PERTH PROTEIN GROUP

AGM program

27-28 November

Harry Perkins Institute of Medical Research Perth WA

perthproteins.org

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PPG Annual General Meeting program

Thursday 27 November 2025

1:30 pm Registration opens

2.00 pm Annual General Meeting

Election of new officials, general business

Tea and coffee

2:30 pm Welcome Address: Joel Haywood (PPG Chair)

2:40 pm Local Capabilities Session

Chair: TBA

2.45 pm **#01 Heng Chooi**

Title: *Precision Fermentation as a Platform for Sustainable Bio-manufacturing*

3.00 pm **#02 Crystal Cooper**

Title: *Bringing Affordable Cryo-Electron Microscopy to WA*

3.15 pm **#03 James Lui**

Title: *Taking proteins into the clinic & beyond using proteomics*

3.30 pm **#04 Olga Shimoni**

Title: *RNA Innovation Foundry: Enabling mRNA Solutions for Tomorrow's Therapeutics*

3.45 pm **#05 Rob Steuart**

Title: Curtin MRI Shared Resource Laboratories and Technology Hubs: Analysis and characterisation from molecules to organisms

4:00 pm Afternoon Tea

PROTEOWA Biotechnology

Poster session

Light refreshments and drinks will be provided

4:20 pm Plenary Speaker

#06 Kate Michie (UNSW Sydney)

Title*: Deep learning is nothing to be salty about*

Chair: TBA

5:15 pm Sundowner

Poster session

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Friday 28 November 2025

9:00 am Morning Tea

9:30 am The Erik Helmerhorst Session (#A)

Chair: TBA

09:35 am **#07 Dayna Holroyd (Adelaide Protein Group)**
Title: *AI-driven structure-guided design of cyclical PCNA-targeting peptides*

10:05 am **#08 Danielle Rudler (UWA)**
Title: *A Genome-Wide CRISPR knockout Screen Reveals Novel Regulators of Mitochondrial Translation*

10:35 am **#09 Blake Payne (UWA)**
Title: *Engineering Fungal Nonribosomal Peptide Synthetases for Novel Bioactive Compounds*

11:05 am Morning Tea

Light refreshments, tea and coffee

11:25 am The Fiona Stanley Session (#B)

Chair: TBA

11.30 am **#10 Fraser Windsor (UWA)**
Title: *The Structure and Function of a Promiscuous Acyltransferase from a Polyketide Assembly Line*

11.50 am **#11 Sanathanee Sachchithananthan (UWA)**
Title: *Designing Synthetic PPR-RNA Tools To Monitor and Regulate Biological Events Using Conformational Changes*

12.10 pm **#12 Hera Nguyen (UWA)**
Title: *Genome mining of the wheat pathogen Parastagonospora nodorum establishes the biosynthesis of methylene-bridged depsides*

12:30 pm Lunch

Light refreshments, tea and coffee

Friday 28 November 2025

1:30 pm The Paul Attwood Session (#C)

Chair: TBA

1.35 pm **#13 Agyeya Pratap (UWA)**

Title: *Protein biomarker discovery, validation and screening method for climate resilience in crops*

1.55 pm **#14 Richard Lipscombe (UWA)**

Title: *Validation of Biomarkers for Esophageal Cancer*

2.15 pm **#15 Désirée Sexauer (ECU)**

Title: *Profiling Autoantibodies in Melanoma Patients with Brain Metastases: A Proteome Array-Based Approach for Biomarker Identification*

2:35pm Afternoon Tea

Light refreshments, tea and coffee

2:50 pm **#Lightning talks**

Chair: Callum Verdonk

3:30 pm The Josh Mylne Session (#D)

Light refreshments and drinks will be provided

4:00 pm **#16 Jie Tang (Monash University)**

Chair: TBA

Title: *Enhancing the delivery efficiency of Biomolecules: From Nanocarriers to Biomodulators*

5:00 pm Closing address and sundowner

Prizes presentation

Sponsors & Support

ASBMB: The Australian Society for Biochemistry and Molecular Biology (ASBMB) unites biochemists and molecular biologists from around Australia. The Society is devoted to promoting research, new developments and education in biochemistry and molecular biology.

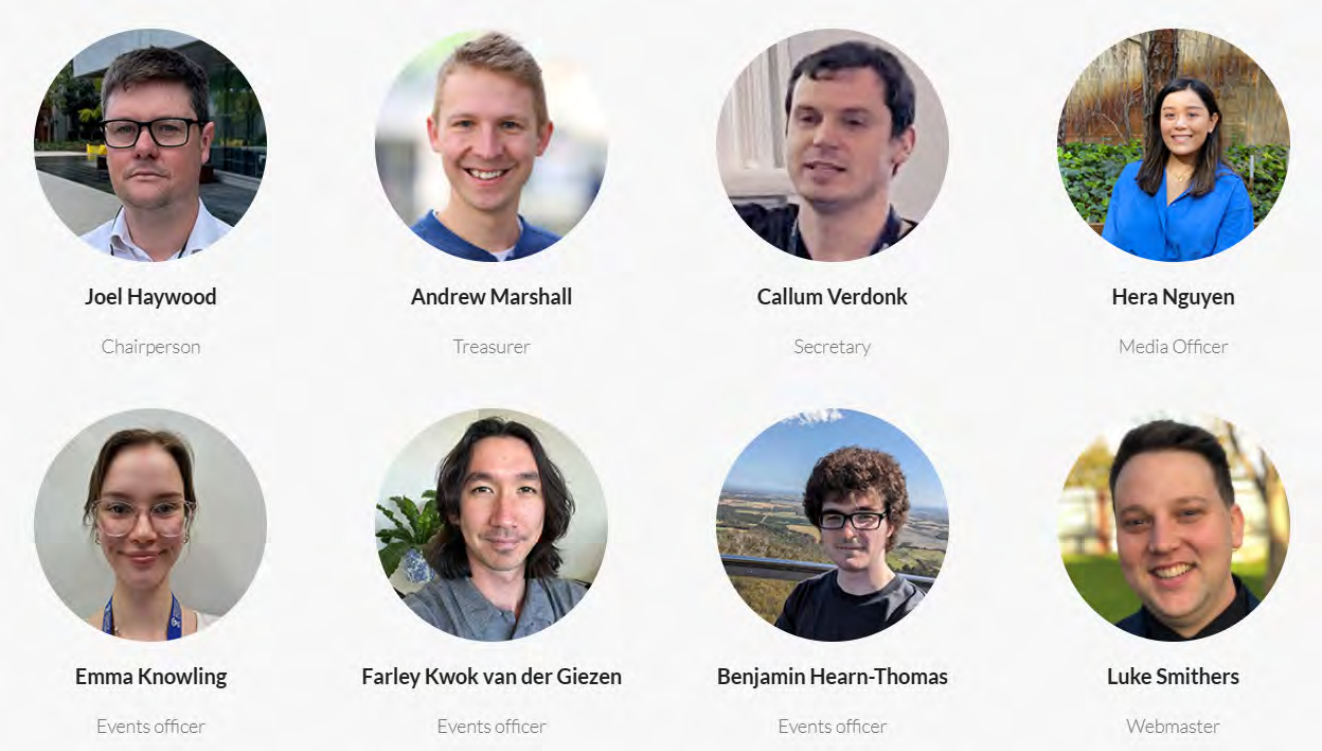
The organising committee

The following people have generously donated their time and talent to make the 2025 Perth Protein Group AGM possible:

Andrew Marshall
Farley Kwok van der Giezen
Joel Haywood
Callum Verdonk
Preet Bal

We would like to thank all of our session chairs and talk and poster judges for their time and assistance.

The Perth Protein Group executive



General information

Registration desk and Venue

Registration is located in Harry Perkins Institute of Medical Research, McCusker Auditorium and will open from 1:30pm on Thursday. Please direct any queries to the organising committee.

Lightning presentations

During the lightning presentation session, you will have 5 minutes to give them a summary of your research. The judges will then have the opportunity to ask you questions. Be aware that this 5 minute limit will be strictly enforced, so it pays to have timed your summary beforehand.

Oral presentations

All sessions will be held in the Harry Perkins Institute of Medical Research, McCusker Auditorium. Unless prior arrangements have been made, speakers should bring their presentation on a USB to the registration desk or to a committee member in the function room at least 20 minutes before their session starts. Speakers should include 5 minutes for questions regardless of allocated time. The session chairs have been asked to enforce these timings.

