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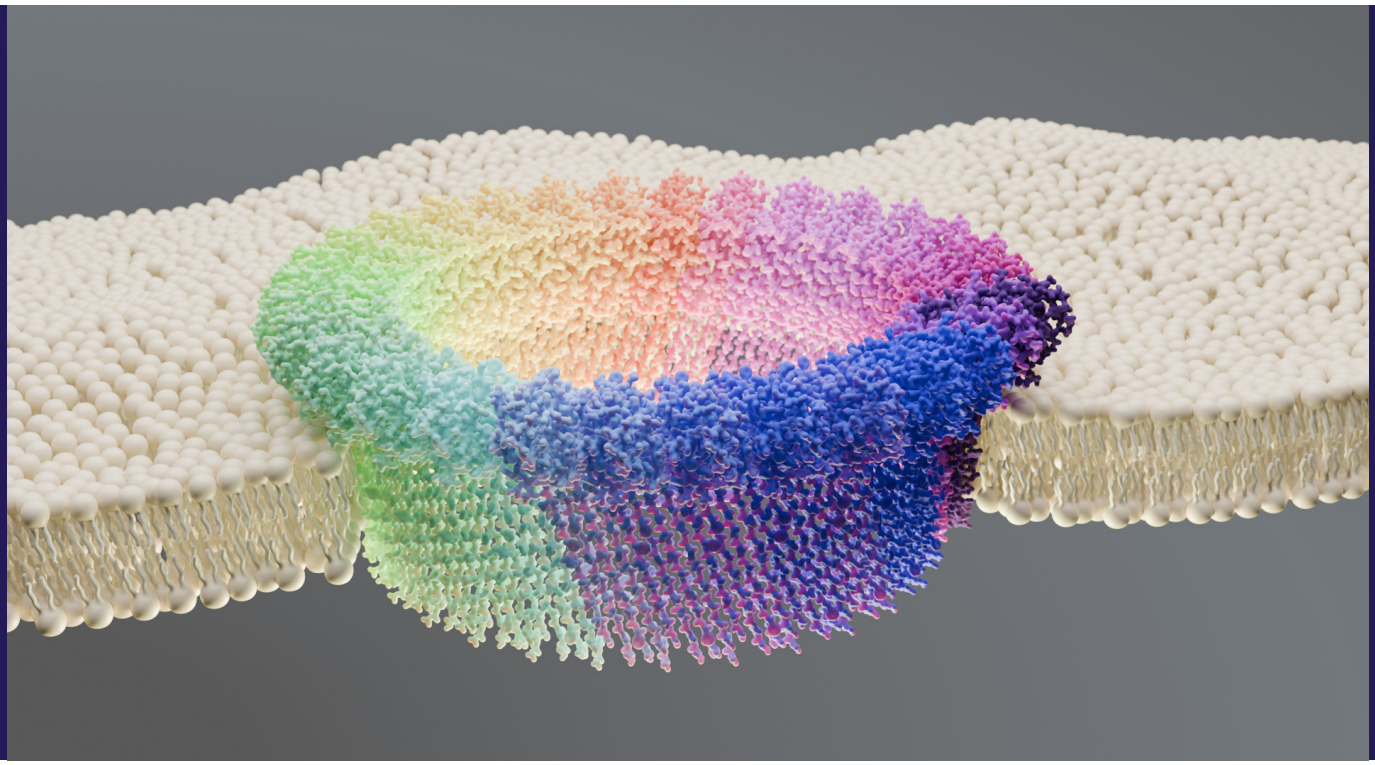

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A cholesterol-dependent cytolysin-like toxin forming a pore within a lipid membrane. Image courtesy of Dr Bronte Johnstone and Professor Michael Parker, Bio21 Molecular Science and Biotechnology Institute, University of Melbourne, and St Vincent's Institute of Medical Research. Created in Blender MolecularNodes. Adapted from *Sci Adv* 2025:11(13):eadt2127 (CC BY 4.0 license).

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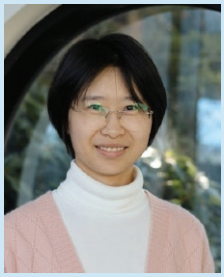

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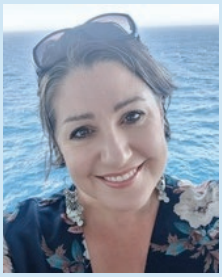

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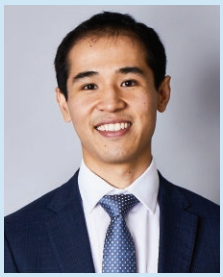

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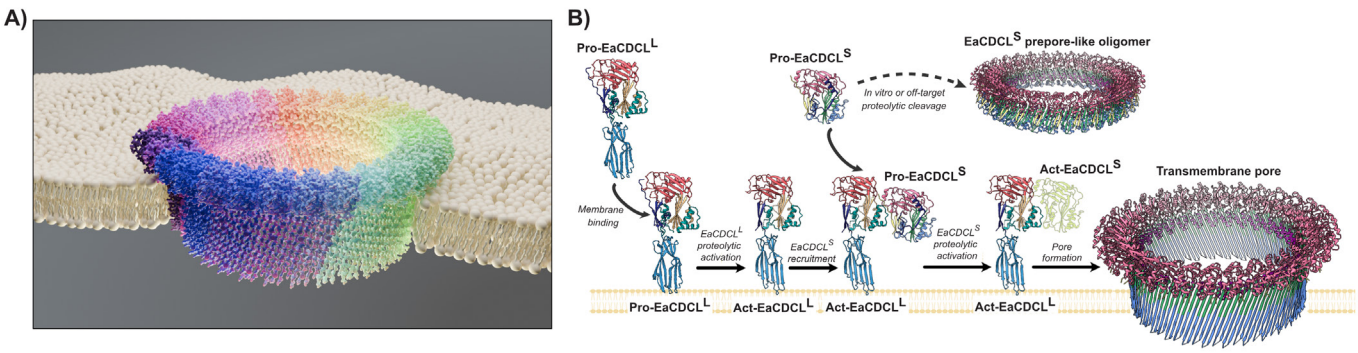
Structural Snapshots During Pore Formation of a Newly Discovered Family of Bacterial Toxins

Johnstone BA*, Christie MP, Joseph R, Morton CJ, Brown HG, Hanssen E, Sanford TC, Abrahamsen HL, Tweten RK, Parker MW*. Structural basis for the pore-forming activity of a complement-like toxin. *Sci Adv* 2025;11:eadt2127.
***Corresponding authors: bronte.johnstone@unimelb.edu.au, mwp@unimelb.edu.au**

Pore-forming proteins are widespread in living organisms where they play key roles in pathogenesis, immunity and cell death via the act of membrane permeabilisation. Prime examples include bacterial pore-forming toxins (PFTs), mammalian complement, perforins and gasdermins which can punch gigantic pores, sometimes more than 150 Å in diameter, in membranes. Pore formation starts with the secretion of water-soluble protomers that oligomerise on contact with a target membrane and undergo a series of complex conformational changes to convert to the membrane-inserted pore. Our lab has been at the forefront of this fascinating field with the determination of the first crystal structure of a PFT called colicin (*Nature*, 1989), the first pore structure by electron microscopy (*Nature*, 1994) and the first crystal structure of a major family of bacterial PFTs called the cholesterol-dependent cytolysins (CDCs) (*Cell*, 1997). PFT structures have been enormously helpful in understanding how these metamorphic proteins transition from water-soluble monomer to membrane-inserted pore, but many mysteries remain.

We discovered a new family of PFTs related to the CDCs based on a shared functionally important five-residue sequence motif (*Nat Commun*, 2024). There are more than 300 of these cholesterol-dependent cytolysin-like (CDCL) proteins and they are common among gut microbes where they are a prevalent means of antibacterial antagonism. CDCLs are unusual PFTs as they act as a bicomponent system consisting of a 3-domain (CDCL-short) and a 4-domain (CDCL-long) subunit. They also require proteolytic activation and, unlike the CDCs, are not dependent on cholesterol, despite their name. Given these distinctive characteristics, we wanted to explore the structural basis of how CDCLs form pores. We combined X-ray crystallography, cryo-electron microscopy (cryo-EM), small-angle X-ray scattering (SAXS) and further biophysical analysis to obtain structural insights across the entire pore-forming pathway for the CDCL pair from *Elizabethkingia anophelis*, a bacterial species found in the gut of mosquitos that can cause neonatal meningitis.

We had previously determined the crystal structures of the CDCL-short and CDCL-long water-soluble forms (*Nature Commun*, 2024). In our new work, we solved the crystal structure of a proteolytically-activated form of CDCL-long, which revealed that proteolytical cleavage replaces the role of cholesterol in CDCs to regulate oligomerisation. SAXS confirmed the crystal structures of all forms were similar in solution. We then determined the cryo-EM structure of the CDCL pore, imaged directly on the surface of liposomes at about 3 Å resolution (**Fig. A**). Surprisingly, we observed stacked complexes of the membrane-inserted pore with a shorter ring on



*(**A**) The CDCL membrane pore inserted within a lipid membrane. Image created in Blender MolecularNodes.*
*(**B**) Graphical summary of the findings and proposed mechanism for EaCDCL pore formation.*
Figure adapted from Sci Adv *2025:11(13):eadt2127 (CC BY 4.0 license).*

top. This short ring appears to be a ring of CDCL-shorts in a 'prepore-like' state and the larger ring the pore with the transmembrane β-hairpins clearly extended. This allowed us to model how CDCL pores assemble (**Fig. B**), revealing the oligomerisation interface, role of the proteolytic cleavage and large conformational changes that progress during the formation of the large ~170 Å β-barrel pore. This cryo-EM structure is the first of a CDCL pore, only the second in the broader CDC/CDCL family and is the first structure solved within a native membrane.

Comparison with members of the mammalian complement/perforin family and the gasdermin superfamily revealed some key similarities with each, suggesting CDCLs straddle all lineages, and we hypothesise that the short form of CDCLs may represent a common ancestor from which others have diverged.

Our work has provided novel insights into this new family of PFTs and highlights the complementary nature of various structural biology techniques to provide a holistic overview of the intricate process of pore formation.

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From left: Bronte Johnstone, Michelle Christie, Riya Joseph, Craig Morton and Michael Parker.

Molecular Insights into Evolutionary Conflict in a Polyspecific Drug/Peptide Transporter

Tanner JD, Richards SN, Corry B*. Molecular basis of the functional conflict between chloroquine and peptide transport in the Malaria parasite chloroquine resistance transporter PfCRT. *Nat Commun* 2025;16:2987.
***Corresponding author: ben.corry@anu.edu.au**

The evolution of drug resistance can sometimes co-opt existing protein functions. This means that pathogens with drug resistance will often be less evolutionarily fit than a drug susceptible isoform in the absence of drug pressure. Exploiting this is potentially a way of combating the dire problem of increasingly prevalent antimicrobial resistance.

Using a method called molecular dynamics simulations, which allow us to see dynamic atomistic motions, we study the origins of a functional conflict in a protein involved in drug resistance in malaria. The protein, called PfCRT, normally functions as a transporter of chemically diverse peptides. However, under selective pressure from the drug chloroquine, a series of mutations evolved which conferred the ability to transport chloroquine and many other clinically important antimalarial compounds. While the consequences of this transport depend on the drug, for chloroquine this results in resistance as it gets transported from its site of action. These resistant isoforms spread globally and chloroquine use subsided. But this resistance came at a cost; chloroquine resistant isoforms tend to have reduced fitness in the absence of drug pressure. In fact, this has contributed to a reduction in chloroquine resistance in some populations, potentially restoring its effectiveness as an antimalarial therapeutic. This fitness cost originates in the chloroquine resistance mutations disturbing PfCRT's ability to transport peptides. Indeed, across PfCRT isoforms, peptide transport rates are strongly anti-correlated with chloroquine transport.

In our study, we found that PfCRT can bind peptides in many ways, but common to all, is an interaction with a centrally located lysine. This lysine also happens to be the only residue that it is necessary (but not sufficient) to be mutated to enable chloroquine transport. When we studied its effect on chloroquine access and binding, we found this same residue blocks the drug from its binding site and disrupts access to the protein's binding cavity. Indeed, none of the resistance mutations appeared to be directly involved in supporting chloroquine binding; they simply improved access to an already existing site. And because of chloroquine's positive charge, improving the drug's access necessarily comes at the cost of the peptide's apparent need for this centrally located lysine.

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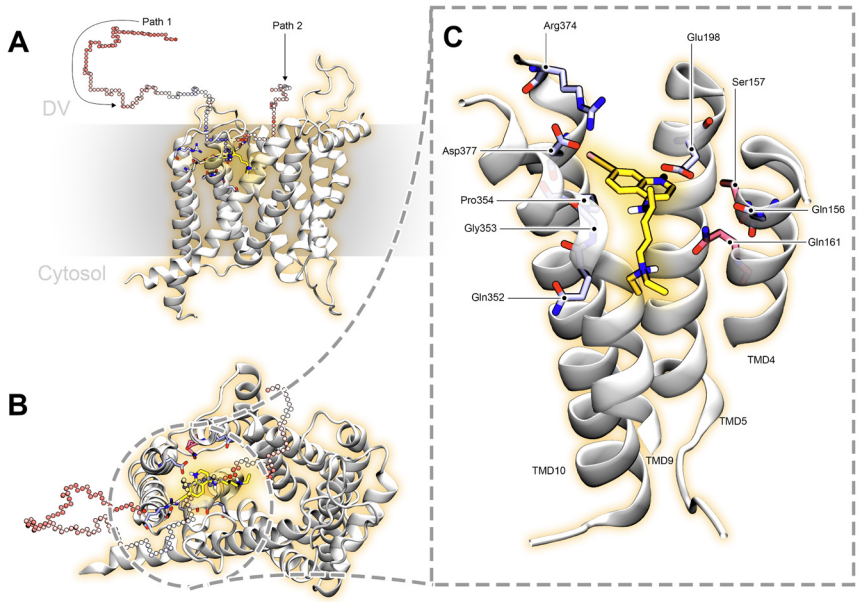

*(**A**) Side view of CQ resistant PfCRT and the two minimum free energy paths from bulk solution to the CQ binding site.*
*(**B**) A top-down view from the vacuolar side of the membrane, of the CQ binding site in CQ resistant PfCRT.*
*(**C**) A close-up of CQ in its binding site. The residues are colored blue and red according to whether their average interaction energy is negative or positive, respectively.*
Figure from Nat Commun *2025;16: 2987 (CC BY-NC-ND 4.0 license).*

We therefore suggest the interpretation that these mutations 're-tuned' the underlying polyspecificity, with the differences in charge shifting the substrate profile of PfCRT from peptides to drug molecules (as positive charge is a common feature of many of these drugs). The differing charge requirements for substrate types then means that these functions struggle to be reconciled, and there is an inverse relationship between their transportabilities. We hope that this work will inform the rational design of PfCRT inhibitors, as well as provide insight into the molecular determinants of drug polyspecificity.

