumulation and determine how altered carbohydrate partitioning contributes to improved abiotic stress resilience in wheat.