General information

#A) The Erik Helmerhorst Proteins Session

Erik Helmerhorst worked on insulin during Honours and PhD at UWA then moved to the University of Toronto to pioneer use of photoaffinity labelling techniques to link insulin to the insulin receptor. Erik returned to UWA as a Teaching Fellow then took an appointment as a Burselum and Healy Medical Research Foundation Fellow to work more on the insulin-receptor interaction. Moving to Curtin in 1988 he started a company to developed orally available insulin mimetics that led to collaboration with UCSD and Eli Lilly. In other work, Erik and Professor Ralph Martins found amyloidogenic Aβ peptide competes with insulin for binding to the insulin receptor, providing a basis for insulin resistance in patients with Alzheimer's disease. Erik was Head of the School of Biomedical Sciences at Curtin for 5 years and the Director of the WABRI, which soon after became the Curtin Health Innovation Research Institute.

#B) The Fiona Stanley Chem 'n' Bio Session

Professor Fiona Stanley was born in Sydney in 1946 and moved to Perth in 1956. She studied medicine at UWA and practised in hospitals for two years before going to the UK and USA for further training in epidemiology biostatistics and public health before returning to WA. She is a vocal advocate for the needs of children and their families and was named Australian of the Year in 2003. In 2004, Professor Stanley was honoured as a "National Living Treasure" by the National Trust. She is also the UNICEF Australia Ambassador for Early Childhood Development. Professor Stanley has published >300 scientific papers and served on many prestigious boards. She was founding Director of the Telethon Kids Institute, established in Perth in 1990. When she retired from the position in December 2011, the TKI had >500 staff and students and an international reputation for its translational research. In 2014 the Fiona Stanley Hospital – a major tertiary hospital in Perth – was named in her honour.

#C) The Paul Attwood Biochemistry Session

Paul Attwood completed his Bachelor of Science and PhD at the University of Bristol in the UK. From 1980 until 1984 he was a Senior Teaching Fellow in Biochemistry at the University of Adelaide. He then worked as a Research Associate in the Department of Biochemistry at the University of Wisconsin until 1986 when he moved to the Merrell Research Institute in Strasbourg, France, as a Senior Research Scientist. In 1988 Paul moved to UWA where he worked up to the rank of Associate Professor and retired in 2020.

#D) The Josh Mylne Session

Professor Josh Mylne completed his PhD at UQ in Botany. Between 2001-2005 Josh carried out post-doctoral studies at the John Innes Centre with Prof. Caroline Dean. Josh then returned to Australia working with Prof. David Craik before obtaining a QEII fellowship (2008-2012) followed by a Future Fellowship (2012-2016) which he undertook at UWA. In 2019 Josh Mylne founded the PPG in 2019 and has played a significant role in its success since then, including acting as Chair (2019-2023). Josh was also responsible for its founding principles in encouraging PhD students and ECRs to present their work in an informal atmosphere. This session aims to continue that legacy.

Plenary speakers

Dr Kate Michie is Chief Scientist of the Structural Biology Facility (MWAC) and a Senior lecturer in BABS.

Kate completed her doctoral degree at the University of Sydney under the supervision of Dr Liz Harry and Professor Gerry Wake, working in the field of bacterial cell division. In 2005 she received a L'Oréal-UNESCO Fellowship researching the structure and function of Structural Maintenance of Chromosome (SMC) complexes and how they exert molecular control over the topological and spatial organization of chromosomes.

In 2015 Kate joined UNSW as a Senior Research Associate working with Professor Paul Curmi working on light harvesting proteins and the Ezrin family of proteins. In 2019 Kate established the Structural Biology Facility (SBF) with MWAC at UNSW

Dr Jie Tang is an NHMRC Emerging Leadership Fellow at Monash University

Since completing her PhD at UQ in 2018, Dr Tang has secured research grants as CI totalling over AU$4 million and etabilished licensing aggreements with industry partners like AstraZeneca. Her research endeavors encompass both fundamental and applied research at the nano-bio interface through nanomaterial innovation. Specifically, Dr Tang's group is dedicated to develop nanoparticle-based platforms tailored for drug and gene delivery, cancer immunotherapy and vaccine adjuvants, leveraging the nanoparticles' unique nanostructure and surface chemistry.

2025 AGM
Selected abstracts

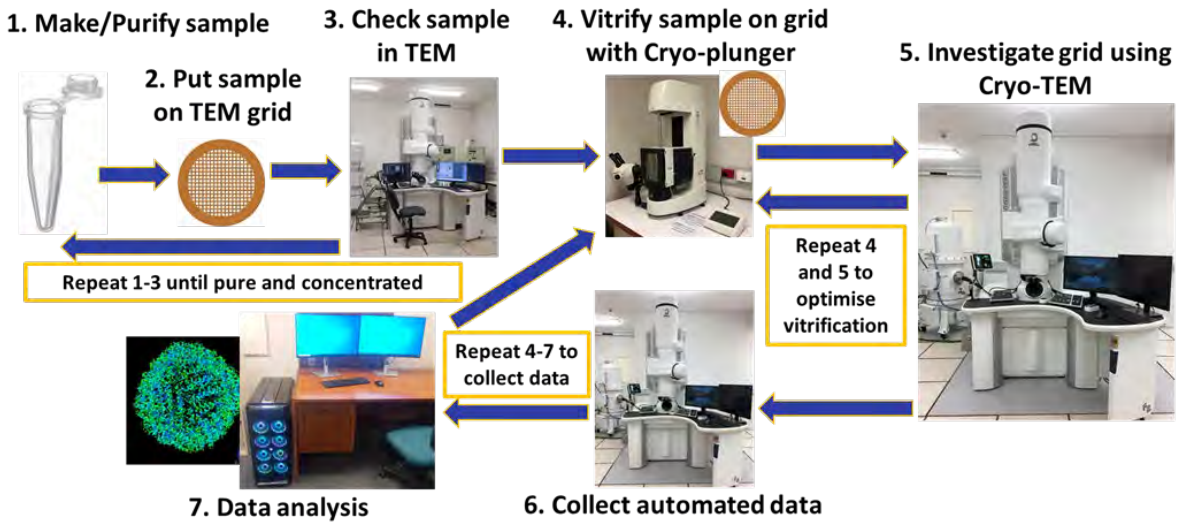
PPG AGM 2025 - #02 (Local Capabilities)

Bringing Affordable Cryo-Electron Microscopy to WA

Crystal Cooper[1]

[1] *Centre for Microscopy, Characterisation and Analysis, University of Western Australia, Australia.*

Cryo-Electron Microscopy (cryo-EM) or Single Particle Analysis (SPA) is a technique used to determine the structure of amorphous macromolecular compounds from tens of thousands of cryogenically frozen (-150°), homogeneous, randomly oriented, and well-dispersed individual molecules. SPA is an essential tool for structural biologists and is fast becoming the gold standard for solving the structure of proteins. The top-end microscopes and associated equipment are expensive to both procure and maintain making it difficult for most researchers to gain access. Over the last decade there has been extensive upgrades to both software and hardware that facilitate bringing affordable SPA to researchers in more remote regions. In 2022, Western Australia installed its first cryo-EM at the Centre for Microscopy, Characterisation, and Analysis at the University of Western Australia. This purchase included a modern side-entry cryo-holder and a cold field emission 200kV TEM fitted with a direct electron detector. We cover our journey with cryo-EM so far including working with polyketide synthases that resemble antibiotic production lines, mitochondrial ribosomes, membrane proteins, RNA binding and editing proteins, and DNA origami. Here about our journey setting up a facility from scratch from installation to achieving our first high-resolution structure and discover how our facility can help your research.