John Tanner, Sashika Richards and Ben Corry
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From left: Ben Corry and John Tanner.

A Mitochondrial Guardian of mRNA Stability

Yang X, Stentenbach M, Hughes LA, Siira SJ, Lau K, Hothorn M, Martinou JC, Rackham O, Filipovska A*. The Vsr-like protein FASTKD4 regulates the stability and polyadenylation of the *MT-ND3* mRNA. *Nucleic Acids Res* 2025;53(4):gkae1261.
***Corresponding author: aleksandra.filipovska@uwa.edu.au**

The mammalian mitochondrial genome may be small and compact, but the regulation of its expression is anything but simple. It relies heavily on a suite of nuclear-encoded RNA-binding proteins (RBPs) to oversee every step – from transcription and processing to stability and translation. Among these is FASTKD4, a member of the FASTK protein family, whose function has remained elusive – until now.

In a recent study published in *Nucleic Acids Research*, our teams, in collaboration with researchers from Switzerland uncovered the structural and functional role of FASTKD4 in stabilising a specific mitochondrial transcript, *MT-ND3* mRNA. This work adds a critical piece to the puzzle of mitochondrial gene expression and highlights how even a single RBP can shape the fate of key metabolic transcripts.

Using crystallography, our team resolved the atomic structure of FASTKD4's RNA-binding domains – FAST1, FAST2 and RAP – revealing a positively charged surface cavity. Interestingly, this structural pocket mimics those found in bacterial endonucleases, yet functional assays confirmed that FASTKD4 does not cleave RNA. Instead, it appears to have evolved a new role: binding and stabilising RNA transcripts, particularly at their polyadenylated tails.

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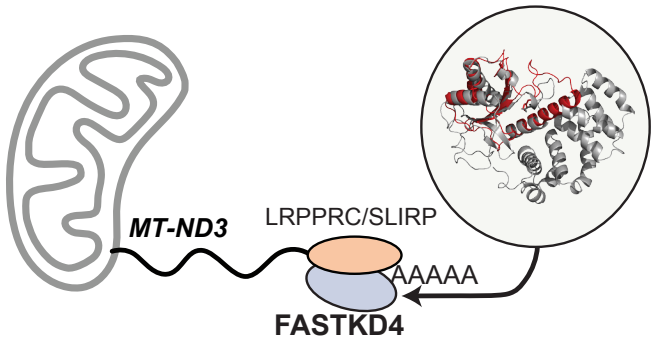

The role of FASTKD4 in mammalian mitochondrial gene expression.

We found that FASTKD4 specifically binds the poly(A) tail of *MT-ND3* mRNA that encodes a component of mitochondrial Complex I and protects it from degradation. In cells lacking FASTKD4, levels of *MT-ND3* mRNA drop dramatically, and the transcript adopts a shortened, non-canonical 3′ end that lacks a functional stop codon. This makes it vulnerable to ribosome-mediated decay, effectively silencing this essential gene. Biochemical studies showed that FASTKD4 interacts with the LRPPRC:SLIRP complex – a known guardian of polyadenylated mitochondrial mRNAs – but only in an RNA-dependent manner. Curiously, while the LRPPRC–SLIRP duo binds a broad range of mitochondrial transcripts, FASTKD4 appears to specialise in specifically binding *MT-ND3*. This suggests a highly selective role for FASTKD4 in fine-tuning mitochondrial mRNA metabolism.

Mutagenesis studies underscored the importance of structural features, that we dubbed the ‘lock’ and ‘key’ helices, within FASTKD4. These elements proved essential for protein stability and RNA binding since mutations in this region destabilised *MT-ND3* mRNAs, validating their functional significance. We also explored the interplay between FASTKD4 and mitochondrial RNA-processing enzymes such as ANGEL2 and Nocturnin. Our results confirmed that while these enzymes contribute to 3′ end shaping, FASTKD4’s absence alone was sufficient to cause *MT-ND3* mRNA instability. Furthermore, translation inhibitors like chloramphenicol can transiently protect mRNA in the absence of FASTKD4, hinting at a delicate balance between translation and degradation.

This work revealed that FASTKD4 is not a nuclease, but a dedicated RNA-binding scaffold that ensures the integrity of a key mitochondrial transcript. Our findings highlight that structural repurposing of proteins supports the streamlined but high-stakes world of mitochondrial gene regulation. As our understanding of these mechanisms grows, so too does the potential to target mitochondrial gene expression defects that cause devastating diseases.

Oliver Rackham and Aleksandra Filipovska
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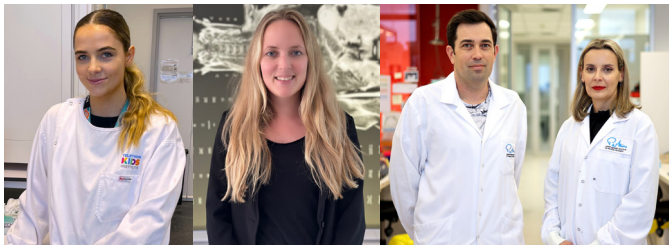
ARC Centre of Excellence in Synthetic Biology
Curtin Medical School and Curtin Medical Research Institute, Curtin University
University of Western Australia



From left: Leatitia Hughes, Maike Stentenbach, Oliver Rackham and Aleksandra Filipovska.

Tethering the Translocases With PINK1

Callegari S*, Kirk NS, Gan ZY, Dite T, Cobbold SA, Leis A, Dagley LF, Glukhova A*, Komander D*. Structure of human PINK1 at a mitochondrial TOM-VDAC array. *Science* 2025;388(6744):303–310.
***Corresponding authors: callegari.s@wehi.edu.au, glukhova.a@wehi.edu.au, dk@wehi.edu.au**

Since the ubiquitin kinase PINK1 was first linked to Parkinson’s disease over 20 years ago, its function has fascinated researchers in both the mitochondrial and ubiquitin fields. PINK1 is a mitochondrial damage sensor. In healthy mitochondria, PINK1 is imported through the import machinery – first through the mitochondrial outer membrane via the translocase of the outer membrane (TOM complex) and then into the inner membrane via the translocase of the inner membrane 23 (TIM23 complex). However, during loss of mitochondrial inner membrane potential, PINK1 import is blocked, trapping PINK1 at the translocases. Its kinase domain then folds on the surface of the TOM complex and when two trapped PINK1 molecules come into close proximity, they dimerise and transautophosphorylate in order to activate their ubiquitin phosphorylation activity. The ability of PINK1 to phosphorylate ubiquitin is unique and a remarkable feature of the ubiquitin code – by phosphorylating the protein modifier ubiquitin, PINK1 essentially alters the ubiquitin message to specifically signal for mitochondrial disposal via mitophagy. Phosphorylated ubiquitin recruits the E3 ligase Parkin, also linked to Parkinson’s disease, which amplifies the signal by adding more ubiquitin substrates for PINK1 to phosphorylate. This phosphoubiquitin signal recruits the phagophore machinery, initiating the process of

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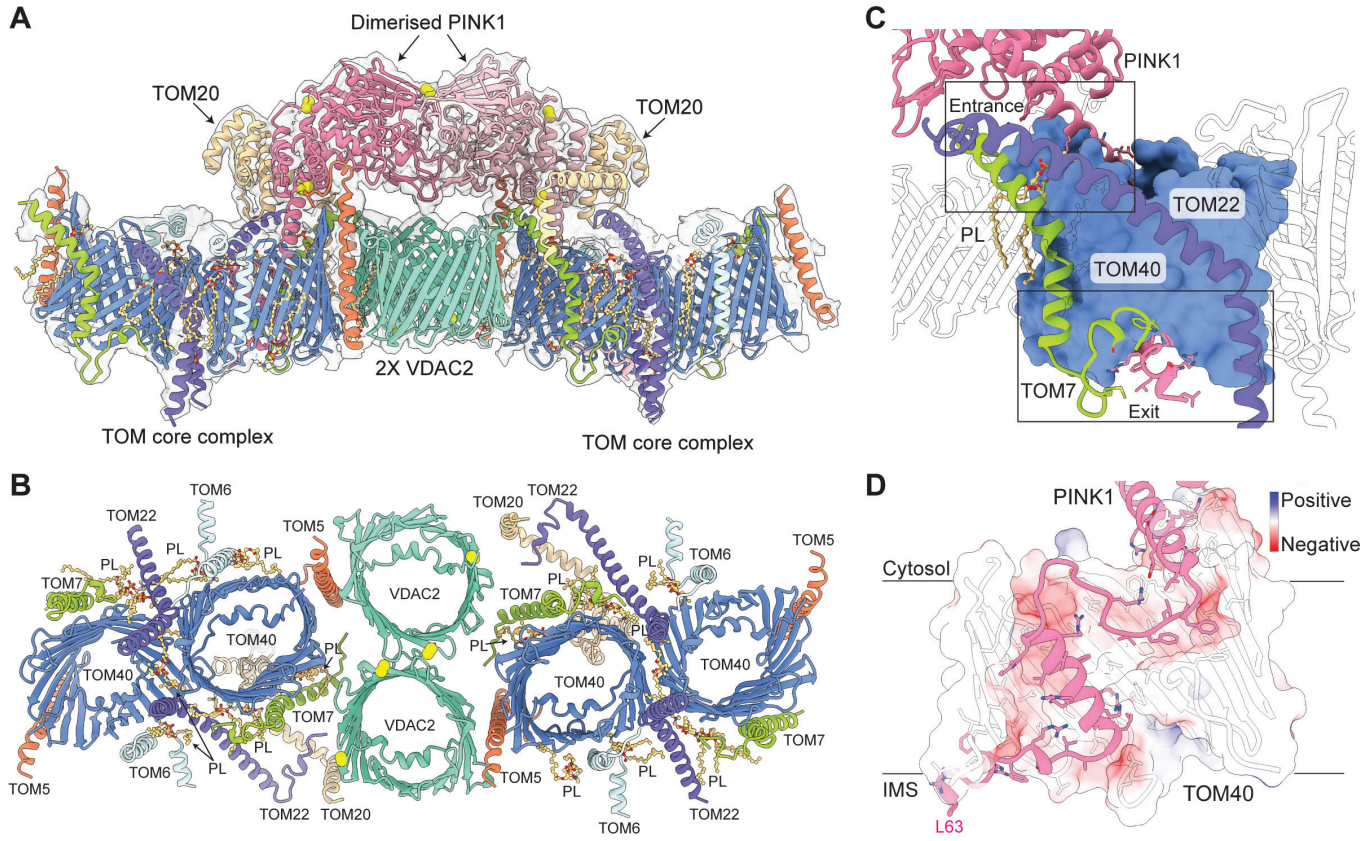

Human PINK1 anchored to an array of mitochondrial translocases.

*(**A**) Colour coded atomic model of the PINK1-TOM-VDAC complex superimposed on the cryoEM density map, as viewed along the plane of the outer mitochondrial membrane. Disulfide bonds are shown as yellow spheres. Phospholipids are shown in stick form.*

*(**B**) As in (A) but viewed from the inter membrane space. PINK1 and TOM20 have been removed from the model to emphasise the composition of the TOM-VDAC2 assembly.*

*(**C**) Interactions of PINK1 upon the entrance and exit of the TOM40 barrel. PL indicates the phospholipid.*

*(**D**) The TOM40 barrel coloured by surface electrostatic potential and segmented to enable visualisation of PINK1.*

Figure adapted from Science *2025;388:303–310 (license 6038660649355).*

mitophagy. Mitophagy is essential for brain health by removing damaged toxic mitochondria that would otherwise accumulate and result in neuronal cell death leading to diseases such as Parkinson's disease.

The mechanisms of PINK1 action have been studied over many years by careful biochemical studies and structural analyses using insect versions of PINK1. However, key pieces of the puzzle were still missing – what does human PINK1 look like and how is PINK1 trapped at the mitochondria? We knew that PINK1 dimerisation is facilitated in oxidative conditions as we could crosslink the dimer in cells upon treatment with hydrogen peroxide (Gan *et al., Nature* 2022). Curiously, while doing these experiments, we observed another hydrogen peroxide induced crosslink between PINK1 and a mystery protein. This mystery protein turned out to be TIM50, a component of the TIM23 complex. We further confirmed that the N-terminal region of PINK1 associates with components of the entire TIM23 complex via chemical crosslink-mass spectrometry experiments. This result was remarkable because it meant that the unfolded N-terminal region of PINK1 was tethering the TOM and TIM23 complexes together. The TOM and TIM23 complexes are on the outer and inner mitochondrial membranes respectively, and only transiently associate upon the import of an unfolded mitochondrial precursor protein to enable precursor handover from TOM to TIM23. The process of how these two complexes associate has largely remained a mystery. PINK1 now represented the first physiological substrate that could trap these two complexes in a supercomplex state and therefore presented the ideal system to structurally elucidate how these two translocases associate.

Obtaining enough PINK1-TOM-TIM23 complexes from cells was always going to be a challenge. To do this, we established the Expi293 mammalian cell expression system (Thermo) in the lab, which allowed us to culture PINK1-FLAG expressing suspension cells in litre batches. We could then extract mitochondria and isolate PINK1-FLAG docked to endogenous TOM-TIM23 complexes. The complexes were further purified

by size exclusion chromatography before vitrifying them on a grid for cryoEM analysis. 2D particle analysis revealed classes of oval shaped discs with six pores and 3D reconstruction resulted in a 3.1 Å cryo-EM map of dimerised human PINK1 docked to an array of six beta barrel proteins. The big surprise was that this array did not just contain the TOM complex, as expected, but in fact comprised of two copies of the TOM complex and a central VDAC2 dimer (**Fig. A** and **B**). This was the first time we had seen such an arrangement of TOM and VDAC complexes in the mitochondrial membrane and, as a bonus, it is also the first structure of human VDAC2.

The N-terminus of PINK1 threads through the barrel of the two proximal TOM40 pores and we could resolve the passage of PINK1 inside the barrel to a resolution of 2.9 Å, thus illuminating the path of a mitochondrial presequence substrate through the TOM40 channel. Although this had been mapped biochemically in previous studies using crosslinking strategies, it had never been visualised. The entrance of PINK1 into TOM40 is guided by TOM7 and a phospholipid (**Fig. C**). PINK1 then follows an acidic route through the barrel (**Fig. D**) and exits at a tunnel facing TOM22 and TOM7, which guide out PINK1 and direct it towards the TIM23 complex. We were unable to obtain a high-resolution model of the very N-terminal 60 amino acid residues of PINK1 that associate with the TIM23 complex, but this is currently the focus of ongoing work.

This PINK1-TOM-VDAC structure enables a greater understanding of PINK1 activation, which has important implications for Parkinson's disease. It is the first time we have visualised human PINK1 and although the kinase domain is similar to that of the published PINK1 insect structures, we observed many new aspects important for PINK1 regulation, including the presence of strategically positioned disulfide bonds that stabilise the dimer conformation of PINK1, suggesting a mechanism of oxidative regulation (**Fig. A**). We can also identify TOM complex components that further stabilise PINK1, including the import receptor TOM20, which clamps the N- and C-helices of PINK1 at its presequence binding site. TOM5 also plays an important role in assembling this activation complex by connecting TOM40 with VDAC2 and additionally seems to act as a pillar, supporting the kinase domain of PINK1 as it hovers above the translocases. The structure explains many patient mutations and paves the way for the structure-based design of PINK1 activators, which would have great therapeutic value for enhancing mitophagy in Parkinson's disease patients with mutations in PINK1.