PPG AGM 2025 - #03 (Local Capabilities)

Taking proteins into the clinic & beyond using proteomics

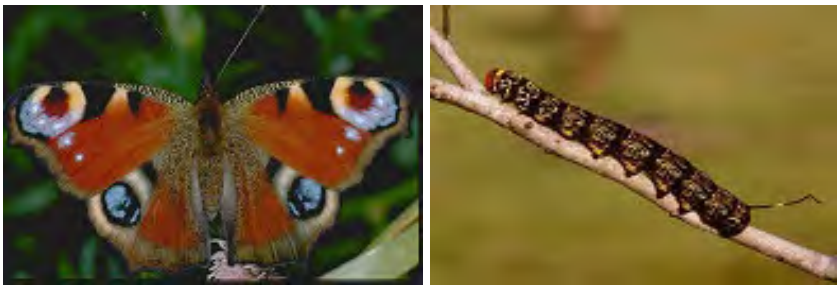
Richard Lipscombe[1], Nikasalee Ediriweera[1], Siobhan O'Connell[1], Aria Kyriakou[1], Scott Bringans[1], James Lui[1]

[1] *Proteomics International, Perth, WA, Australia*

Proteomics International Laboratories (ASX:PIQ) is a pioneering medical technology company operating at the forefront of predictive diagnostics and precision medicine. Founded in 2001,Proteomics International's mission is to improve the quality of lives by the creation and application of innovative tools that enable the improved treatment of disease.

Proteomics International provides protein analytical services to the WA science community via the WA Proteomics Facility which it has operated since 2006, becoming the WA node of BioPlatforms Australia in 2010. The WA Proteomics Facility is now a collaborative Public Private Partnership jointly managed by Proteomics International and UWA. The Facility brings together deep scientific and technological expertise to translate protein-based biological markers that impact human health, agriculture, and environmental systems into practical and effective tools to answer problems encountered in everyday life.

Same genome



PPG AGM 2025 - #06 (Plenary)

Deep learning is nothing to be salty about…

Kate Michie[1]

[1] *Structural Biology Facility, Mark Wainwright Analytical Centre, The University of New South Wales, Sydney, NSW*

Deep learning methods (otherwise known as AI) have come to biomolecular science with a rush. If you follow any social media you'll probably be aware of the AI hype cycle- those that sing its praises and those that call it a doomsday event. Here I present a story of how deep learning in biomolecular science can complement traditional methods, in a discovery of a likely symbiotic relationship of a bacterium and an archaeum isolated from stromatolites from Shark Bay, WA. I'll work through how some of the deep learning tools can be used and on the way also illustrate some limitations, provide other case study examples and discuss the newest tool developments.

PPG AGM 2025 - Poster

Ultrasound-induced modifications in functional, rheological and structural attributes of high protein lupin milk powder

Barsha Adhikari[1], Keshav Raghav Hegde[1], Sruthi N U[1], Stuart Johnson[2], and Rewati Raman Bhattarai[1]

[1] School of Molecular and Life Sciences, Faculty of Science and Engineering, Curtin University, Australia; [2] Ingredients by Design Pty Ltd, Australia

Recent trends for plant-based diets, coupled with consumer concerns over animal proteins, have driven the demand for alternative plant protein sources. Australian sweet lupin (*Lupinus angustifolius*) can help address the alternative plant protein gap due to its high protein content (30-40%), low allergenicity, and unique amino acid profile. However, the commercial use of lupin is limited due to poor techno-functional properties. This research investigated the effect of ultrasound treatment (UT) on the various structural and functional properties of freeze-dried high-protein lupin milk powder (LMP) and compared it with soymilk powder (SMP). The results showed significant differences in solubility (99.62%), dispersibility (87.76%), sinkability (0.869) and wetting time (36 s) of ultrasound-treated LMP when compared with untreated LMP as well as untreated and treated SMP. Likewise, the incorporation of UT to LMP exhibited good flowability (CI = 12.75%), less cohesiveness (HR = 1.14) and significant alteration on its secondary structure. These outcomes could provide food industries with a stable food ingredient to meet the growing plant protein demand.

PPG AGM 2025 - Poster

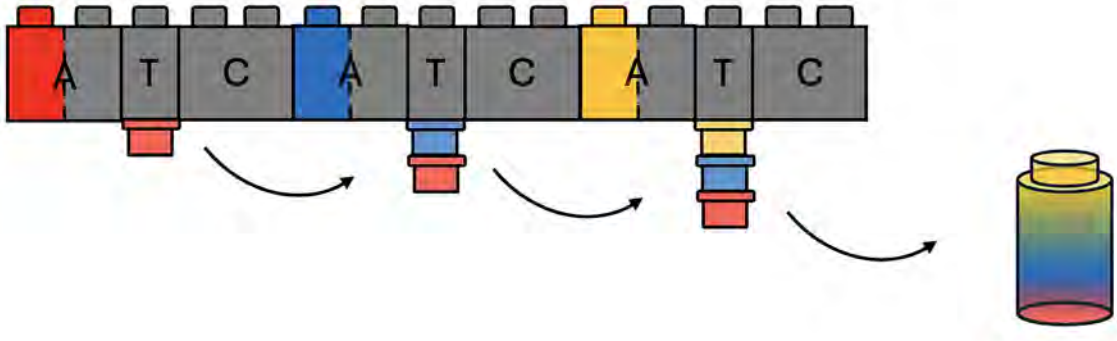
Biology Blocks:

Non-Ribosomal Peptide Synthetase Edition

Licia Benedict, Luke Smithers, Blake Payne, Hera Nguyen, Heng Chooi

School of Molecular Sciences, University of Western Australia, Australia

Non-ribosomal peptide synthetases (NRPSs) are bacterial and fungal enzymes that synthesise natural products. Natural products have a wide array of applications from antibiotics in the medical and agricultural industries to pigments in paint. NRPSs are made up of modules, each which add on a substrate that is incorporated into a growing chain to form a natural product. The modules are made up of three domains: the adenylation (A) domain, thiolation (T) domain and condensation (C) domain. This opens up the possibility of changing the modular makeup of NRPSs to create numerous novel products. Although, changing a whole module from A through to C domain seems like the straightforward method, it is not always successful. Alternative methods have been developed, such as changing modular parts that are between T domains, between C domains, and more specifically changing the region surrounding the A domain, which is involved in selecting the substrate. We propose a new high-throughput method, changing a part of the A domain, with the rationale that this part, specifically, is involved in selecting the substrate.



PPG AGM 2025 - Poster

Molecular studies of the nuclear transcription factor complex PPARγ and RXRα as a function of ligand binding

Deborshi Chanda, Yvonne Mukuka, Jasmine King, Matthew Piggott, Luke Smithers, Alice Vrielink

[1] *School of Molecular Sciences, University of Western Australia*

Peroxisome proliferator-activated receptor gamma (PPARγ) is a ligand-inducible nuclear receptor that regulates gene expression through heterodimerization with retinoid X receptor alpha (RXRα) and subsequent binding to DNA. PPARγ plays a central role in metabolic homeostasis and cancer progression, making it an important therapeutic target. Structural studies using X-ray crystallography suggest that ligand-induced conformational rearrangements within the ligand-binding domain, particularly involving helix-12, play a role in modulating receptor activation and coregulator recruitment. Our group has recently observed ligand-induced spatial–conformational changes, involving residues that may be involved in the PPARγ–RXRα interaction surface. This suggests a novel phenomenon that could alter the mechanism of action of this heterodimer complex based on the ligands bound to it. To further probe this novel mechanism, we characterised the PPARγ–RXRα interaction as a function of different covalent ligand classes (antagonist, inverse agonist and partial agonist) using microscale thermophoresis. Preliminary results from these studies reveal differences in the PPARγ–RXRα binding affinity as a function of ligand class. Structural analyses of PPARγ in the presence of these ligands suggest that binding alters the protein conformation as a function of ligand class. Our current studies are focused on elucidating structures of different ligand-bound PPARγ–RXRα–DNA complexes in order to better explain the binding affinities observed. These findings aim to further probe the molecular basis of PPARγ activation and repression, providing a structural framework to guide the design of selective modulators with therapeutic potential for cancer, metabolic disorders and other PPARγ-linked conditions.

PPG AGM 2025 - Poster

Structural and Functional Characterization of *Neisseria meningitidis* Capsular Transporter

Weixin Chen[1], Luke Smithers[1], Alice Vrielink[1]

[1] School or Molecular Science, University of Western Australia, Australia

The capsular polysaccharide (CPS) is a principal virulence factor responsible for the pathogenesis and treatment challenges of meningococcal disease caused by *Neisseria meningitidis (Nm)*. A comprehensive understanding of the transporter responsible for CPS export is therefore essential. The capsule transport protein (Ctr) complex, an integral component of the *Nm* envelope, is hypothesized to form a channel across the two bacterial membranes. This complex is composed of four protein subunits: outer membrane CtrA and inner membrane CtrB are both channel proteins, while CtrC and CtrD form an ATP-binding cassette (ABC) transporter that is anchored in the inner membrane and associated with CtrB.