Sylvie Callegari and David Komander
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La Trobe University

From left: Alisa Glukhova, Nicholas Kirk, Sylvie Callegari and David Komander. Credit: WEHI.

Lysosome, Interrupted: *Coxiella* Remodels the Host Lysosomal Compartment Through Removal of Cathepsin B

Bird LE, Xu B, Hobbs AD, Ziegler AR, Scott NE, Newton P, Thomas DR, Edgington-Mitchell LE*, Newton HJ*. *Coxiella burnetii* manipulates the lysosomal protease cathepsin B to facilitate intracellular success. *Nat Commun* 2025;16(1):3844.
***Corresponding authors: laura.edgingtonmitchell@unimelb.edu.au, hayley.newton@monash.edu**

Avoiding degradation by host lysosomes is critical to the success of an intracellular pathogen. Yet, *Coxiella burnetii*, the causative agent of Q fever, has the unique ability to thrive within a lysosome-derived compartment termed the *Coxiella*-containing vacuole (CCV). To date, the mechanisms used by *Coxiella* to withstand this harsh intracellular environment and resist lysosomal degradation are poorly defined. In this study, we report that *Coxiella* actively modifies the repertoire of host lysosomal proteases present in the CCV, remodelling the normally bactericidal compartment into a friendlier home by removing the host cathepsin B.

C. burnetii is unique in its ability to thrive in a part of the cell where other pathogens go to die: the acidic, degradative phagolysosome. From within this membrane-bound compartment, *Coxiella* use a type 4B secretion system (T4SS) to translocate bacterial effector proteins into the host cell, where they are trafficked to distinct subcellular compartments and

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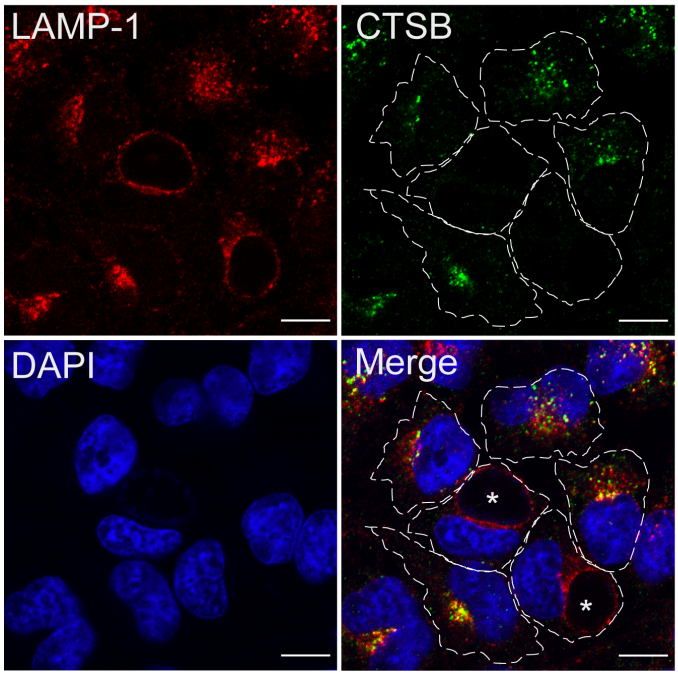

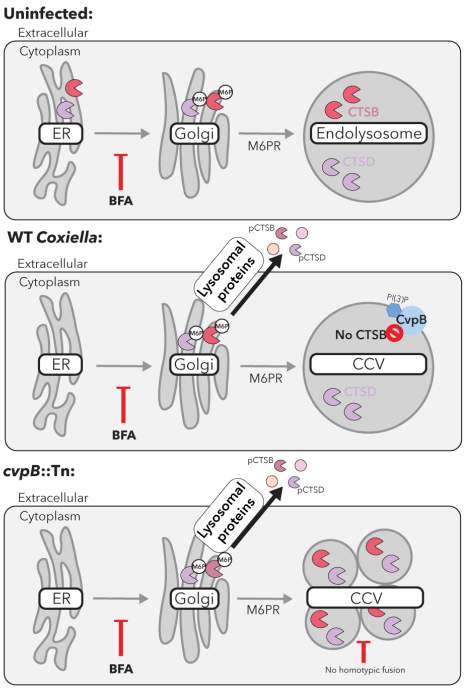

Left *Coxiella infection of mammalian cells leads to loss of cathepsin B.* Coxiella*-infected cells were immunostained with antibodies against LAMP-1 (red) or cathepsin B (green). Infected cells (marked with asterisk) show dramatic loss of cathepsin B.*

Right *Schematic representation of lysosomal protease modulation by* Coxiella*.*

Figure adapted from Nat Commun *2025;16(1):3844 with permission.*

manipulate a plethora of pathways. Although the CCV has historically been characterised as a lysosome-like niche, the cohort of lysosomal proteases present and active in this compartment has never been comprehensively examined – until now.

We aimed to determine if *Coxiella* downregulated lysosomal protease activity to aid survival in a lysosome-derived vacuole. Using a combination of cell biology and proteomic techniques, we identified that cathepsin B – a major workhorse of lysosomal proteolysis – is completely removed from *Coxiella*-infected cells in a T4SS-dependent manner. Overexpression of cathepsin B disrupted both bacterial replication and CCV morphology, pointing to a strong selective pressure for its removal. Using a library of *Coxiella* mutants, we learned that cathepsin B removal required CvpB, a T4SS effector which promotes CCV fusion. The relationship between cathepsin B and CvpB was indirect, giving rise to the hypothesis that CvpB-dependent modulation of the CCV generates a vacuole in which (i) cathepsin B has reduced stability, or (ii) another *Coxiella* virulence factor is activated which drives cathepsin B clearance.

In addition to removing cathepsin B, we report that *Coxiella* incites the host cell to secrete a broad range of lysosomal proteins to the extracellular space to maintain lysosomal homeostasis. This occurred independently of the T4SS and could be inhibited by brefeldin A. It remains to be determined whether secreted lysosomal proteases are active in the extracellular space, and future work will examine the consequence of lysosomal protein secretion for infection progression.

Collectively, this research highlights the intricate interplay between host and pathogen, shedding light on how a unique intracellular microbe subverts mammalian cell biology to cause disease. In addition to furthering our understanding of *Coxiella* pathogenesis, this study opens avenues for exploring lysosomal biology in human health and disease.

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From left: Hayley Newton, Laura Edgington-Mitchell and Lauren Bird.

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The ASBMB Education Feature is coordinated by Tracey Kuit (tracey_kuit@uow.edu.au) and Amber Willems-Jones (amber.willems@unimelb.edu.au). This issue was supported by Maurizio Costabile (University of South Australia) and Alyssa Van Dreumel (University of Western Australia).

Getting to the CoRe of Flow Cytometry: a New Teaching Framework

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Flow cytometry is a cornerstone technique across many disciplines including biochemistry, immunology and microbiology, providing the ability to analyse thousands of cells within seconds while simultaneously measuring multiple markers on a single cell. Despite its importance, the complexity of flow cytometry has grown from simple three-colour machines to instruments capable of measuring over 30 parameters, presenting significant challenges in teaching and learning. As part of a large team of renowned experts, we contributed to the first collection of protocols for the correct use of cytometric techniques in the field of immunology, published in the *European Journal of Immunology* community guidelines (1,2). However, these guidelines lack specific recommendations on how to effectively teach these key topics and core concepts.

In response to this challenge, we propose a novel application of the conceptual tool, CoRe-Flow-Matrix, an adaptation of the content representation (CoRe) matrix (3,4), originally designed to support science educators in developing their pedagogical content knowledge (PCK) – that is, the integration of subject matter expertise with effective teaching strategies.

The need for a structured teaching framework

To effectively use flow cytometry in academic teaching and research settings, undergraduate and graduate students must develop competency in three fundamental areas:

1. Conceptualisation and preparation: experimental design, reagent selection and sample preparation.
2. Operations: machine setup, calibration and data acquisition.
3. Data analysis: gating strategies, compensation and statistical interpretation.

Currently, these components are often taught in isolation, with students, researchers and facility staff acquiring knowledge at varying levels and through different pedagogical approaches and research training. This fragmented learning can lead to incorrect result acquisition, uninformed analysis and misinterpretation of data creating significant ethical dilemmas and can also lead to expensive machine repair or waste of costly resources. Few studies have explored the effectiveness of flow cytometry education (5,6). One study showed that even an eight-week intensive course is insufficient to fully grasp the technique, with students requesting extended learning opportunities (7). A lack of comprehensive education not only affects experimental outcomes but also presents ethical dilemmas when misinterpreted data leads to incorrect scientific conclusions.

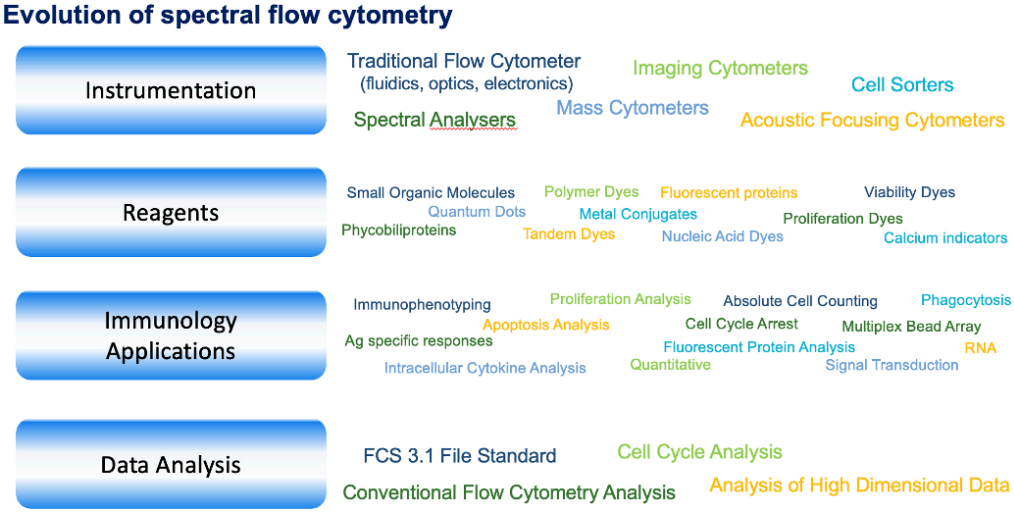

Fig. 1. Main skills required for graduate research students to learn in flow cytometry. *As an expert group, we have started to identify the main skills categories and associated tasks that are required for graduate research students to learn flow cytometry.*

The role of pedagogical content knowledge

A major factor influencing the effectiveness of flow cytometry education is the PCK of instructors (8). An individual's PCK is influenced by their experience, developed through their teaching practice, subject mastery and engagement with student learning behaviours. Three key dimensions of PCK for science educators include (9):

1. Suitable subject matter knowledge.
2. Practical teaching and classroom experience.
3. Understanding of student learning behaviours and attributes.

For flow cytometry, PCK is not limited to university educators; postdoctoral researchers, graduate students and technical staff also play a crucial role in teaching the technique. However, due to the technical complexity of flow cytometry, few have a sufficient PCK framework for effectively teaching this topic.

Table 1. Flow cytometry topics should be developed through identifying underlying associated core concepts. *The CoRe-Flow-Matrix requires a topic (first column) to be divided into multiple core concepts. This is an example of the breadth topics for correct sample preparation and acquisition, and the associated core concepts that require pedagogical content knowledge for robust sample data generation.*

Skill category	Task
Conceptual	Understanding how a flow cytometer works
	Understand how the fluidics and optics systems enable multicolor analysis of a single cell
	Explain how flow cytometry data is generated and presented
	Identify current applications of flow cytometry and selecting the current cytometry equipment for your experiment
Technical	Compensate fluorescence cross talk on a flow cytometer
	Quantify cell viability on a flow cytometer
	Stain membrane bound antigens for flow cytometric analysis of immunophenotyping and antigen-specific responses
	Stain intracellular antigens for flow cytometric analysis
	Quantify cell proliferation on a flow cytometer
	Quantify cell death on a flow cytometer
Analytical	Design properly controlled multicolor flow cytometry experiments to address research question and troubleshoot
	Analyse and interpret flow cytometry data

Introducing the CoRe-Flow-Matrix tool

With the evolution of flow cytometry becoming increasingly broad and exquisitely technical (**Fig. 1**), as an expert group, we have started to identify the main skill categories and associated tasks required for graduate research students to learn flow cytometry (**Table 1**). We propose a universal framework is required for students to effectively acquire competency in all three fundamental areas of flow cytometry, and for educators, researchers and facility staff to share their PCK together in a community of practice through the CoRe-Flow-Matrix.

The CoRe-Flow-Matrix framework aims to bridge the gap between expertise and education in flow cytometry. The tool aims to assist educators assess their own PCK and refine their teaching methods to improve student outcomes. The proposed CoRe-Flow-Matrix is a diagrammatic representation of aspects of expert academics' collective PCK related to the teaching of flow cytometry topics.

The CoRe-Flow-Matrix format shows each topic (first column) in flow cytometry broken down into key core concepts (**Table 2**). For each concept, educators consider eight pedagogical questions (rows) designed to explore the most effective ways to teach the topic (**Table 3**). This structured framework enables instructors to:

- Align teaching strategies with fundamental principles.
- Identify common misconceptions and challenges in the teaching and learning flow cytometry.
- Ensure consistency and comprehensiveness in training.

For example, a fundamental topic such as sample preparation might be divided into core concepts like reagent selection, cell viability and isotype controls. Each concept can then be analysed using the CoRe-Flow-Matrix to determine the best teaching approach. Table 3 demonstrates the application of the CoRe-Flow-Matrix to isotype controls. The content can continually be evaluated as more instructors within the community of practice contribute their PCK on the topic using the CoRe-Flow-Matrix.

This ongoing initiative will enhance the quality of flow cytometry education, ensuring that future researchers receive structured, high-quality training that allows them to apply the technique effectively in their scientific careers.