The objective of this project is to conduct structural studies on the Ctr complex and characterize the binding affinities of the transporter subunits by microscale thermophoresis studies. Preliminary work has established a foundation for this investigation. CtrA has been successfully expressed in *E. coli* strains, yet its purification requires optimization to attain higher purity protein for structural and functional studies. CtrB has been purified and preliminary analysis via negative stain electron microscopy and single particle cryo-electron microscopy analysis is in progress. CtrC has been successfully crystallized, but its crystallization conditions need to be optimized. The expression and purification of the CtrD remain challenging.

The goal of this research is to characterize the complete structure of this critical transporter and reveal its polysaccharide export mechanism. *Nm* meningococcal disease is associated with high mortality and can progress despite treatment. Findings from this project will provide a molecular basis for designing novel antibiotics targeting capsule assembly, addressing the urgent need to overcome antibiotic resistance of this pathogen.

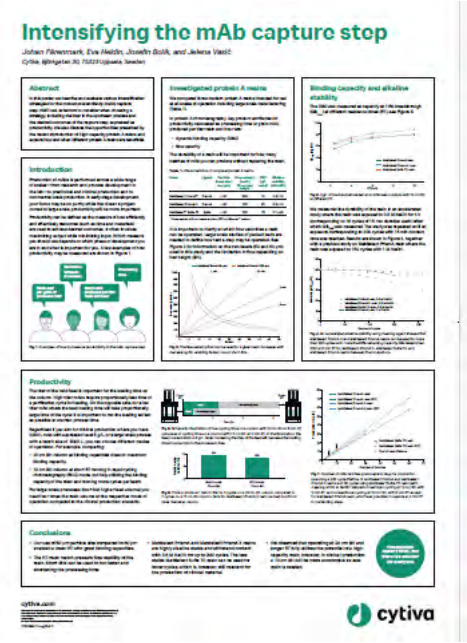
PPG AGM 2025 - Poster

Intensifying the mAb capture step

Emma Dal Maso[1], Johan Färenmark[2], Eva Heldin[2], Josefin Bolik[2] and Jelena Vasić[2]

[1] Global Life Sciences Solutions Australia Pty Ltd DBA Cytiva, Australia; [2] Cytiva, Björkgatan 30, 75323 Uppsala, Sweden

In this poster, we describe and evaluate various intensification strategies for the monoclonal antibody (mAb) capture step. We'll look at factors to consider when choosing a strategy, including the titre in the upstream process and the desired outcomes of the capture step, expressed as productivity. We also discuss the opportunities presented by the recent introduction of high-capacity protein A resins and explore how and when different protein A resins are beneficial.



PPG AGM 2025 - Poster

Preliminary Structural Studies of a Mitochondrial tRNA Importer

Maren Pantring[1], Javier Ting[1], Crystal Cooper[2], Luke Smithers[1], Alice Vrielink[1]

[1] School or Molecular Sciences, University of Western Australia. [2]Centre for Microscopy, Characterisation and Analysis, University of Western Australia

Transfer RNA (tRNA) import is a crucial process for maintaining mitochondrial gene expression in plants, but the localization and structural features of the proteins involved in tRNA import are not well understood.

In this study, tRNA import component 1 (Tric1), a putative tRNA importer from *Arabidopsis thaliana* was investigated using an integrated structural, bioinformatic and experimental approach. Tric1 is composed of a preprotein and amino acid transporter (PRAT) domain and a sterile alpha motif (SAM) domain. PRAT domain proteins are a family of membrane proteins found in chloroplasts and mitochondria, important for the transport of preproteins and amino acids. SAM domains are often associated with protein-protein, protein-nucleic acid interactions. Membrane-associated Tric1 was recombinantly expressed and purified to enable preliminary structural analysis. Visualisation of the protein via both negative-stain and cryo-electron microscopy showed that the protein appears to assemble as an oligomer and may not be associated with detergent micelles. Further studies revealed that the protein may also be found in the soluble fraction of the *E. coli* cells. This hypothesis was examined through *in silico* analyses indicating that the Tric1 PRAT domain is not predicted to be membrane associated. Experimental validation involving purification of the cytosolic fraction, followed by SDS-PAGE and Western blot analysis confirmed that Tric1 is also present in the cytosolic fraction.

Results presented in this study raise new questions regarding the mechanism and the localization of Tric1. These findings provide new structural and mechanistic insights into the *A. thaliana* tRNA importer and establish a foundation for future studies of plant tRNA transport.

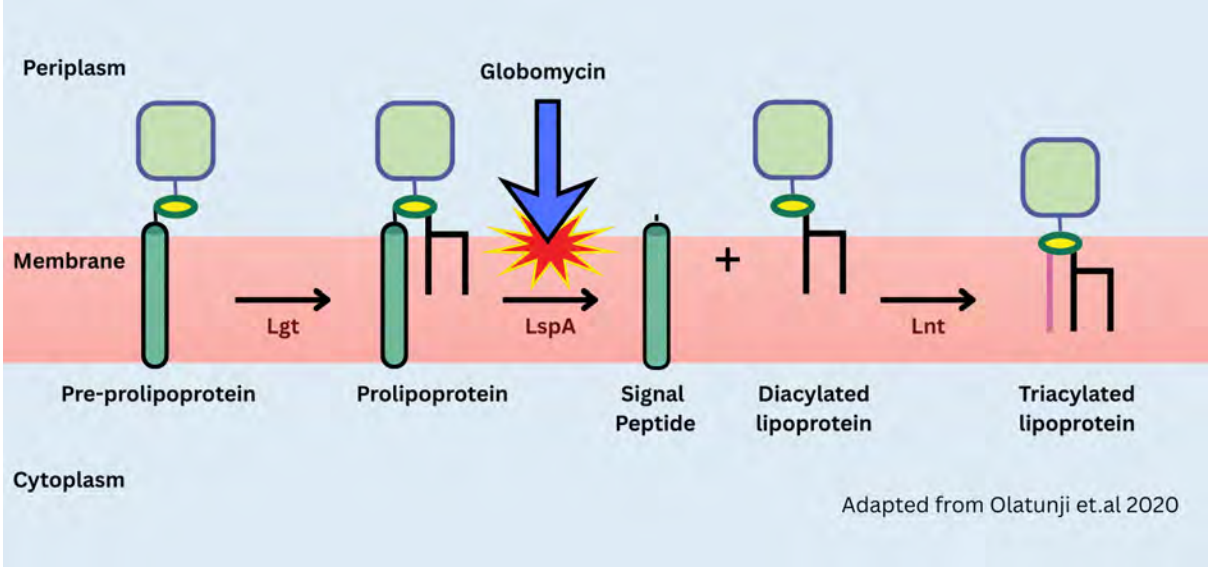
PPG AGM 2025 - Poster

Structure-Function study of LspA from *N. meningitidis*

Bidisha Roy[1], Luke Smithers[1], Alice Virelink[1], Mitali Sarkar-Tyson[2]

[1]School of Molecular Sciences, University of Western Australia, Australia; [2]School of Biomedical Sciences, University of Western Australia, Australia

Neisseria meningitidis is a Gram-negative bacterium that can spread rapidly and cause meningococcal disease and sepsis if not treated urgently. Bacterial lipoproteins are essential for survival and virulence, unique to bacteria, and are an attractive target for antibiotic development. LspA is a key enzyme responsible for the maturation of Bacterial Lipoproteins. Structural and functional analysis of LspA from *Pseudomonas aeruginosa* (DOI: 10.1126/science.aad3747) and methicillin-resistant *Staphylococcus aureus* (DOI: 10.1038/s41467-019-13724-y) has revealed that the antibiotic globomycin inhibits the function of LspA by binding to its active site and stabilizing an intermediate conformation. Analysis of LspA from *N.meningitidis* with globomycin will provide valuable insights into its interaction for structure-based drug design.



PPG AGM 2025 - Poster

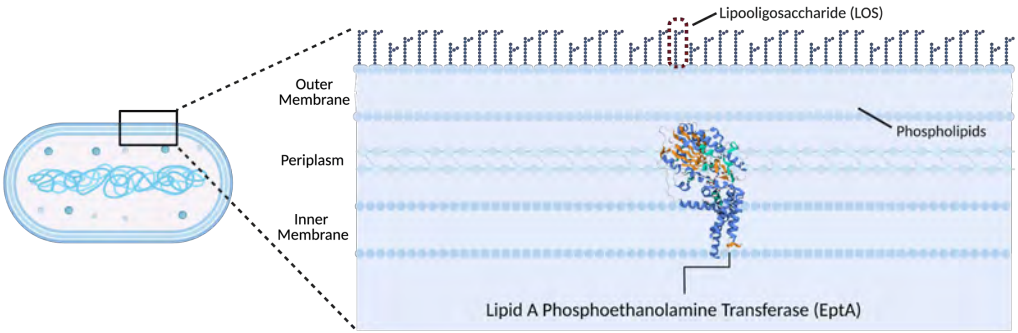
Targeting EptA in *Neisseria gonorrhoeae*

Javier Ting[1], Luke Smithers[1], Crystal Cooper[2] Alice Vrielink[1]

[1] *School of Molecular Sciences, University of Western Australia, Australia*
[2] *Centre for Microscopy, Characterisation and Analysis, University of Western Australia, Australia*

The emergence of multidrug-resistant *Neisseria gonorrhoeae* is a growing global health threat, with resistance to last-line antibiotics driven by the lipid A-modifying enzyme EptA. EptA is an inner-membrane phosphoethanolamine transferase that alters the bacterial outer membrane, reducing susceptibility to multiple antibiotics. Despite its clinical relevance, structural and mechanistic insights into EptA remain limited, partly because detergent molecules used during purification can occupy the active site, potentially obscuring key functional features.

This study combines structural and functional approaches to characterize EptA. High-purity EptA is being analysed using X-ray crystallography and cryo-electron microscopy to resolve its native fold and active site configuration without interference from detergent molecules. A newly-developed complementary liposome-based assay provides a native-like membrane environment to examine enzyme activity, substrate interactions, and small-molecule inhibitor interactions. This enables direct measurement of EptA activity and inhibitor potency in a physiologically relevant context. In this setup, EptA interacts with the liposome surface, and preliminary assays comparing conditions with and without EptA have demonstrated that the enzyme retains functional activity in the presence of lipid membranes. Future work will incorporate small-molecule inhibitors to assess their effects on EptA activity and binding. Together, these approaches aim to elucidate EptA function and membrane interactions, providing a platform for strategies to restore antibiotic efficacy against multidrug-resistant *N. gonorrhoeae*



PPG AGM 2025 - #07 (Session A)

AI-driven structure-guided design of cyclical PCNA-targeting peptides

Dayna Holroyd[1]

[1] *School of Biological Sciences, The University of Adelaide, Adelaide, South Australia, Australia*

Proliferating Cell Nuclear Antigen (PCNA) is a nuclear protein with an essential role in DNA synthesis and cellular proliferation. PCNA slides along DNA to facilitate the binding of over 400 interacting proteins to its large hydrophobic surface pocket. PCNA is upregulated in ~90% of cancer types to handle their high proliferative demand. Interestingly, PCNA inhibition demonstrates selective suppression of cancer cell proliferation, with minimal toxicity in non-cancerous cells. This emphasises PCNA as an exceptional target for the development of broad-spectrum cancer therapeutics. An effective strategy to inhibit PCNA is by competing with all PCNA-interacting proteins at the canonical binding pocket. Peptides display promising therapeutic properties to target PCNA's large pocket, despite cell and nuclear uptake being major hurdles for peptide-based inhibitors thus far. Using AI-driven structure-guided approaches, we have identified a cyclised peptide which targets PCNA's hydrophobic pocket, with enhanced cellular stability and membrane permeability. This novel peptide makes multiple key interactions upon binding PCNA, as confirmed with X-ray crystallography. A solvent-exposed interface has also been identified, allowing for rational peptide modification with a fluorescein tag, to provide fluorescence imaging capabilities *in vitro*. Confocal microscopy demonstrates the co-localisation of this fluorescein-tagged peptide within the nuclei of cancer cells. Furthermore, this peptide demonstrates the on-target inhibition of PCNA through proximity ligation assays. Importantly, this modified peptide maintains a low micromolar affinity for PCNA (biophysical assays) and an anti-proliferative effect in ovarian, breast and cervical cancer cell lines. Whilst this novel peptide lends itself to further optimisation to improve affinity and potency, it provides a strong foundation for the development of AI-designed cyclical peptides to target PCNA for cancer therapeutic application.

PPG AGM 2025 - #08 (Session A)

A Genome-Wide CRISPR knockout Screen Reveals Novel Regulators of Mitochondrial Translation.

Danielle L. Rudler[1,2]

[1] School of Human Sciences, The University of Western Australia; [2] ARC Centre of Excellence in Synthetic Biology

The complex interplay between cellular organelles is essential for homeostasis, but the pathways governing their co-regulation are not systematically defined. Mitochondria are energy producing organelles that dynamically respond to changing metabolic conditions. This flexibility is mediated by an array of proteins involved in the communication between the mitochondrion and cellular environment. While there have been advancements in characterising the mitochondrial proteome, an understanding of the relationship between mitochondrial gene expression and the rest of the cell is severely lacking. To identify novel regulators of mitochondrial biogenesis, we performed a whole-genome CRISPR knockout screen using a mitochondrial ribosomal protein as a sensor of mitochondrial stress. We identified hundreds of enriched genes associated with mitochondrial defects and validated these via the generation of stable cell knockouts. This presentation will discuss the primary findings, highlight new regulatory pathways, and connect these results to their broader roles in inter-organelle biogenesis and mitochondrial transport.

PPG AGM 2025 - #09 (Session A)

Engineering Fungal Nonribosomal Peptide Synthetases for Novel Bioactive Compounds

Blake Payne[1], Luke Smithers[1], Licia Benedict[1], Yit-Heng Chooi[1]

[1] *School of Molecular Sciences, The University of Western Australia, Australia*

Fungal nonribosomal peptides (NRPs) are a vital source of bioactive compounds with broad applications in medicine and agriculture. The modular nature of their biosynthetic factories, nonribosomal peptide synthetases (NRPSs), provides a blueprint for engineering novel molecules. This presentation will discuss our work reprogramming NRPSs by swapping key functional domains and sub-domains to alter the final peptide product. Building on these efforts, we are now leveraging emerging computational tools in the aim of more precise re-engineering of the adenylation (A) domain, which acts as the gatekeeper for substrate selection. The framework of this computational strategy will be presented, along with preliminary data used to score and rank promising new enzyme designs for future experimental validation.

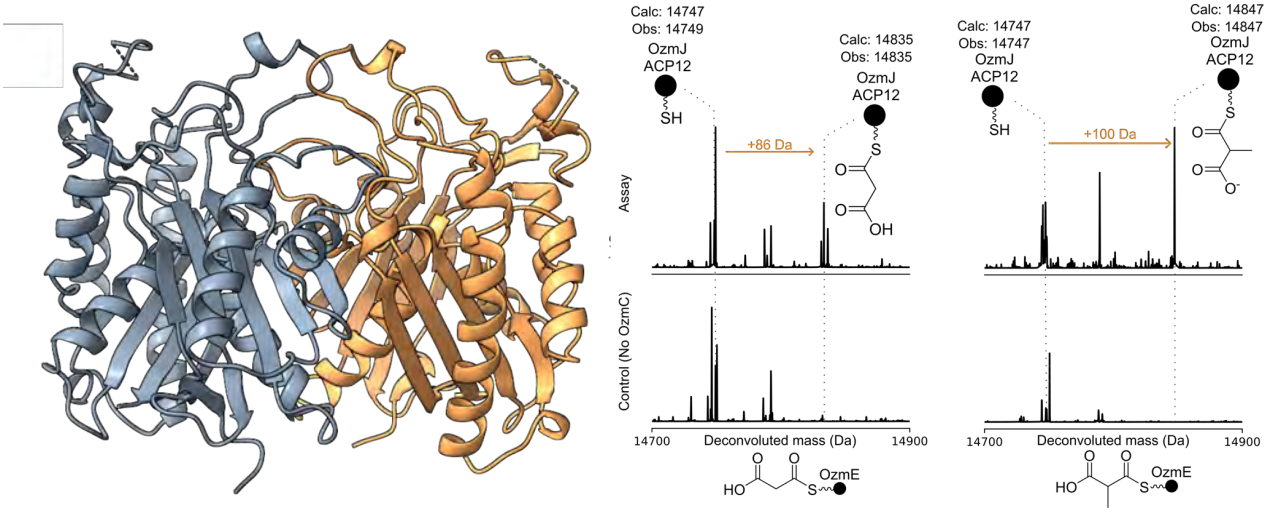
PPG AGM 2025 - #10 (Session B)