Table 2. CoRe-Flow-Matrix for a science educator's PCK. *Adapted from* Res Sci Ed *2011;41(3):341–355.*

Skill category	Topic	Core concept 1	Core concept 2	Core concept 3
Conceptual	**Understand the cells or tissue** you are using and prepare your experiment accordingly.	Some cells are more fragile than others. Be vigilant on your single cell suspension preparation to ensure the cells are in good shape to appropriately generate your data.	Kinetics are important! Ensure your cells are kept at appropriate temperate and media conditions.	Cells die. Unless you want these in your data, use a viability exclusion marker.
Technical	Certain **sample requirements** are essential in flow cytometry to ensure problem free acquisition of samples and accurate downstream analyses.	Whole blood samples should be processed as soon as possible to minimise cell loss that may cause downstream cell enumeration errors. If samples can't be processed immediately, overnight storage at room temperature is preferred to storage at 4˚C.	Monoclonal antibodies can bind non-specifically to dead cells. Although dyes that discriminate between live and dead cells are available, starting with a sample that displays high viability will improve the accuracy of data collected.	If cells are stuck to each other, the signals detected from them can provide inaccurate data. Care should be taken to ensure samples are well resuspended prior to acquisition. This minimises the risk of a sample clogging the flow cytometer and reduces the number of doublets that need to be gated out during analysis.
Analytical	**Controls** are vital in any flow cytometry experiment to provide the context within which one can interpret test samples to reliably distinguish the results from background variation and non-specific effects.	Isotype controls are not real controls.	FMO samples are controls required to minimise spectral overlap.	Secondary only antibody control is required when using two-layer staining.

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Table 3. Development of a CoRe-Flow-Matrix tool to enhance flow cytometry PCK.

Key: Knowledge of Flow principles; Knowledge of students' understanding of Flow; Knowledge of Flow instructional strategies; Knowledge of assessment of effective Flow practices

Topic: Controls are vital in any flow cytometry experiment to provide the context within which one can interpret test samples to reliably distinguish the results from background variation and non-specific effects	**Core concept 1:** Isotype controls are not 'real' controls
What is most important for students to know about this idea?	It is **almost impossible to achieve a useful isotype control** as it should be the same isotype, both in terms of species, heavy chain (IgA, IgG, IgD, IgE, or IgM) and light chain (kappa or lambda) class, the same fluorochrome (PE, APC, etc.), and have the same F:P ratio.
Why it is important for students to know this?	Classically isotype controls were meant to show what level of nonspecific binding you might have in your experiment. The idea is that there are several ways that an antibody might react in undesirable ways with the surface of the cell but **not all undesirable binding can be directly addressed by an isotype control.**
What else do you know about this idea (that you do not intend students to know yet)?	Viability dyes are essential for removing **dead cells that will loose membrane integrity, become sticky and non-specifically uptake antibodies** like isotype controls.
Difficulties connected with teaching this idea	Isotype controls were historically used for flow cytometry experiments and **still described in many texts book as appropriate controls**. Many supervisors and paper reviewers still request the inclusion of isotypes.
What do you know about students' thinking that influences your teaching of this idea?	Ensure that the **learning is scaffolded**. The antibody structure (heavy chain, light chain), flurochomes, F:P are explained individually. The students need to be able to understand and visualise how all concepts influence each other.
Other factors that influence your teaching of this idea	To **avoid misconceptions, alternatives to isotypes must be discussed** and the context of their use, e.g. FMOs in multicolour analysis when spectral overlap is occurring, Fc-block if using myeloid cells.
What teaching strategy/ies will you use to support student learning of this idea? Why were they chosen?	**Activity presenting students with different experimental questions/conditions to select a more appropriate control** than isotypes, e.g. cell signaling and the requirement for unstimulated control or phosphorylation inhibitors), inclusion of protein knockout.
How will you ascertain students' understanding or confusion around this idea after teaching them?	Mix and match; practice questions using experimental data.

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Preparing the Next Generation of Students for AI-Driven Biomedical Research: Opportunities in Higher Education

Joshua Hardy, Dylan Silke, Ashley Weir, Daniel Brown, Kerry Ko, Brendan Ansell, Jessica Borger and Megan Taylor

Walter and Eliza Hall Institute of Medical Research and Department of Medical Biology, University of Melbourne

The rapid advancement of artificial intelligence (AI) in biomedical research has accelerated scientific discovery, particularly in fields like *de novo* protein design. A recent University of Melbourne, Bachelor of Science Honours project, jointly supervised in the Lucet and Papenfuss labs, at the Walter and Eliza Hall Institute of Medical Research (WEHI) exemplified this potential, showcasing the power of interdisciplinary collaboration between experimental and computational scientists in *de novo* protein design. Recognising the need to prepare future biomedical researchers for an AI-embedded research landscape, we have conceptualised a new subject that incorporates coding and AI literacy in a biomedical research context.

ProteinDJ: where bench science meets AI

Protein binders can be engineered to recognise and specifically bind to a defined target protein to support its visualisation or enact post-translational modifications, relocalisation or degradation.

ProteinDJ, a new tool for *de novo* protein binder design, was developed using funding from the NHMRC. It was part of a novel research project that brought together a supervisor with extensive structural biology knowledge and a student with strong computational skills and AI expertise.

ProteinDJ integrates deep learning AI tools AlphaFold2 (1) and ProteinMPNN (2) with the *de novo* protein design tool RFDiffusion (3), to generate novel functional protein binders. Using AI and coding, the student developed this user-friendly package that can leverage high-performance computing systems, dramatically speeding up binder generation (**Fig. 1**). ProteinDJ implements new metrics to evaluate binder quality, including their biochemical attributes such as hydrophobicity, size and charge, with visual plotting of results to help with design filtering and selection. The designs can then be validated by wet lab researchers, using *in vitro* binding assays and assessing functional impact.

The success of the ProteinDJ project highlights the importance of collaboration between experimental and computational scientists to integrate traditional wet lab techniques with cutting-edge AI technologies. To address the rapidly evolving landscape of biomedical research and the growing role of AI, the Scientific Education team at WEHI have developed a new Master of Biomedical Science elective subject, Coding and Data Analysis in Biomedicine, at the University of Melbourne.

Preparing biomedical graduates for AI-integrated biomedical research

The Coding and Data Analysis in Biomedicine graduate subject combines theoretical lectures and tutorials presented by leading experts in biomedical research with hands-on coding workshops. The subject aims to equip students with the core skills needed to succeed in an AI-embedded research environment.

The lecture series exposes students to a broad range of computational approaches used in biomedical research. For example, one lecture introduces students to core principles of machine learning and how these tools are evaluated and applied in biomedical datasets (4). In another, Professor Jodie McVernon explores the use of modelling techniques in interdisciplinary settings,

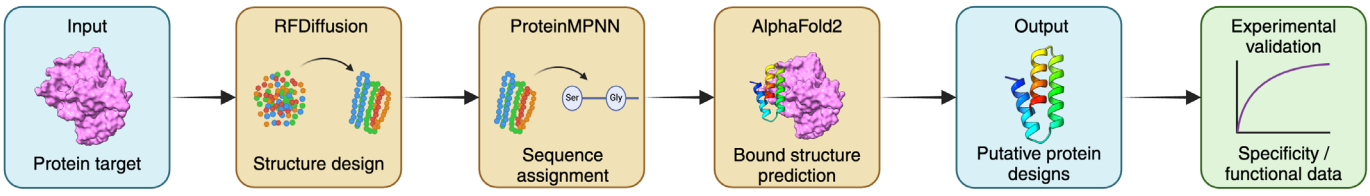

Fig. 1. Overview of the ProteinDJ* de novo *protein binder design pipeline. *The target protein structure is supplied to RFDiffusion, which generates thousands of potential binder structures through iterative refinement. The output structures are supplied to ProteinMPNN, which generates a feasible sequence for each putative binder. Finally, AlphaFold2 is used to validate each binder–target structure. The putative protein must then be validated experimentally to check for specificity of binding to its target and functional impact. Created in biorender.com*

such as COVID-19, demonstrating how computational tools can inform public health decision-making (5).

In parallel, the subject offers a series of coding workshops in which students learn to program using R. These workshops build foundational coding skills and expose biomedical students to one of the languages commonly used by computational biologists. This shared understanding enhances communication between biomedical and computational researchers, fostering more effective interdisciplinary collaboration. For some of the biomedical science students, these workshops may serve as an entry point into computational biology and may inspire a transition into AI and machine learning careers.

Ultimately, this subject aims to build students' confidence in using AI tools and navigating the intersection of computational and biological approaches. By integrating these skills, students will be better prepared to undertake research projects that combine AI and biomedical science, accelerating discoveries and contributing to the next generation of AI-embedded biomedical research.

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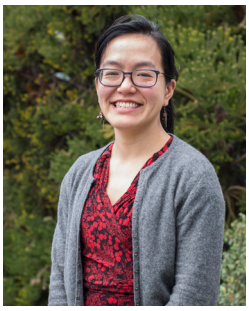

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Education Activities at the 31st FAOBMB Conference in Busan, Korea

Tracey Kuit

School of Science, University of Wollongong

Tracey Kuit presents the 2025 FAOBMB Education Award Plenary.

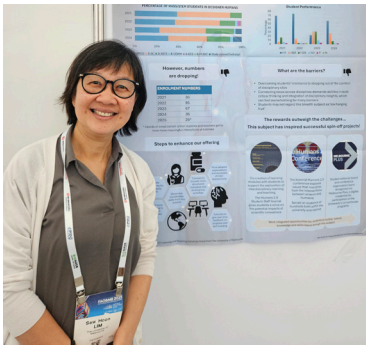
FAOBMB 2025 provided a space for education enthusiasts across the globe to gather, share ideas and explore future opportunities in a relaxed atmosphere, supported by a great location, venue and wonderful hosts. The Education activities started with three fantastic presentations in a session chaired by Professor Yang Mooi Lim (Universiti Tunku Abdul Rahman, Malaysia) and Professor Gracia Fe Yu (University of the Philippines). Associate Professor Zhi Xiong Chen (National University of Singapore), who is involved in the education of medical, dental, pharmacy and life sciences students, shared with us how he is exploring ways to broaden education for health professionals and promote transdisciplinary learning. Zhi Xiong shared his specific interests of the role of medical sciences in health professions practice, faculty development, student affairs and medical education technology. Zhi Xiong also shared the importance of medical education focussing on pressing global health challenges, such as unhealthy aging, metabolic disorders and mental health. He shared his experiences in creating a common curriculum across diverse courses in medicine, pharmacy, dentistry and nursing using a systems-based approach and pedagogical reform to integrate disciplines and use of supportive GenAI technology.

Dr Matthew Clemson (University of Sydney) was next to present on approaches to assessment and the creation and utilisation of a GenAI tool using the Cogniti platform to create a Socratic Tutor – Dr MattTabolism. Matt took the audience through the journey of creation of the GenAI-driven tutor, the affordances to make learning biochemistry more accessible and enjoyable for students, but also the space it creates for the teaching team. Dr MattTabolism helps the students think critically and clarify their understanding through a prompted conversation. Matt took us through various ways the student conversations with the GenAI-driven tutor can be used to understand emerging themes of confusion for students, increasing student use of technical terms or higher levels of learning, whilst also understanding the AI's pedagogical approaches. These are a few of the areas Matthew has explored in his groundbreaking AI-based approach to biochemical education.

Professor Mo Mo Than (Defence Services Medical Academy (DSMA), Myanmar) shared with us the journey of transitioning DSMA, one of Myanmar's medical universities, to an outcome-based integrated program in line with the World Federation for Medical Education Basic Medical Education Standards. She shared the team's approach and subsequent evaluation that shows significant progression towards a quality culture. Concluding that structural improvements, regular training programs and ongoing evaluation are essential to strengthening the internal quality assurance framework and fostering a quality culture at DSMA. The successful implementation of quality assurance program depends on teamwork amongst leadership, academics and all stakeholders. This presentation was supported by a poster during the Education poster session.

Following these presentations, Associate Professor Nirma Samarawickrema (Monash University) and Professor Ferhan Sağın (Ege University, Turkey) facilitated a joint FAOBMB–FEBS interactive session on active learning strategies in constrained spaces. In the workshop, attendees explored the importance of active learning strategies, reflecting on how this could be achieved within their differing contexts. Participants joined in Kahoot games, IF-AT scratch cards, videos, team discussions and sharing. Much fun (and chocolate) were had by all.

Associate Professor Saw Hoon Lim (University of Melbourne) presented a poster on the roadblocks and rewards of interdisciplinary teaching through an exploration of the subject Designer Humans: Prospects and Perils. This subject, taught by a team from the School



Saw Hoon Lim presents her poster.

ASBMB Education Feature

of Biomedical Sciences and the School of Historical and Philosophical Studies, has students explore challenging topics through the lens of scientific, technical, ethical, legal and social implications. An ongoing challenge is supporting students to step out of the comfort of their disciplinary silos.

Professor Tracey Kuit (University of Wollongong) gave the FAOBMB Education Award Plenary Lecture. Tracey focussed on how modern science education can support students to tackle real-world sustainability challenges through a focus on interdisciplinarity and teamwork. Tracey shared examples of how she has scaffolded learning within and outside formal curriculum to bring interdisciplinary teams of students together to tackle the targets of the United Nations Sustainable Development Goals. Using the principles of Universal Design for Learning to support student choice and creative problem-solving, Tracey has teamed with academics, industry, community and students in this design and delivery, ultimately showing the development of key transferrable skills in critical thinking, creative problem-solving, communication and teamwork.

The next major conference on Education in Biochemistry and Molecular Biology in the FAOBMB region is the IUBMB Education Symposium 2025 in Kuala Lumpur, Malaysia, from 25–26 August 2025.

Education presenters and chairs, from left: Gracia Fe Yu, Mo Mo Than, Zhi Xiong Chen, Matthew Clemson, Joon Kim (FAOBMB President), Ferhan Sağın, Nirma Samarawickrema and Yang Mooi Lim.

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From Pipettes to Partnerships: Turning a Life Science PhD Into SME Impact at CSIRO

Rhea Cornely

Mid-way through my PhD in cell biology, everything that could go wrong did. Experiments sputtered, the mouse colony bred off-schedule, and my supervisor and I were pulling in different directions… a postdoc, let alone an NHMRC grant, suddenly felt like a long shot.

Still, I wasn't ready to walk away from science. So, I wrapped up my thesis and started knocking on new doors, doors that opened onto research–industry collaborations rather than traditional academia.

My first stop after the PhD was selling high-end cell separation reagents. I'd never carried a sales target before, but years of decoding protocols meant I could translate dense chemistry into plain English – exactly what lab managers needed. Talking with scientists from different fields, but with similar methods, felt like a breath of fresh air.

When budgets tightened and sales dipped, I had to change to a different sales role with a portfolio centred around pipetting. When a customer mentioned an opening in a university next-gen sequencing facility, I swapped suits for lab coats and began programming liquid-handling robots and streamlining sample pipelines. I arrived knowing little about sequencing but armed with classic PhD super-powers: experimental design, troubleshooting, and obsessive documentation. I discovered I love teaching machines to pipette.

Those automation and sequencing tricks landed me in a biosensor start-up, where my team and I were building biosensor prototypes. The can-do energy was exhilarating, but science is fickle, and the functioning sensor we had our hearts set on was not going to be realised anytime soon. Time to pivot again.

Scrolling job boards, one ad jumped out: Facilitator, CSIRO SME Connect – Kick-Start.

CSIRO Kick-Start offers Australian startups and small businesses dollar-matched funding of $10,000–$50,000 and a direct line to CSIRO expertise. Since 2017, it has supported over 280 projects, channelled $24 million into R&D, and helped alumni top $2 billion in combined value.