The Structure and Function of a Promiscuous Acyltransferase from a Polyketide Assembly Line

Fraser Windsor[1], Loreli Masselot--Joubert[1], Joel Haywood[2], Brodie Bulcock[1], Marriane Costa[3], Alice Vrielink[1], Yit-Heng Chooi[1]

[1] School of Molecular Sciences, University of Western Australia, Australia; [2] Centre for Crop Disease and Management, Curtin University, Australia; [3] Olgram, France

Polyketide synthases (PKSs) are large, multi-active site enzymes that synthesise a variety of bioactive molecules, notably used as antibiotics, by the repeated condensation of small acyl building blocks. The assembly-line structure of PKSs has generated interest in engineering them to produce novel bioactive molecules. *Trans*-acyltransferases are standalone enzymes which can select building blocks for PKS assembly lines. These enzymes have potential as tools to change building block use in PKSs, altering their products. However, known *trans*-acyltransferase domains select for a limited range of building blocks. OzmC is a proposed *trans*-acyltransferase from the biosynthesis of oxazolomycin where it is proposed to select for a building block that is unique among known *trans*-acyltransferases. Studies by *in vitro* assays analysed by intact protein mass spectrometry revealed OzmC to accept multiple different acyl building blocks. The structure of OzmC was solved by X-ray crystallography which revealed that the tertiary structure of OzmC is unique among known *trans*-acyltransferase domains. OzmC's promiscuity and unique structure among *trans*-acyltransferases make it an interesting case within the landscape of polyketide biosynthesis and an attractive engineering target to produce novel bioactive molecules.



PPG AGM 2025 - #11 (Session B)

Designing Synthetic PPR-RNA Tools To Monitor and Regulate Biological Events Using Conformational Changes

Sanathanee Sachchithananthan [1], Kim T Melville[1], Ian D Small K[1, 2], Andrew C Marshall[1], Charles S Bond[1]

[1]School Molecular Sciences, University of Western Australia, Australia; [2]ARC Centre of Excellence for Plant Energy Biology, University of Western Australia, Australia.

Proteins undergo conformational changes upon interacting with other proteins, nucleotides, or other molecules. Understanding these structural shifts is key to elucidating protein function and designing controllable molecular tools. Pentatricopeptide repeat proteins (PPR) are composed tandem α-helical motifs and exhibit sequence-specific RNA binding. These proteins undergo conformational change upon binding to RNA targets, adopting a compressed super helical conformation compared to their unbound state. This study investigates how RNA-induced conformational changes in PPR proteins contribute to protein function, and how such changes can be exploited to design RNA-responsive PPR-based synthetic tools. Previous studies with chemically labelled PPR proteins demonstrated conformational upon RNA-binding change using fluorescence resonance energy transfer (FRET). Building on this, a 9 repeat S class PPR protein was protein was engineered with Now-GFP and mRuby2 (9S-FP) fused to the N- and C-terminus. To investigate the binding affinity and conformational shifts, 9S-FP was analysed using analytical size-exclusion chromatography (SEC) and FRET, whereas micro scale thermophoresis was used to analyse the binding affinity of 9S control PPR protein without FP. Analytical SEC confirmed RNA binding of 9S-FP, with the protein:RNA complex eluting at a distinct retention time from protein- or RNA-only samples. In vitro FRET assays showed an increasing FRET signal upon RNA titration, consistent with a binding-induced conformational change. MST analysis of the control 9S protein revealed an RNA-binding affinity of 60 nm. The results indicate that the PPR protein retains RNA-binding ability and undergoes conformational changes despite FP attachments at both terminals. However, a stronger FRET pair is needed to improve the signal. Furthermore, a similar system can be employed to longer PPR proteins where the FPs will be fused in between the PPR tracts for FRET studies. This system has potential as the basis for RNA-responsive biosensors.

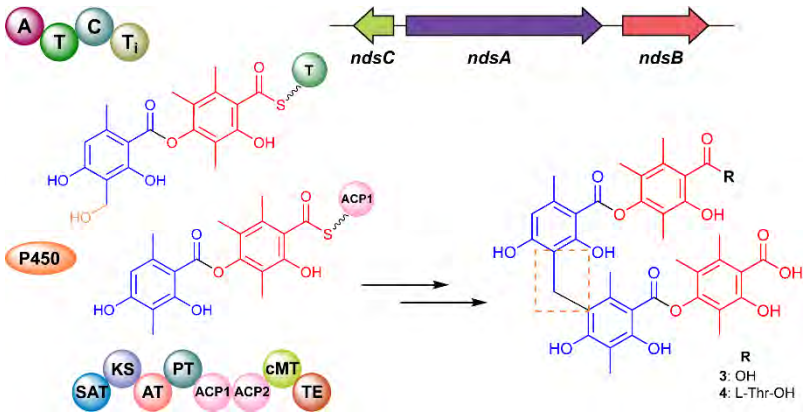
PPG AGM 2025 - #12 (Session B)

Genome mining of the wheat pathogen *Parastagonospora nodorum* establishes the biosynthesis of methylene-bridged depsides

Hera T. Nguyen,[1] Nicolau Sbaraini, [1] Joe Bracegirdle, [1] Luke Smithers,[1] Stephen A. Moggach,[1] Daniel Vuong,[2] Ernest Lacey,[2,3] Joel Haywood,[4] Andrew M. Piggott[2] and Yit-Heng Chooi[1]

[1] School of Molecular Sciences, The University of Western Australia, Perth, WA; [2] Microbial Screening Technologies Pty. Ltd, Smithfield, NSW; [3] School of Natural Sciences, Macquarie University, Sydney, NSW; [4] Centre for Crop and Disease Management, Curtin University, WA

Depsides are polyphenolic natural products commonly found in lichens but also produced by some free-living fungi. Here, we report the discovery and functional characterisation of an *in planta*-upregulated biosynthetic gene cluster (*nds*) in the wheat fungal pathogen *Parastagonospora nodorum* SN15, comprising a non-reducing polyketide synthase (NR-PKS; NdsA), a non-ribosomal peptide synthetase (NRPS; NdsB) and a cytochrome P450 oxygenase (NdsC). Heterologous expression of the *nds* cluster in *Aspergillus nidulans* LO8030 yielded previously reported depsides, CJ-20,557 (**1**) and duricamidepside (**2**), alongside two novel dimeric methylene-bridged depsides, nodoraside A(**3**) and B (**4**). Combinatorial gene expression and precursor feeding experiments revealed that hydroxylation of CJ-20,557 by the cytochrome P450 NdsC, followed by non-enzymatic dehydration, generates an *ortho*-quinone methide intermediate, which reacts with a second depside unit to form methylene-bridged depsides. Notably, this crosslinking occurs only in the presence of NdsAand NdsB *in vivo*, indicating a possible requirement for protein–protein interactions or enzyme co-compartmentalisation. Methylene-bridged depside natural products are rare, and this study provides the first insight into their biosynthetic origin.



PPG AGM 2025 - #13 (Session C)

Protein biomarker discovery, validation and screening method for climate resilience in crops.