My day now? I screen founders with innovative ideas across food tech, renewables, health and mining who need R&D support for their products. When there's a good fit, I connect them with the CSIRO researchers who can make it happen. My role combines the following aspects of my career experience:

- Critical thinking and experimental design skills I developed during my PhD enable me to detect flawed hypotheses and missing controls before any financial commitment is made.
- My technical expertise from sales and automation enables me to understand the connection between business terminology and laboratory scientific methods.

So, I still "do science", but from the vantage point of a matchmaker, connecting problems with people who can solve them.

Three takeaways for PhD and ECR readers

- **Track your portable skills early.** Jot down what every experiment really teaches you, like data wrangling, project planning, persuasion.
- **Treat each coffee as fieldwork.** My sales break began with cold calls; many Kick-Start projects still surface over conference chats or a LinkedIn DM. Curiosity compounds.
- **Industry links supercharge careers.** CSIRO Kick-Start, for example, values individuals who can convert research concepts into business ideas. Your discipline knowledge is a feature!

Links

CSIRO Kick-Start
CSIRO SME Connect

Rhea Cornely studied biochemistry in Germany and completed a PhD in immunology and cell biology at UNSW Sydney. Today, Rhea helps connect small businesses with CSIRO researchers to develop new innovative products.
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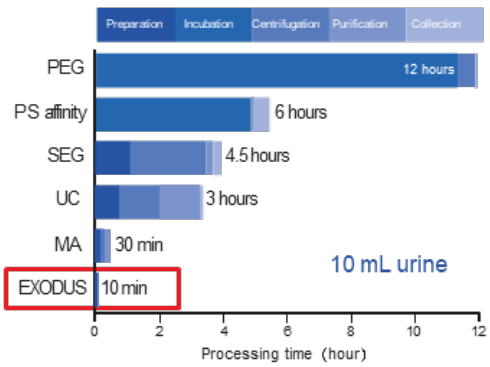

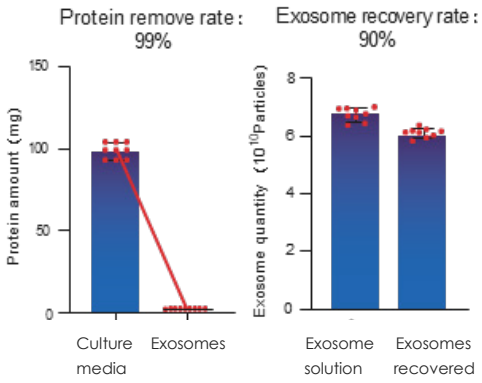

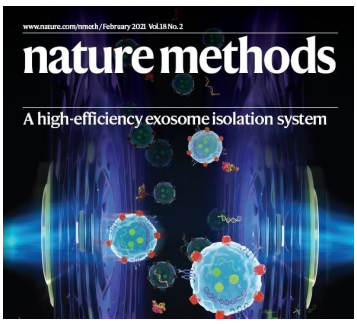

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Science Meets Parliament 2025

Praveena Thirunavukkarasu at Parliament House, Canberra.

Science Meets Parliament (SMP) is the flagship event hosted each year by Science & Technology Australia (STA), bringing together professionals from the science, technology, engineering and mathematics (STEM) sectors with the nation's policy-makers. This year marked a remarkable milestone for SMP, as it celebrated its 25th anniversary, reinforcing its role in fostering meaningful connections between researchers and policy-makers. SMP has provided scientists with invaluable opportunities to engage with parliamentarians, enhancing their ability to communicate research effectively and contribute to science-informed policy-making.

A week prior to the SMP event, we received instructional videos on *Practice Your Pitch* by Dr Lila Landowski (Vice President, STA, and Lecturer, University of Tasmania) and Tanya Ha (Director of Engagement, Science in Public). They highlighted the importance of delivering a compelling pitch, incorporating an analogy to effectively engage parliamentarians and communicate our science. Additionally, we had a video on *Preparing to Meet a Parliamentarian*, led by ATSE CEO Kylie Walker and Associate Professor Jeremy Brownlie. This session provided insights into what to expect during the meetings, strategies for a successful interaction and best practices for follow-up.

I had the privilege of attending the two-day event in Canberra on 12–13 February. It was an eye-opening experience. The program provided deep insights into how the government and policy-makers work towards the advancement of science in Australia. Through keynote sessions, panel discussions and interactive workshops, I gained a better understanding of the policy-making process, the role of advocacy in science and how researchers can effectively contribute to national decision-making.

Day 1 kicked off with a welcome to the country from Ngunnawal Traditional Custodian and Elder, Aunty Serena Williams, followed by an opening address from STA President Professor Sharath Sriram and STA CEO Ryan Winn, marking the opening of SMP2025. The first session, *Navigating Democracy: A Beginner's Guide to Civics*, featured a conversation with Anna-Maria Arabia (Chief Executive of the Australian Academy of Science) and the Hon Bill Shorten (Vice-Chancellor and President of the University of Canberra). They discussed how to effectively communicate research while aligning with policy-makers' interests. They encouraged us to be ambitious in what we ask for and to articulate our claims with clarity.

The second session on *Leading with Science: Elevating STEM for Economic Growth* encompassed a panel discussion with Professor Sriram, Jas Chambers (President-Elect, STA), Dr Raj Aseervatham (National President and Chair, Engineers Australia) and Professor Reuben Bolt (Deputy Vice-Chancellor First Nations Leadership, Charles Darwin University, Northern Territory). The discussion highlighted the lack of awareness and education about STEM careers, and how discovery science requires decades to yield results.

This was followed by a session where current and former policy advisors shared their insights into their roles in supporting Ministers, Members of Parliament and Senators in the policy-making process. The sessions, titled *From Research to Reality: The Role of Policy Advisors in Decision-Making* and *Turning Passion into Action*, explored how advisors help translate research into practical policies and guide evidence-based decision making. Afterward, we watched a National Press Club Address by the Hon Ed Husic MP, Minister for Industry and Science, who underscored the significance of quantum computing, its potential for early bushfire detection to the next generation of robotics.

Pitch Perfect: How to Talk About Your Science to the Media featured distinguished speakers including Dr Lila Landowski, Tanya Ha, Dr Nicholas Coatsworth (former Deputy Chief Medical Officer, Australian Government) and Dr Vanessa Pirotta (Chief Scientist, Wild Sydney

From left: Dr Praveena Thirunavukkarasu, Dr Simone Li and Dr Claudia Del Campo (all Monash University).

Science Meets Parliament 2025

Science & Technology AUSTRALIA

Harbour). Two key messages were that "science is not finished until it is communicated" and "be yourself – because everyone else is already taken." The session reinforced the need to make an impact, capture people's attention and tailor communication to the audience while speaking clearly, confidently and passionately.

We concluded the day with a Welcome Reception and Gala Dinner, with the theme *A Night at the Museum*, a spectacular black-tie event with a record 500 attendees. We enjoyed a vibrant dance performance by Aunty Serena and her children, and had the chance to network with scientists from various backgrounds. A highlight of the evening was the presence of Her Excellency, the Hon Sam Mostyn AC, Governor-General of the Commonwealth of Australia, who delivered a speech reflecting on the significant achievements of SMP over the past 25 years. She left us with two key thoughts: the critical role of collaboration and trust in science, as well as their broader impact on civic life. She emphasised that these principles are essential to the nation's progress and success.

The Day 2 sessions highlighted the parliamentarians' perspectives on policy development and the research that happens behind the curtain to support policy-making. I was intrigued to learn that hundreds of dedicated researchers work at the Parliamentary Library, providing confidential insights to parliamentarians and supporting the policy-making process. A key session focused on *Using STEM for the greater good*, where Professor Brett Sutton (Director of Health and Biosecurity, CSIRO) and Senator Dr Mehreen Faruqi (Deputy Leader, Australian Greens) shared their experiences of transitioning from the lab into the realms of politics and industry to drive national progress. They discussed the importance of perseverance, encouraging us to embrace challenges and leverage our expertise to influence policy-making and create a meaningful impact on the nation's future.

I had the opportunity to meet the ALP Member for Adelaide, Steve Georganas MP, in his office, alongside two fellow scientists. We began by introducing ourselves and presented our research, with each of us delivering a brief pitch. I spoke about my T cell research, explaining their critical role in combating infections and their significance in the immune system. I also discussed how we use the Australian Synchrotron to study the molecular structure of various protein–protein complexes. I was pleasantly surprised by Mr Georganas' genuine curiosity and engagement with our work. He asked thoughtful questions, demonstrating a keen interest in understanding the details of our research. This meeting was a unique and valuable experience, allowing me to communicate complex scientific concepts to a policy-maker. Additionally, I took the opportunity to advocate for increased and recurring funding for early-career researchers, and the importance of sustained investment in scientific research to drive innovation and progress.

Since it was a Parliament sitting week, I was fortunate to attend a one-hour tour of Senate Question Time. It was fascinating to observe how Members of Parliament debated pressing national issues. The discussions covered topics such as tax changes affecting Medicare and bulk billing, as well as the approval of certain medications for various diseases.

SMP2025 was an inspiring and transformative experience that allowed me to see science beyond the laboratory and understand its crucial role in shaping policy decisions. The event highlighted how scientific expertise is valued in policy-making and reinforced the importance of effective science communication in influencing national strategies. I highly recommend that scientists participate in SMP in the future, as it provides a unique opportunity to see science through the lens of politicians, engage in meaningful discussions with policy-makers, and advocate for evidence-based decision-making. The experience not only broadened my perspective, but also strengthened my ability to communicate the impact of my research in a way that resonates with stakeholders beyond the scientific community.

I would like to express my sincere gratitude to the ASBMB for supporting my participation in this event. SMP was an unparalleled opportunity to appreciate the significance of my research and explore ways to contribute more effectively to Australia's scientific and policy landscape. This experience has further motivated me to actively engage in science advocacy and work towards the betterment of Australian science and innovation.

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From left: Dr Kristina Konstas (CSIRO), Dr Amy Wilson (Ovarian Cancer Research Foundation), Steve Georganas MP and Dr Praveena Thirunavukkarasu.

ASBMB Awards 2026

SOCIETY MEDALS, AWARDS AND FELLOWSHIPS NOW OPEN

Nomination/application forms for the
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Nominations/applications must be submitted
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There are membership requirements for all
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NOMINATIONS FOR MEDALS AND AWARDS

*The **Lemberg Medal** is awarded to a distinguished ASBMB member who will present the Lemberg Lecture at the ASBMB annual scientific meeting. The Medal is presented in memory of Emeritus Professor M.R. Lemberg who was the Society's first President and Honorary Member. The award will be made to an individual who has demonstrated excellence in biochemistry and molecular biology and who has made significant contributions to the scientific community. An honorarium is provided by ASBMB.*

*The **Shimadzu Research Medal** is awarded to an outstanding ASBMB member with no more than 15 years since the award of the PhD degree (or equivalent taking any career disruption into account) at the nominated deadline. The successful candidate will present the Shimadzu Medal Lecture at the ASBMB annual scientific meeting. An honorarium is provided through the courtesy of Shimadzu.*

ASBMB Awards 2026

APPLICATIONS FOR TRAVEL AWARDS AND FELLOWSHIPS

*The **Eppendorf Edman ECR Award** is awarded to an ASBMB member with no more than 7 years postdoctoral experience (or equivalent taking any career disruption into account), in recognition of their outstanding research work. The Award provides funds to assist the recipient to attend an overseas conference in a field associated with biochemistry or molecular biology or to visit briefly a research laboratory in Australia or elsewhere to access specialised equipment or to learn new research techniques. The recipient will give a talk at the ASBMB annual scientific meeting. The contribution to travel expenses is provided through the courtesy of Eppendorf South Pacific.*

*The **SDR Scientific Education Award** rewards outstanding achievement in education in biochemistry or molecular biology, especially innovation and creativity in education, with a view to fostering leadership in this important area of the Society's objectives. The Award will enable the recipient to participate in an international conference with a significant focus on education, or to spend a period of time at another institution for the purposes of undertaking developments in education in biochemistry and molecular biology. The recipient will present a lecture within the Education Symposium at the ASBMB annual scientific meeting. The contribution to travel expenses is provided through the courtesy of SDR Scientific.*

*The **Boomerang Award** is awarded to an outstanding expatriate Australian biochemist or molecular biologist to allow them to return to Australia to present their work in a symposium the ASBMB annual scientific meeting and to give seminars at universities or research institutes. This will provide the awardee with exposure in Australia and will facilitate interactions with local researchers. The Award makes a significant contribution to the cost of a return airfare and accommodation for the ASBMB annual scientific meeting, and towards domestic travel expenses to visit at least one other Australian city. Applicants must have been awarded their PhD not more than 10 years prior to the closing date (or equivalent taking any career disruption into account). The contribution to travel expenses is provided by ASBMB.*

*The Awards Committee will also award several **ASBMB Fellowships** to postgraduate students who are no more than 2 years prior to the completion of their PhD degree or recently graduated postdoctoral researchers no more than 2 years subsequent to the award of their PhD degree. The contribution to travel expenses is provided by ASBMB. The most outstanding ASBMB Fellowship applicant may receive the **Fred Collins Award**. These travel grants are awarded to early career researchers, normally resident in Australia, in recognition of their outstanding work in an area of biochemistry and molecular biology. The Fellowships provide funds to assist the recipient to attend an overseas conference in a field associated with biochemistry or molecular biology, or to visit briefly a research laboratory in Australia or elsewhere to access specialised equipment or to learn new research techniques.*

Patenting Insights From Researchers-Turned-Patent Professionals

Dr Harriet Keenan (Associate) from FPA Patent Attorneys speaks to colleagues about their work as patent attorneys.

Harriet Keenan.

Introduction

I asked three colleagues, Dr Lap Hing (Leo) Chi, Dr Marie-Claire Giel, and Dr Andrew (Andy) Foers, to share some thoughts about how their views on patenting and the role of patent attorneys changed upon recently transitioning from working as research scientists, to working as patent scientists (trainee patent attorneys).

This article aims to provide some insights from "the other side" and dispel some common misconceptions that researchers (including us in our past vocational lives) may hold regarding the patenting process.

The role of patent attorneys and preparing patent applications

Patent attorneys in Australian and New Zealand can be confused as lawyers, but there are distinct differences. Firstly, registered trans-Tasman patent attorneys must have a technical background. Patent attorneys in the life sciences often have PhD qualifications and prior experience as academic researchers. Secondly, a key function of patent attorneys is to draft (prepare) and file patent applications, which intellectual property (IP) lawyers in Australia or New Zealand are not permitted to do, unless they are supervised directly by a registered patent attorney.

Leo's initial view of patent attorneys was that they focused mainly on the legal aspects, but Leo found they in fact have a strong technical background and focus on understanding the underlying technology in the context of patent law: "While the law is a critical component of patent attorney work, patent attorneys need to hone in on the science of the inventions so as to understand and effectively protect them. Patent attorneys can also provide insights as to what further experimental data may overcome potential hurdles and even suggest experimental designs."