Agyeya Pratap[1,2,3,4,5], Madan Pal[6], Viswanathan Chinnusamy[6], Kadambot H.M. Siddique[1], Nicolas L. Taylor[1,2,3,4,5] *

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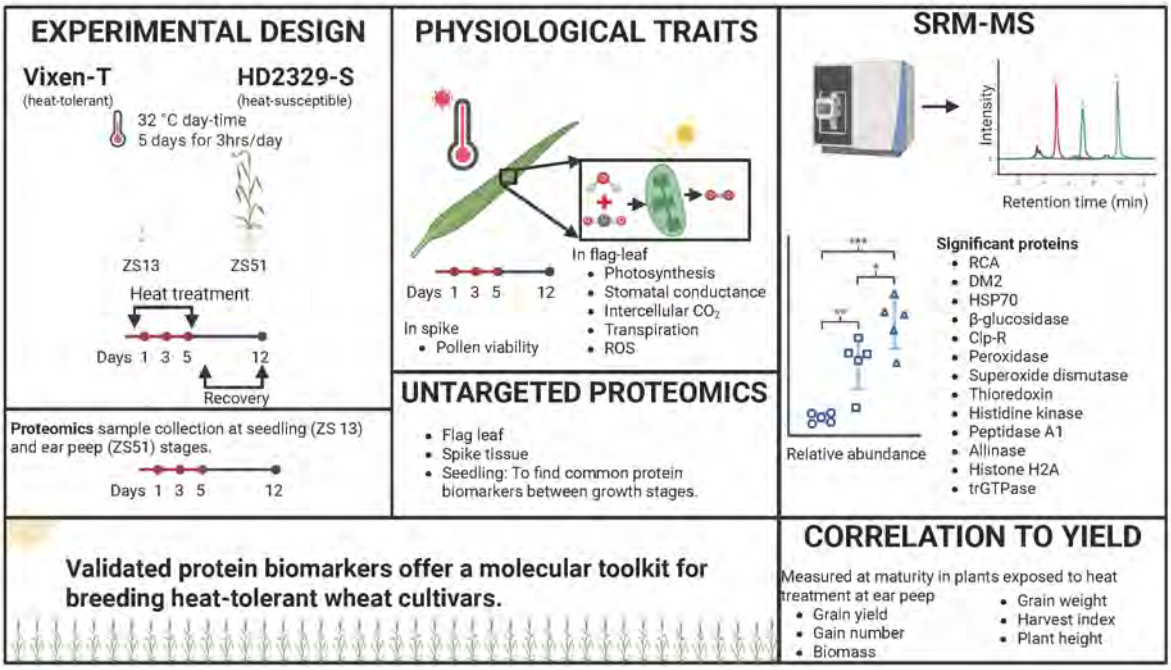
Climate change poses a significant threat to global crop production, negatively impacting both yield and quality. Accurate prediction of stress tolerance, particularly at the flowering stage, is critical for breeding resilient crop cultivars. In this study, we demonstrate that protein biomarkers offer a sensitive and specific approach for assessing flowering-stage heat tolerance in wheat, even at the seedling stage. Using untargeted proteomics, we identified candidate protein biomarkers associated with heat tolerance during the ear peep stage. These candidates were subsequently validated through targeted proteomics at both seedling and ear peep stages. Our findings reveal that protein biomarkers indicative of heat tolerance at flowering can be reliably detected at the seedling stage, enabling a high-throughput and scalable screening method for development of heat-tolerant wheat cultivars. This approach offers a promising tool for accelerating wheat breeding programs.


EXPERIMENTAL DESIGN
Vixen-T
(heat-tolerant)
HD2329-S
(heat-susceptible)
32 °C day-time
5 days for 3hrs/day
ZS13
ZS51
Heat treatment
Days 1 3 5 12
Recovery
Proteomics sample collection at seedling (ZS 13) and ear peep (ZS51) stages.
Days 1 3 5 12
PHYSIOLOGICAL TRAITS
Days 1 3 5 12
In flag-leaf
Photosynthesis
Stomatal conductance
Intercellular CO_2
Transpiration
ROS
In spike
Pollen viability
UNTARGETED PROTEOMICS
Flag leaf
Spike tissue
Seedling: To find common protein biomarkers between growth stages.
SRM-MS
Intensity
Retention time (min)
Relative abundance
Significant proteins
RCA
DM2
HSP70
β-glucosidase
Clp-R
Peroxidase
Superoxide dismutase
Thioredoxin
Histidine kinase
Peptidase A1
Allinase
Histone H2A
trGTPase
Validated protein biomarkers offer a molecular toolkit for breeding heat-tolerant wheat cultivars.
CORRELATION TO YIELD
Measured at maturity in plants exposed to heat treatment at ear peep
Grain yield
Gain number
Biomass
Grain weight
Harvest index
Plant height

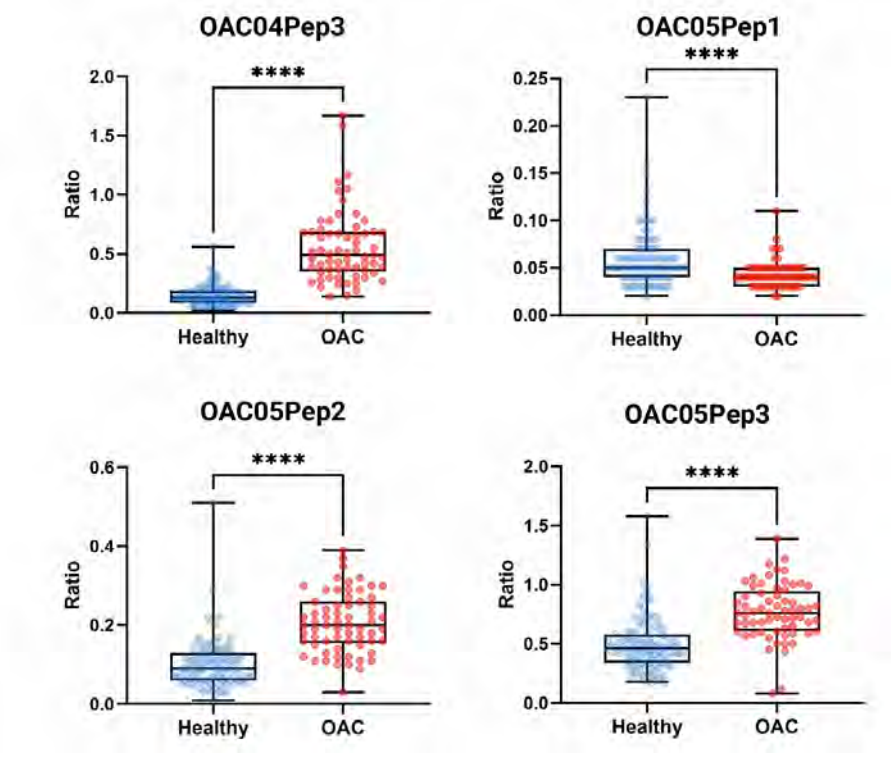
PPG AGM 2025 - #14 (Session C)

Validation of Biomarkers for Esophageal Cancer

Scott Bringans[1], Elizna Schoeman[1], Natalie Scott Dorta[1], Rui Wang[1], Peter Galettis[1], Richard Lipscombe[1]

[1] *Proteomics International, Perth, WA, Australia*

Esophageal cancer is the sixth leading cause of cancer-related deaths worldwide, with esophageal adenocarcinoma (EAC) now the most common subtype in Western populations. Early-stage EAC is often asymptomatic, leading to delayed diagnosis. Current detection methods, such as endoscopy with biopsy, are invasive, expensive, and usually performed only after symptoms appear. To improve early detection, PromarkerEso has been developed as a non-invasive, blood-based test to identify individuals at higher risk of EAC who may benefit from confirmatory endoscopy.
PromarkerEso uses a serum glycoprotein biomarker panel analysed through a lectin-based magnetic bead pulldown method targeting O-linked galactose structures, followed by liquid chromatography-mass spectrometry. Quantified peptide ratios distinguish EAC-positive from negative samples. Preliminary data show strong discriminatory performance, with ongoing validation to improve reproducibility and assess independent cohorts. PromarkerEso offers a promising triage tool to prioritize high-risk patients for endoscopy, supporting earlier detection and potentially improving patient outcomes.