Marie-Claire found patent attorneys were more involved in commercialisation than she expected. An appropriate patent filing strategy is closely intertwined with commercial goals, for example: what should be drafted and when in consideration of expected commercial milestones, should there be single application to manage costs, or multiple applications to produce a diverse patent portfolio. Commercial factors similarly interplay with patent prosecution strategy – e.g. which claims are required for the patent to have commercial value versus which claims can be amended or deleted, and in which countries/jurisdiction should patent protection be pursued.

Leo initially thought that patent drafting would be a simple process of just copy-pasting data provided by inventors and using standard legal language. However, Leo found that patent specifications are complex legal documents and that their preparation requires critical analysis and iterative, ongoing communication between patent attorneys and inventors. To draft a valuable patent application that accurately protects the commercial invention whilst also preventing competitors from easily designing-around the invention to avoid patent infringement, Leo says that "most of the statements written in a patent application are the result of carefully considered and balancing thoughts."

The importance of patentability assessments

Many technology transfer (TT) or commercialisation offices at research institutions undertake patentability assessments of potential inventions, which researchers describe in an invention disclosure form. Patent attorneys are often enlisted to assist with these processes and provide a recommendation regarding whether the invention would meet requirements to be eligible for patent protection, and could form the basis for filing a patent application.

Leo was unaware of how valuable these initial patentability assessments could be before filing a patent application: "the process prevents wasting resources on inventions that are identified as clearly lacking in novelty due to a so-called "knock-out" prior art document."

Marie-Claire was surprised by the strong focus on identifying prior art that could render an invention lacking novelty, rather than assessing inventive step, during patentability assessments. She explains that whilst inventive step objections are commonly raised by patent examiners during the patent prosecution process, and are almost to be expected, it is very difficult to assess the prior art and predict which particular documents may be raised by the examiners. During patentability assessments, a strategy is often to consider potential inventive step arguments that you make later If objections are raised, based upon the core advantages of the invention.

I was surprised by what is considered likely to be legally inventive or non-obvious – it can often be less innovative or ground-breaking than you would think. Working in academic science, I assumed that many of the experiments I was involved in were the next obvious step, because I was following on from what I had done before in a way that made sense to me in view of my expertise in that particular research area.

Patenting Insights From Researchers-Turned-Patent Professionals

From left: Andy Foers, Marie-Claire Giel and Leo Chi.

However, researchers are frequently surprised that what they consider an obvious step may arguably not be obvious in a legal sense, when considered in view of the hypothetical "skilled person" (a person skilled in the field of the invention but not applying inventive input). The choices/selections that scientists make, particularly combinations of choices, can result in an inventive product or method if it can be argued that the selections were not routine and/or provided an unexpected result compared to other possible selections. Moreover, the path chosen to overcome a development problem may not be obvious to the skilled person, which can support an argument of inventiveness.

Disclosures

Public disclosures that make up the prior art for novelty and inventive step assessment can include a range of documents and activities, not just published journal articles. Other forms of potential disclosures relevant to academic research settings include conference presentations, posters, abstracts, online pre-prints (e.g. bioRxiv), and non-confidential funding applications. Leo stressed that pre-prints can often be overlooked because they are not considered a "final" product, but by being published online, they can represent a disclosure that could jeopardise future patenting prospects.

Andy recalls the tension he experienced as a postdoctoral researcher, trying to present exciting new data at a conference, but coming up against IP disclosure restrictions from the pharmaceutical company that was funding his position. As part of his fellowship contract, Andy had to send his conference abstract to the company for approval before presenting. The company did not approve him presenting the data at the conference, and Andy felt he had been blocked from an opportunity to receive valuable feedback from his peers regarding the project. However, after six months working as a trainee patent attorney, Andy now says he completely understands the company's decision; agreeing that "even a simple poster presentation at an academic conference would be considered prior art that could negatively impact the patentability of the invention."

Ultimately, for Andy's research to have translational impact via the pharmaceutical company's engagement and investment, ensuring a safe IP position was more important. Of course, there are options other than simply not presenting at a conference that can reduce the risk of a harmful disclosure, whilst facilitating academic participation and knowledge-sharing.

With his increased awareness for patents in general, Leo was also interested to notice that many published academic journal articles declare earlier patent filings associated with the work. This is indicative of a strategy where inventors ensure their patent application is filed first, to secure a priority date and pursue patent protection for their inventions, before disclosing said inventions in an academic journal article.

Leo now recommends that academic researchers include searching patent literature as well as scientific literature. Patent applications disclosed by other parties can be used to the advantage of academic researchers when conducting literature searches to identify new research avenues and "gaps" in a given field. Searching patent literature, like Google Patents or WIPO Patentscope, can identify previous work not yet published academically but disclosed in patent filings.

Data for patent applications

Both Leo and Marie-Clarie's perceptions shifted regarding how much data is needed to file a patent application when they became trainee patent attorneys. Leo learned that limited data can still form the basis of an initial provisional filing, with more data added later when the complete/PCT application is filed, rather than needing a full data package upfront. Marie-Claire agreed, "I think there is a misconception that the data requirements for patents are higher than they are. There is a conflation that what is needed for journal article acceptance or grant funding approval is exactly what is needed for a patent application."

Adding to this, Leo emphasised "the more data the inventors provide, the more likely it may be that a broader scope of patent protection is obtained. However, waiting for more and more data might not be justified if

Patenting Insights From Researchers-Turned-Patent Professionals

it significantly delays a patent filing, which in turn could delay paper submissions, grant applications, and/or commercial negotiations."

The value of patents

As an academic researcher, Leo feels he underestimated the importance of patents as a core feature of the commercialisation pipeline for pharmaceuticals. He now sees securing IP as critical for enabling companies to invest in drug development and to ultimately recover costs, which is essential for translating research into practical applications. And from Leo's experience, "patent coverage assessment is a key component of due diligence before companies invest in the development of a drug," so it is important that patents which are granted have claims that accurately "cover" and provide protection for the commercial product.

Take-home messages

Thank you to Leo, Marie-Claire and Andy for their contributions! Some key themes arose when comparing what they know now as trainee patent attorneys, to what they thought then as academics:

- Patenting, including drafting patent applications, is a complex, collaborative process between inventors and patent attorneys, where patent attorneys require a strong understanding of the technical details of the invention as well as legal requirements.
- Researchers should be aware that even seemingly innocuous public disclosures, like poster presentations or pre-prints, can compromise future patent protection – and careful IP management is essential for research to have commercial impact.
- Conducting initial patentability assessments can save valuable resources by identifying early inventions that are unlikely to meet the legal requirements for patent protection.
- The data requirements for filing a patent application are often less than researchers assume, and the amount of data needed is not the same as that for a journal article or grant application.
- The value of patents, particularly for translating research into commercial outcomes, is often underappreciated by academics – patents play a critical role in enabling investment and drug development.

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30th FAOBMB Conference

Phillip Nagley and Dominic Ng report on the FAOBMB Conference held in Busan, Korea, and the FAOBMB Council meeting.

FAOBMB2025, the 31st FAOBMB Conference and Korean Society for Biochemistry and Molecular Biology (KSBMB) International Conference, was held at the Busan Exhibition and Convention Center (BEXCO), South Korea, from 20–23 May 2025. The pleasant springtime weather enabled visitors to enjoy the local sights, including Haeundae Beach.

Professor Bong-Kiun Kaang led the organisation, together with Professor Joon Kim (President of FAOBMB). Preceding the conference, there was a Young Scientist Program from 18–20 May (see report on page 36) and the FAOBMB Council Meeting on 19 May.

FAOBMB2025 was hosted by the KSBMB. The conference attracted over 4,000 participants from 27 countries across the region and beyond. There were 43 participants from Australia. The theme of the conference was Revolution in Biomedical Science. The majority of presentations (and all of the Plenary Lectures) described research using molecular approaches to problems that had application in a wide range of biomedical sciences, including neuroscience, genetic diseases, cancer, immunology and physiology.

Sand sculptures at Haeundae Beach. Bottom, from left: Phillip Nagley, Terry Piva, Melody Tang, Rasika Perera, Chyan-Leong Ng and Shannon Au.

FAOBMB Council Meeting

The FAOBMB Council Meeting was held before the commencement of the conference. Delegates to Council of 16 of the 20 Constituent Members of FAOBMB (national Societies or Groups) were represented at the meeting, either in person or on Zoom, in addition to the six members of the Executive Committee (EC) and a number of observers from various countries. Australia was represented by Terry Piva (Secretary General and FAOBMB Regional Ambassador of IUBMB), Nirma Samarawickrema (Chair of the Education Committee), Phillip Nagley (Archivist and Secretary) and Dominic Ng (ASBMB Representative to FAOBMB). The Council Meeting was chaired by Professor Joon Kim and Professor Terry Piva. In his President's report, Joon Kim noted that the activities of the Federation have returned to normal following the challenges of the COVID-19 pandemic. However, participation in conferences, symposia and congresses had been relatively low and declined further during the pandemic. He emphasised that now is the time to reverse this trend by actively encouraging attendance at FAOBMB annual meetings.

Shannon Au (Treasurer) reported on the financial status of the FAOBMB accounts, the subscription status of constituent members and the budget plans for 2025 and 2026. In his Fellowships Chair report, Rasika Perera reported on the role of FAOBMB in providing YSP Fellowships awarded both in 2024 to the YSP associated with the Congress in Melbourne (26 participants from the FAOBMB region, with ten more from other regions, given that this YSP was also supported by IUBMB) and in 2025 to the YSP event in Busan (30 international participants). Regarding Education Special Travel Fellowships, one had been awarded to participate in the Congress in Melbourne in 2024, and one was awarded to Professor Lt Col Mo Mo Than (Myanmar) to enable her participation in the Conference in Busan in 2025 (see the report on the Education Activities at FAOBMB2025 on page 19). Finally, one FAOBMB Exchange Fellowship had been awarded in late-2024 to a student from Birla Institute of Technology and Science (BITS) India, to travel to UNSW to undertake the laboratory work required for part of his PhD research.

Nirma Samarawickrema reported on the planning of the Education Activities at the Busan Conference. She outlined progress in establishing a cohort of Education Lead people within various Constituent Member countries in the FAOBMB region. There are now BMB Education Leads in six countries (Australia, New Zealand, Thailand, Sri Lanka, Malaysia and China). Following publication online of the first Education Newsletter, the FAOBMB Education Committee invites submissions for the newsletter (500–600-word writeups from educators about an education-related issue/event/innovation/teaching approach).

Reports were presented from the 26th IUBMB–17th

FAOBMB2025 Co-Chairs Joon Kim (left) and Bong-Kiun Kaang.

FAOBMB Council Meeting participants.

FAOBMB Congress (Melbourne, 2024) and the 31st FAOBMB Conference (Busan, 2025). Progress reports on planning the next two annual meetings of FAOBMB were discussed, concerning the 32nd FAOBMB Conference (Hong Kong, 2026) and the 18th FAOBMB Congress (Kuala Lumpur, Malaysia, 2027). Bids to host the subsequent three annual events were accepted, the 33rd FAOBMB Conference (Bali, Indonesia, 2028), the 34th FAOBMB Conference (Tokyo, Japan, 2029) and the 19th FAOBMB Congress (Bengaluru – formerly Bangalore – India, 2030).

From the commencement of 2025, the offices of President-Elect and Secretary-General had been taken up by Chun Hung Hans Lin (Taipei, China) and Terry Piva (Australia), respectively. Expressions of interest will be called later in 2025 for the position of Treasurer, as the term of office of Shannon Au (Hong Kong, China) is due to end on 31 December 2025.

The FAOBMB2025 Conference

After the Opening Ceremony on 20 May, the scientific program commenced with the Lecture by this year's recipient of the FAOBMB Award for Research Excellence, Professor Sheng-Cai Lin (China). His lecture was entitled 'Glucose-sensing and pathophysiological implications in health and lifespan'. He focused on AMP kinase (AMPK) and mTORC1 as focal points for the sensing of low and high glucose, respectively, and applied his research to a wide range of issues in metabolic control in health and ageing, and also to cancer cells. He contrasted the actions of metformin (a general activator of AMPK) with those of a more focussed AMPK agonist aldometanib, which also has beneficial effects on fitness and lifespan in mice, as well being useful as an anticancer drug in some circumstances. The third pharmaceutical he considered was lithocholic acid, which mimics the effects of caloric restriction in mice, and whose downstream pathway of action intersects that of metformin. He emphasised that periods of caloric restriction or starvation are beneficial for longevity, working through glucose sensing pathways that aim to keep glucose as low as feasible for optimal function. The system operates across a range of metabolic checkpoints with control by AMPK being central to this.

The FAOBMB Education Award Lecture was delivered by Tracey Kuit (Australia), 'Tackling real-world sustainability challenges through a focus on interdisciplinarity and teamwork'. She described her personal and professional journey into BMB education and emphasised the importance of connections to promote a sense of belonging. To engender such sense of connection and belonging in first-year students, Tracey described a series of activities involving student team projects for a class of 800 students. These activities demonstrably opened the horizons of the students across a range of disciplines, instilled a sense of connection to other students, and developed their confidence through teamwork and self-expression within the student team project. Student peer evaluation protocols were central to being able to implement this approach in a large class. A further aspect concerned the topic of sustainability, which for many young people presents a depressing outlook. Tracey's approach was to develop team projects addressing microplastic pollution of seas and waterways, the outcome of which was not only about the scientific and technical feasibility of possible solutions, but also to instil hope in the minds of students to see pathways to a brighter, more sustainable future. In all of this, staff engagement must precede student engagement.

We were treated to a set of amazing Plenary Lectures, as well as the FEBS Lecture. Plenary Lecture 1 was delivered by Marcia Haigis (USA) who spoke on 'Lessons learnt from studying mitochondria in health and disease'. She first focused on the skewed metabolic processes in cancer cells (relative to normal cells) and how the expression of oncogenes may have an impact on such metabolic profiles. Further, she spoke on metabolites and ageing, in relation a number of topics, such as how obesity may affect anti-tumour immunity via impairment of T-cell activity, and how age affects the progression of lung cancers. She noted that a particular type of lung cancer can be suppressed in young patients by an antioxidant approach, which does not work for the same cancer in old patients (because they have depleted glutathione levels). Strikingly, glutathione-S-transferase inhibitors can alleviate certain lung cancers in young patients, but they exacerbate similar lung cancers in old patients. This has implications for how oncologists treat the same type of cancer in patients of various ages.

David Liu (USA) delivered a masterful Plenary Lecture 2 on the latest developments in gene therapy and genome editing to provide effective treatments (in some cases cures) for genetic diseases, 'Mutation-specific, mutation-agnostic, and disease-agnostic therapeutic genome editing'. Asserting avoidance of methods that involve double-stranded DNA breaks (as occurs with techniques

Tracey Kuit receives the FAOBMB Education Award from FAOBMB President Joon Kim.

Plenary Lecturer David Liu.

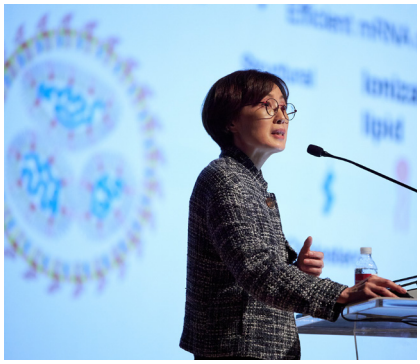
based on CRISPR-Cas9), he showed how base editing and prime editing can generate changes in specific bases in DNA at target sites in the human genome, illustrated by successfully treated patient cases. Liu described work with Sam Sternberg in the development of more efficient CRSPR-associated transposases (CASTs) using phage-assisted continuous evolution (PACE), which will be applied to the improved integration of novel gene-sized cassettes to modify target disease-causing genes. He outlined a novel approach aimed at using suppressor tRNA molecules to provide effective treatments for genetic disorders, involving readthrough of premature termination codons in the mRNA encoded by many disease-causing genes.

Nobel Laureate Thomas Südhof (USA) presented Plenary Lecture 3 on 'Molecular insights into long-term memory circuits'. He was awarded the Nobel Prize in Physiology or Medicine in 2013, for his discoveries on how nerve cells communicate with one another in the brain. He had identified the molecular machinery that responds to an influx of calcium ions and directs neighbour proteins rapidly to bind vesicles to the outer membrane of the nerve cell, causing release of neurotransmitters. Südhof's research explained how temporal precision is achieved and how vesicles' contents can be released on command. His talk focussed on the neural circuitry in the brain that underlies memory formation, at molecular, physiological and behavioural levels. In the context of the various steps in formation of memory, he expounded on his recent research into sensory inputs (including social interactions), memory acquisition (short-term memory), memory consolidation, memory storage, and memory recall and reconsolidation (long-term memory). Using a mouse model involving food preferences in context of socially exposed or solitary mice, he reported on his discoveries of the key molecular players in the acquisition and consolidation of memory, and on the distinct pathway for formation of long-term memory. As with his Nobel Prize-winning work on synaptic transmission, he showed that timing is everything for establishment of these neural circuits and emphasised the different regions of the brain in which these processes occur.

Plenary Lecture 4 was delivered by Narry Kim (South Korea) on 'mRNA stability control: Lessons from viruses and RNA therapeutics'. She began by outlining the now widely used process of introduction into cells of therapeutic mRNA wrapped in lipid nanoparticles (LNP), as is used in the so-called mRNA vaccines. Her research has determined the regulatory mechanisms impacting on exogenous therapeutic mRNAs, by conducting genome-wide knockout systems to find positive and negative regulators, the end-point assay being translational efficiency of particular test mRNAs. Both cell surface molecules (e.g. heparin sulphate proteoglycan) and internal enzymes (e.g. V-ATPase that acidifies endosomes) turned up as positive regulators, while negative regulators included TRIM25, an RNA-binding protein that interacts with proinflammatory factors. She also discussed viral RNA control in mammalian cells, particularly relating to the downstream Poly A tails on viral mRNA and their elaboration by terminal nucleotide transferases, especially TENT4 family members. TENT4 proteins can elongate Poly A tails with mixed sequences, delaying deadenylation and extending mRNA half-life. Using lessons learnt from what Kim termed the virosphere, application of such TENT4 -mediated modification of polyA tails to exogenous therapeutic mRNA increased protein output and duration of expression, both at the cellular level and *in vivo* in mice.

In Plenary Lecture 5, Kazutoshi Mori (Japan) first provided the background to his research on 'Dynamics of function and regulation of the endoplasmic reticulum', by taking the audience through his fascinating career, during which he discovered that the endoplasmic reticulum (ER) is a critical stress-sensing organelle. He discussed his seminal work identifying many of the protein components involved in the signalling mechanism that detects the accumulation of unfolded proteins in the ER, a process known as the ER stress response or the unfolded protein response (UPR). He shared insights from his more recent research on the knockout of AXER, an ATP/ADP exchanger on the ER membrane. This knockout leads to persistent ER stress and heart failure, highlighting the critical role of the UPR in the progression of various diseases.

The FEBS Lecture was presented for the first time in the context of the newly signed co-operative arrangement between FAOBMB and FEBS. This lecture was delivered at FAOBMB2025 by Irene Diaz-Moreno (Spain) on the topic of 'Biomolecular condensates and the hidden architecture of cells: from chaos to molecular order in health and disease'. The theme of this talk was based on the phenomenon of liquid–liquid phase separation (LLPS) that generates compartmentalisation of proteins to control biochemical reactions spatially and temporally. Nucleolar trafficking and arrest of mRNA translation in stress



Plenary Lecturer Narry Kim.

FEBS Lecturer, Irene Diaz-Moreno (left), and Jerka Dumic (session co-Chair).

granules (SGs) are two examples of processes dependent on LLPS. The assembly of the relevant protein complexes depends upon intrinsically disordered regions of key proteins. For example, NPM1 involved in nucleoli can capture cytochrome *c* – which migrates from mitochondria to the nucleolus in response to DNA damage – in the cavity formed by a set of 'arms', namely, the disordered acidic middle regions of NPM1. In turn this causes the expulsion from the nucleolar condensate of the ARF tumour-suppressor, arising from a major conformational change in NMP1 (induced by cytochrome *c*). Another example occurs in SGs, where TIA-1 is responsible for SG formation by aggregation in a prion-like manner. TIA-1 is also involved in alternative splicing, thus modulating the translational output of particular mRNAs. In exploring mutations that affect phosphorylation of TIA-1 at key sites, which have been linked to aberrant SG formation and neurodegenerative diseases (ALS and frontotemporal dementia), Diaz-Moreno emphasised the need for a clear understanding of the structural changes in TIA-1. Such changes entail its initial capacity to form a β-hairpin, thus moving the protein from a disordered to an ordered state (and then on to its self-association and consequent SG formation). Understanding the liquid demixing of TIA-1 may provide new avenues for developing therapeutics.

Across the three full days of the conference, there were five parallel sessions. These included 25 symposia sessions covering a wide array of topics, various joint symposia, short talk sessions (selected from abstracts submitted) and various special sessions, among which were the FAOBMB Education Session and the FAOBMB–FEBS Interactive Session. The KSBMB Award Lectures were delivered in various sessions (in Korean), in addition to the KSBMB Council Meeting and General Assembly. An interesting feature was the Workshops and Spotlight Sessions, organised by commercial companies supplying instrumentation and resources to the research community in Korea. There were long queues of participants for these sessions. There were more than 1,000 posters presented during the conference, and 155 exhibitors who sponsored passport competitions.

There were several satellite meetings and joint symposia, including a joint KSBMB–ASBMB satellite meeting (see report on page 46) and a symposium within the program entitled Korea–Australia Joint Symposium: Protein Folding, Aggregation and Homeostasis.

Social activities

The Welcome Reception was held on the first evening, Tuesday 20 May, the Gala Dinner was held on Wednesday evening 21 May, and a Presidential Dinner on Thursday 22 May. There was a series of speeches and toasts, made by speakers from various cultures, including Korean *(gun-bae!)*, Japanese *(kampai!)* and Australian *(cheers!)*. Entertainment was provided by a crew of young K-pop dancers; the song that received the greatest audience acclaim was, of course, Gangnam Style.

Closing session

K-pop dancers at the Gala Dinner.

The closing session comprised thank you speeches and the announcement of the poster award winners. Brief presentations were made by the organisers of the next three FAOBMB Meetings: the 32nd FAOBMB Conference in Hong Kong, China, 10–13 August 2026 (Dong-Yan Jin), the 18th FAOBMB Congress in Kuala Lumpur, Malaysia, 24–27 August 2027 (Antony Ho and Chyan-Leong Ng) and the 33rd FAOBMB Conference in Bali, Indonesia, 12–14 September 2028 (Sarmoko Sarmoko).

Phillip Nagley is an Honorary Member of ASBMB and is the Archivist of FAOBMB
Dominic Ng is Secretary of ASBMB and is the Delegate of ASBMB to FAOBMB Council

Dominic Ng and Phillip Nagley at the Gala Dinner.

Young Scientist Program in Busan

Daniel Fox presents his talk, AI-designed protein inhibitors can inhibit growth of pathogenic E. coli.

I was privileged to have been awarded a Young Scientist Program Fellowship and an ASBMB Fellowship to attend FAOBMB2025 and the associated Young Scientist Program (YSP). The YSP was held prior to the conference at Prestige Biopharma Innovative Discovery Center (IDC), a new state-of-the-art biotech hub for new drug discovery and development located in Busan, South Korea.

The YSP was attended by roughly 60 PhD students and ECRs from 16 countries, including South Korea, the Philippines, Vietnam, Japan, Myanmar, Sri Lanka, Thailand, Iran, Bangladesh, China, Indonesia, Malaysia, Pakistan, India, New Zealand and Australia. Australia was well represented by Francesca Alves (University of Melbourne), Nicole Fenton (UNSW), Sara Assar Kashani (Macquarie University), Sina Shadfar (Macquarie University), Jing Zhi Anson Tan (University of Queensland), Zeinab Takalloo Bighash (Macquarie University), Yoon Lim (University of South Australia), Lucy Fitschen (University of Wollongong), Ram Prasad Bhusal (Monash University), Yezhou Yu (Griffith University), Pamali Fonseka (La Trobe University), Naveen Vankadari (University of Melbourne) and myself, Daniel Fox. We gave both an oral and poster presentation at the YSP, which I found personally beneficial given we could present our work in more detail during our talks and then have more informal discussions at our posters afterwards, which I think helped with engagement and interest in our work. These informal sessions were also such an invaluable opportunity as it allowed us to expand our networks more, especially with those from other countries or in other disciplines. A highlight was guest lectures from Professor Marcia Haigis (Harvard University) and Professor Kazutoshi Mori (Kyoto University), preeminent experts in the fields of metabolic reprogramming in cancer and the unfolded protein response, respectively. It was also particularly insightful for students and ECRs to hear more about the progression of their careers.

The Australian contingent at the YSP

YSP participants on tour at Songdo Beach.

Prestige Biopharma Innovative Discovery Center.

We were given a behind-the-scenes tour of the IDC, went on a tour of the beautiful Songdo beach region in Busan and were treated to some delicious Korean lunches and a shabu-shabu dinner on the last night, which were great opportunities to get to know the other attendees and share our science. The YSP was a highlight of my career thus far, and I would like to express my sincere thanks and gratitude to both the ASBMB and FAOBMB YSP for the award of the Fellowships that made it possible for me to attend this amazing event. I would also like to thank Associate Professor Sung-Min Ahn, Assistant Professor Kyung-Sun Heo and the rest of the YSP committee for organising such an enriching and stimulating program.

Daniel Fox, Monash University and the University of Melbourne

2nd ASBMB–KSBMB Joint Meeting

2nd ASBMB–KSBMB Joint Meeting.

The 2nd ASBMB-KSBMB Joint Meeting was held from 18–20 May at the POSCO International Center on the Pohang University of Science and Technology (POSTECH) campus in Pohang, South Korea. Building on the success of the inaugural ASBMB–KSBMB Joint Meeting in Melbourne in September 2024, this year's event further strengthened the scientific and collaborative ties between our societies.

The 2025 meeting showcased an exceptional scientific program over two days, featuring 26 high-quality talks from leading researchers across Australia and Korea. Seven ASBMB members were invited to present their cutting-edge research, covering a broad spectrum of topics within molecular biology and biochemistry.

Professor Megan Maher (President, ASBMB, University of Melbourne) delivered a fascinating presentation on the role of zinc in bacterial infection and immunity, highlighting how understanding trace metal biology provides new insights into host–pathogen interactions. Dr Han Chow Chua (University of Sydney) provided structural and functional insights into sodium leak channels, an emerging area with significant implications for neuronal physiology.

Associate Professor Julia Pagan (University of Queensland) presented her latest work on the molecular mechanisms of mitophagy, shedding light on how cells maintain mitochondrial quality control. Associate Professor Steven Zuryn (University of Queensland) explored the epigenetic regulation of mitochondrial DNA heteroplasmy, providing a new understanding of the impact of mitochondrial genetics on organism fitness.

We also heard from Dr Laura Edginton-Mitchell (University of Melbourne) on novel tools for studying proteases, which are central to understanding disease processes such as cancer and inflammation. Dr Qi Zhang (SAiGENCI, University of Adelaide) discussed the role of the PRC2 complex in chromatin remodelling. Finally, Professor Ross Hannan (Past President, ASBMB, Australian National University) shared the exciting journey in developing a novel RNA polymerase I inhibitor for cancer treatment, illustrating the potential of targeting fundamental biological processes for therapeutic benefit.

There were 19 KSBMB speakers. Professor Tae Soo Kim (Ewha Womans University) presented his cutting-edge research on the epigenetic regulation of cryptic *cis*-regulatory elements, a crucial aspect of gene expression control. Dr Ara Koh (POSTECH) spoke about the implications of microbial metabolites in the gut–brain axis signalling. Associate Professor Dongsung Lee (Seoul National University) showcased advances in 3D genomic and epigenomic profiling for understanding genome organisation in health and disease.

We also learned from Dr Yun Ha Hur (POSTECH) about tissue injury sensing and repair pathways, highlighting molecular mechanisms underlying tissue homeostasis and regeneration. Professor Ho Min Kim (KAIST) demonstrated the exciting potential of AI-based protein design in immunotherapy and antiviral treatments. Professor Soung-Hun Roh (Seoul National University) discussed the latest applications of cryo-electron tomography to bridge high-resolution molecular imaging with electrophysiological properties of individual neurons.

Beyond the excellent science, the meeting offered opportunities to experience Korean culture and hospitality. Delegates were treated to a variety of delicious Korean cuisine, both traditional and modern. A particular highlight was the cultural excursion to the nearby Gyeongju Historic Areas, where we explored the UNESCO World Heritage Site, the Donggung Palace and Wolji Pond of the ancient Silla dynasty (57 BCE–935 CE).

A strong sense of community and collaboration was fostered between Australian and Korean scientists. The two-day event provided numerous opportunities for networking, exchanging ideas and forging new friendships that we hope will lead to lasting scientific collaborations. This spirit of partnership aligns with the goals set out in the Memorandum of Understanding signed between ASBMB and KSBMB in January 2025, which aims to promote sustainable, long-term academic exchange between our societies.

We extend our deepest gratitude to the local organisers, Professor Tae-Kyung Kim and Professor Sekyu Choi (POSTECH), for their efforts in ensuring the success of the meeting. We also thank Professor Bong-Kiun Kaang (President, KSBMB), Professor Ho Jeong Kwon (Past President, KSBMB) and Professor Joon Kim (President, FAOBMB) for their leadership and support. We are also grateful for the financial support from the Australia–Korea Foundation (Australian Department of Foreign Affairs and Trade), POSTECH, ASBMB and KSBMB.

Looking ahead, we anticipate the 3rd ASBMB–KSBMB Joint Meeting to take place in Sydney, coinciding with ComBio2026. We encourage anyone interested in being involved in organising this exciting event to contact us.