PPG AGM 2025 - #15 (Session C)

Profiling Autoantibodies in Melanoma Patients with Brain Metastases: A Proteome Array-Based Approach for Biomarker Identification

Désirée Sexauer[1,2], Lydia Warburton[1,2,5], Anna L Reid[1,2], Wei Yen Chan[3,4] , Jenny H Lee[3,4], Ashleigh Stewart[3,4], Russell J Diefenbach[3,4], Alexander M Menzies[4,6,7], Georgina V Long [4,6,7], Aaron B Beasley[1,2,], Elin S Gray[1,2], Helen Rizos[3,4†], Pauline Zaenker[1,2†]

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Context: Brain metastases in melanoma are typically diagnosed following neurological symptoms or imaging, often at advanced stages. Early detection of asymptomatic brain metastases is crucial, as progression can lead to severe neurological decline, diminished quality of life, and death.

Methods: This study investigated tumour-associated autoantibodies in baseline blood samples from melanoma patients. Sera from 33 patients with brain metastases and 58 patients with extracranial-only metastases were analysed.

IgG and IgA autoantibody profiling was performed using high-density human proteome microarrays (HuProt™), containing approximately 17,000 full-length human proteins, each printed in duplicate. Arrays were scanned immediately using the InnoScan 710 (Innopsys), and fluorescence intensities quantified with Mapix microarray image analysis software (Innopsys). Prior to analysis, array quality was assessed using ArrayQualityMetrics, and signal intensities normalised via the robust linear model (RLM) approach implemented in PAWER (Protein Array Web ExplorerR).

Results: From the filtered dataset ($p < 0.01$, $\log2FC > 1.5$), 203 candidate IgG autoantibodies were identified, including 49 IgG markers with AUC ≥ 0.7, which were elevated in patients with brain metastases.

Conclusion: These preliminary findings highlight the potential of tumour-associated autoantibody combinations as minimally invasive biomarkers for the detection of melanoma brain metastases. Validation in an independent cohort using custom focused protein microarrays is underway.

PPG AGM 2025 – #L1 (Lightning talks)

Model Protein-based Biomolecular Condensates

Dilruka V Kasturiarachchi[1], Andrew C Marshall[1], Charles S Bond[1]

[1] *School Molecular Sciences, University of Western Australia, Australia*

Liquid-liquid phase separation (LLPS) is a fundamental biological phenomenon in which a uniform mixture of biomolecules spontaneously separates into distinct, coexisting liquid phases. This results in the formation of concentrated assemblies known as biomolecular condensates which are essential for cellular organization, enabling dynamic compartmentalization of biomolecules without membrane boundaries. Certain proteins have the intrinsic ability to undergo LLPS. Beyond their biological significance, harnessing the phase-separating ability of proteins has promising applications in synthetic biology and biotechnology, including metabolic engineering, and biocatalysis. This project focuses on characterizing the phase behaviour of *Drosophila* Behaviour/Human Splicing (DBHS) proteins, an RNA-binding family of proteins known to undergo LLPS, and investigating their ability to recruit the model enzyme cytochrome P450 BM3 and one of its substrates. Through *in vitro* assays, fluorescence imaging, and biochemical analysis, I will examine DBHS protein phase separation and their capacity for selective recruitment. I will also explore droplet maturation, defined as the time-dependent transition of condensates from dynamic, liquid-like assemblies to more rigid, gel-like states, to understand its influence on condensate dynamics, protein recruitment and enzymatic activity. By establishing relationships between condensate composition, phase behaviour, and biochemical function, this study aims to demonstrate precise and dynamic control of chemical reactions using biomolecular condensates, potentially advancing their application in synthetic and industrial biotechnology.

PPG AGM 2025 – #L2 (Lightning talks)

Harnessing structural bioinformatics and pathogenicity mechanisms for advancing crop protection and pathogen control

Pavel Misiun[1], Kristina Gagalova[1], Callum Verdonk[1], Mark Derbyshire[1]

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Fungal pathogens cause crop diseases that are of major importance to the agricultural industry and global food security. Underlying this are incredibly complex interactions between host and pathogen, facilitated by fungal 'effector' proteins. Identifying and characterising interactions at the level of individual proteins has major implications for the development of crop varieties with durable disease-resistance. This, however, is made difficult by the unique evolution of fungal pathogens and their effectors, and the complexity of disease mechanisms. The rapidly evolving landscape of artificial intelligence and deep learning, along with its continued application in the field of bioinformatics, has the potential to accelerate this research. Through my PhD project, I aim to develop tools and resources that enhance the discovery and characterisation of effectors and their interactions with hosts, leveraging advances in structural prediction, generative protein design, and novel machine-learning architectures such as protein language models. I am particularly interested in applying these methods for automated, large-scale protein-protein interaction discovery, structural conservation-based effector prediction, and investigations of effector evolution and function. Given that the project is in a very early stage, this talk will give a general outline of its aims and preliminary research, inviting discussion and feedback to refine its trajectory.

PPG AGM 2025 - #L3 (Lightning talks)

Biomass Concentration and Specific Growth Rate Using a Dissolved Oxygen Soft-Sensor for Expression Systems in Automated Dense Fed-Batch Culture

Shaman Gaspar[1]

[1] Infors Southeast Asia; [2] Infors AG, Switzerland

The study involves the role of soft-sensor technology through a data driven, machine learning AI that allows real time analysis of specific growth rates and biomass from a bioreactor using input from an optical dissolved oxygen sensor. The function allows tailored growth profiles leading to automated actuation of carbon source delivery through the feed pump in exponential fashion. An oxygen soft-sensor for online monitoring of x and μ was programmed into eve® software platform and applied during the cultivation of a recombinant Escherichia coli strain. The sensor used the dissolved oxygen concentration (pO2) in the media as input value. The pO2 signal is a pertinent parameter, considering that majority of bioreactors are equipped with a pO2 probe.

PPG AGM 2025 – L4 (Lightning talks)

Structural characterization of CquiOR136-DEET complex in *Culex quinquefasciatus*

Samar Mahmood[1], Wei Xu[1], Aniruddha Agnihotri[1]

[1] *School of Agricultural Sciences, Murdoch University, Australia.*

Culex quinquefasciatus is a primary vector of diseases such as West Nile virus and lymphatic filariasis. The vector relies on the functioning of odorant receptors (ORs) to detect environmental cues, including host-derived odors and insect repellants. DEET (N, N-diethyl-3methylbenzamide) is the gold standard mosquito repellant available in the market. CquiOR136 has been identified as the primary DEET-sensing odorant receptor in mosquitoes, acting in conjunction with co-receptor Orco. Understanding the structural basics of CquiOr136 interaction with DEET is crucial for guiding the development of more effective repellants. This research focuses on the structural characterization of the CquiOR136-CquiOrco receptor complex from *C. quinquefasciatus* bound to the insect repellent DEET. The project employs generation of recombinant protein expression in insect cells using the baculovirus expression system. The process will be followed by ligand-stabilization screening, detergent optimization, and affinity purification of the receptor complex in the presence of DEET. The membrane protein will be purified using Affinity and size exclusion chromatography. The purified complex will undergo lipid cubic phase crystallization, and X-ray crystallographic structure determination. Preliminary results are expected to identify the DEET binding pocket at CquiOR136 and Orco, revealing the allosteric modulations by DEET. These results will confirm the structure of CquiOR136-Orco-DEET complex. The structure will provide atomic level insights into the DEET induced alterations in conformation and dynamics of the receptor. These findings will deliver the first high-resolution structural basis for repellent recognition in mosquitoes. Understanding the molecular basis of DEET-receptor interactions will provide insights into mosquito olfaction and inform the rational design of improved insect repellents.

PPG AGM 2025 - #16 (Plenary)

Enhancing the Delivery Efficiency of Biomolecules: From Nanocarriers to Biomodulators.

Jie Tang[1]

[1]*Drug Delivery, Disposition and Dynamics, Monash Institute of Pharmaceutical Sciences, Monash University*

This talk will explore innovative nanotechnology-based strategies for enhancing the intracellular delivery of therapeutic peptides and proteins, with a ocus on mucosal and non-invasive administration routes. Our research investigates how the physicochemical properties of nanoparticles influence their ability to traverse biological barriers, interact with mucosal environments, and engage cellular uptake pathways. I will highlight our work on biomimetic nanoparticles engineered to mimic gut microbes, enabling efficient mucus penetration, epithelial transcytosis, and cytosolic delivery of macromolecular cargo. These platforms have been applied to the oral and inhalable delivery of pDNA, mRNA, and proteins, offering new opportunities for developing non-injectable vaccines and protein-based therapeutics with improved patient compliance and global accessibility.