Mihwa Lee, University of Melbourne
Victor Anggono, University of Queensland

Annual General Meeting of the Australian Society for Biochemistry and Molecular Biology Inc.

The 69th Annual General Meeting of the Australian Society for Biochemistry and Molecular Biology Inc. will be held on Tuesday 30 September 2025. The meeting will be conducted at the University of Queensland, St Lucia Campus. Time and lecture room are to be determined and will be released with the meeting program.

AGENDA

1. Apologies
2. Confirmation of the Minutes of Annual General Meeting No. 68
3. President's Report
4. Treasurer's Report
5. Fees for 2026
6. Elections to Council
8. Amendments to Constitution and By-laws
9. Any Other Business

Dominic Ng
Secretary, ASBMB

Election of Council 2026

Nominations are called for the following positions on the Council of the Australian Society for Biochemistry and Molecular Biology Inc for 2026: President Elect, Secretary, Treasurer, Editor, Education Representative, FAOBMB Representative, Secretary for Sustaining Members and State Representatives.

Eligible for re-election
§ Position open

The ASBMB Council for the period 1 January 2025 to 31 December 2025 is composed of the following members:	President	M Maher
	Past President	R Hannan
	Secretary	D Ng §
	Treasurer	A Achuthan #
	Editor	T Soares da Costa #
	Education Representative	T Kuit #
	FAOBMB Representative	D Ng #
	Secretary for Sustaining Members	S Parsons
Representatives for:	ACT	C Suraweera #
	NSW	T Christie #
	QLD	C Wang #
	SA	M Roach #
	TAS	A Holloway #
	VIC	S Stewart #
	WA	A Van Dreumel §

Nomination forms are available on the ASBMB website and are to be submitted online: https://www.asbmb.org.au/asbmb/council-nomination/Site/Register. Nominations for all vacant positions must be signed and seconded by members of the Society. The nominations must be signed by the nominee to indicate his/her willingness to stand. If more than one nomination is received for any position, a ballot will be held at the Annual General Meeting. All members will be notified of any elections and members not attending the Annual General Meeting may submit a proxy form available from the Secretary.

NOMINATIONS MUST REACH THE SECRETARY BY 5PM 15 SEPTEMBER 2025
(PRIOR TO THE ANNUAL GENERAL MEETING TO BE HELD ON 30 SEPTEMBER 2025).

Queensland Protein Group: an ASBMB Special Interest Group

The Queensland Protein Group (QPG) was established in 1987 and operates under a constitution accepted in 2004. The QPG committee comprises members from a range of institutions including the University of Queensland (UQ), Queensland University of Technology (QUT), Griffith University (Nathan and Gold Coast campuses) and the Queensland Institute of Medical Research. The current QPG Office Bearers are Thomas Ve (President), Kevin Chen (Treasurer) and Larissa Dirr (website/communications coordinator). Committee members include Victor Anggono, James Antoney, Michael Healy, Natsumi Maruta, Yu Low, Hilary Yong and Dalton Ngu.

The primary activities of QPG include coordinating the biannual East Coast Protein Meeting (ECPM) with the Sydney Protein Group (SPG), and organising the annual local Ross Smith ECR Award Symposium.

ECPM aims to provide a platform for postdoctoral researchers and students to present their work across all areas of protein science. The meeting is distinguished by its strong emphasis on oral presentations from students and postdoctoral researchers, offering more opportunities for emerging researchers than traditional conferences typically do. In 2024, the QPG organised the ECPM at Opal Cove Resort, Coffs Harbour from 17–19 July. The program featured plenary lectures by Professor Wai-Hong Tham (WEHI) and Professor David Ascher (School of Chemistry and Molecular Biosciences, UQ). A highlight of the event was the ECR Career Advice Panel, which included both plenary speakers and Professor Glenn King (Institute for Molecular Bioscience, UQ), offering valuable insights into career development for young scientists.

The meeting also recognised excellence through several awards, including prizes for the best postdoctoral researcher and student presentations, travel grants and the Biomolecular Horizons (BMH) 2024 Award, which provided an ECR with a speaking opportunity at BMH2024 and covered registration costs.

Travel awards (sponsored by the ASBMB)
Felicia Lie, University of Sydney
Junyu Liu, UQ
Bryan Lim, UQ
Yan Zhou, UQ

Best student poster (sponsored by Sarstedt and BMG Labtech)
Aidan Compton, University of Wollongong
Brayden Williams, University of Sydney
Alexandra Shanahan, University of Wollongong
Cebrina Nolan, UQ

Best postdoctoral researcher poster (sponsored by MedChem Express)
Chun Yuen Chow, UQ

Best student talk (sponsored by ATA Scientific)
Solace Roche, UQ
Elise Wilkinson, University of Wollongong

Best postdoctoral researcher talk (sponsored by Cytiva)
Sam Robinson, UQ

BMH2024 Award (sponsored by SPG and QPG)
Taylor Szyszka, University of Sydney

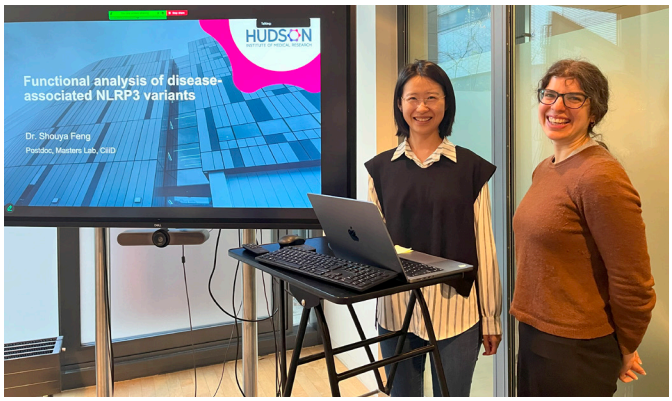
2024 East Coast Protein Meeting.

The QPG Ross Smith ECR Award Symposium was first held in 2021. It honours Professor Ross Smith, an eminent local protein scientist who was instrumental in founding the QPG in 1987. The symposium features presentations from ECRs and students, alongside keynote addresses by more established scientists. Two prizes for outstanding presentations are awarded at the symposium, the Ross Smith ECR Medal and the QPG Student Prize. In 2023, the Ross Smith ECR Award Symposium featured keynote talks from Dr Frank Sainsbury (Griffith University) and Professor Avril Robertson (UQ). The winner of the ATA Scientific sponsored Ross Smith Medal was Dr Michael Healy (UQ), while Ada Quinn (UQ) was awarded the ASBMB-sponsored student prize. In 2025, the symposium will take place on 1 August at the Queensland Brain Institute, UQ. The event will feature keynote presentations by Dr Rosemary Cater (UQ) and Dr Freda Jen (Griffith University), and the Ross Smith ECR price will include a speaking opportunity at ASBMB2025, along with complimentary registration. The symposium will also serve as a chance to welcome new members. We're eager to hear from anyone interested in helping carry the QPG's traditions and activities into the future.

Thomas Ve, QPG President
t.ve@griffith.edu.au
qld.protein@gmail.com
www.asbmb.org.au/queensland-protein-group

ASBMB Fellowship Report

Inflammasomes Across Borders



Shouya with Dr Cassandra Harapas at DRFZ.

It was a great honour to receive the ASBMB Fred Collins Award, which supported my travel to visit Professor Eicke Latz's lab at the Deutsches Rheuma-Forschungszentrum (DRFZ) in Berlin and to attend the 13th Meeting of the International Society of Systemic Autoinflammatory Diseases (ISSAID) in Paris.

Professor Latz is one of the most highly cited researchers in immunology and his pioneering work has established the critical role of the NLRP3 inflammasome in the pathology of many common diseases, including arthritis, diabetes and Alzheimer's disease. His Berlin lab was the first stop on my European trip. There, I presented my recent work on the functional analysis of disease-associated NLRP3 variants, which has now been published in *Nature Immunology*. I was excited to meet many researchers at DRFZ who share my interest in NLRP3. We had insightful discussions on how NLRP3 variants with different levels of activity contribute to infectious and chronic diseases. I was also invited to collaborate on a project to further characterise the frequently identified NLRP3 variants.

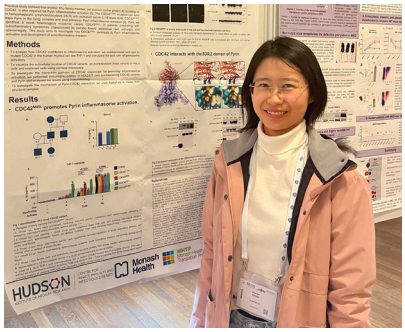
It was fascinating to learn about the Latz lab's recent progress in studying the role of inflammation in ageing, and how alternative splicing in innate immune sensors contributes to inflammation in various disease contexts. Dr Cassandra Harapas and Dr Daniel Simpson kindly gave me a tour of the lab, and Dr Ana Kitanovic demonstrated the robotic system designed for drug screening projects. Professor Latz's enthusiasm for cutting-edge technologies, coupled with his lab's advanced research equipment, significantly enhances the research capabilities of his lab.

Next, I travelled to Paris for the ISSAID conference that brings together both research scientists and clinicians working in autoinflammatory diseases. The conference covered a broad range of topics, from foundational molecular mechanisms to clinical observations. I presented a poster introducing our recent findings on how Pyrin inflammasome activation is regulated by the cytoskeletal regulator CDC42. My poster attracted many researchers with similar interests, and I had a valuable discussion with Dr Jérôme Delon, whose team discovered that CDC42 can also regulate STING signalling, which is another important innate immune sensing pathway.

The main conference featured presentations by leading researchers on autoinflammatory pathways and inflammasome activation mechanisms. My supervisor, Professor Seth Masters, presented our recent publication on NLRP3, which helped reinforce the impact of our work in the autoinflammatory disease field. More clinicians are now aware of our findings and are incorporating them into clinical practice. Our development of a high-throughput functional screening assay has also sparked interest from other research groups. At the conference, I learned that Professor Thomas Henry and his team have developed a single-cell sequencing-based assay to assess the functional activity of all variants of another inflammasome sensor.

Many clinician–scientists shared findings from patients experiencing different complications of autoinflammatory diseases and highlighted cases involving drug tolerance. A notable feature of ISSAID was the case-based discussion forum, chaired by Professor Rae Yeung, who compared disease progression and phenotypes in Still's disease and Kawasaki disease, both of which involve the NLRP3 inflammasome. These discussions inspired me to further explore inflammasome regulatory pathways to develop novel treatments with broader disease applications.

Many other talks and posters caught my interest, and I had the pleasure of reconnecting with old friends and making new ones. I also had dinner with Seth and collaborators at a lovely French restaurant nestled in a beautiful garden. These networking opportunities allowed for deeper scientific discussions beyond the formal sessions.



Shouya with her poster at the ISSAID conference.

Finally, I would like to express my deepest gratitude to the ASBMB for supporting this incredible opportunity. This exceptionally fulfilling experience has not only deepened my understanding of autoinflammatory diseases but also expanded my professional network and inspired new directions in my research.

Dr Shouya Feng is a postdoctoral researcher in the Centre for Innate Immunity and Infectious Diseases at the Hudson Institute of Medical Research.

King's Birthday Honour for ASBMB Member

Emeritus Professor John Carver was awarded a Medal of the Order of Australia (OAM) for service to science in the fields of chemistry and biochemistry.

John is a retired professor at the Research School of Chemistry (RSC), Australian National University. His peripatetic career commenced with an undergraduate degree at the University of Adelaide majoring in chemistry and physics. His Honours year in Inorganic Chemistry, supervised by Stephen Lincoln, engendered his interest in NMR spectroscopy for molecular characterisation. John's PhD at the ANU, supervised by Howard Bradbury, investigated the structure of haem proteins by solution NMR. The latter was enhanced by a postdoctoral fellowship in the Department of Biochemistry, University of Oxford, working with Iain Campbell FRS where he utilised newly developed two-dimensional NMR techniques to determine the solution structures of membrane-interacting peptides and small proteins. He then spent two years in the Department of Biochemistry, University of Adelaide, working with John Wallace on biophysical studies of peptides and proteins, including pyruvate carboxylase. In 1988, John took up a Lectureship in Chemistry at the University of Wollongong where he instigated a research program into eye lens crystallins, molecular chaperones, protein misfolding and aggregation and their relationship to age-related disorders such as cataract, Alzheimer's and Parkinson's diseases. Structure–function studies of antimicrobial peptides derived from native Australian frogs were also commenced. The research utilised a variety of spectroscopic, biophysical, protein chemical and cell biological techniques.

In 2004, John moved to the University of Adelaide as Head of the School of Chemistry and Physics. In 2008, he became Deputy Executive Dean of the Faculty of

Sciences and, for all of 2009, was also Head of the School of Molecular and Biomedical Science. From 2013 to 2019, he was Director of the RSC, ANU. In addition to significant involvement in administration at both universities, he had roles in research management nationally and internationally.

His research interests expanded into an examination of the mechanism of protein amorphous or amyloid fibrillar aggregation, and their prevention by chaperones and small molecules. In addition to disease involvement, these factors are of relevance to the interactions of milk casein proteins within the casein micelle and under industrial processing conditions. His research program is characterised by extensive national and international collaborations with leading researchers in the peptide, chaperone and protein folding/unfolding areas.

John has received a variety of prizes and fellowships, including a University of Canterbury Erskine Fellowship and a Royal Australian Chemical Institute Distinguished Fellowship. He has published over 200 articles and supervised nearly 70 Honours, Masters and PhD students who have made the majority of contributions to the research outcomes.

Australian Society for Biochemistry and Molecular Biology Inc
PUBLICATION SCHEDULE FOR *AUSTRALIAN BIOCHEMIST*, volume 56, 2025

Issue	ASBMB Content	Copy Deadline	Issue Date
April 2025 56(1)	Profiles of medal, award and fellowship winners Nominations for Executive/Council	Monday 3 February	Monday 31 March
August 2025 56(2)	Nominations for medals, awards and fellowships Notice of AGM/proposed constitutional changes	Monday 2 June	Monday 4 August
December 2025 56(3)	Annual reports ASBMB meeting report	Monday 6 October	Monday 1 December

ASBMB Member Elected Fellow of the Australian Academy of Science

On 22 May 2025, the Australian Academy of Science announced the election of 26 Fellows, including ASBMB members, Professor Christina Mitchell and Professor Anthony Weiss.

Christina Mitchell.

Professor Christina Mitchell AO is a physician scientist (MBBS, FRACP, PhD). She completed her medical degree at the University of Melbourne before undertaking specialist training in general medicine and haematology. She later earned a PhD from Monash University, investigating the anticoagulant protein S. Christina practiced as a general physician from 1990 to 2000 and as a specialist haematologist from 1990 to 2011 in the Department of Haematology at Box Hill Hospital. She undertook a postdoctoral fellowship at Washington University, St Louis, USA, for three years.

In 2000, she was appointed as Head of the Department of Biochemistry and Molecular Biology at Monash University, a role she held until she was promoted to Head of the School of Biomedical Sciences in 2006. In 2011, she was appointed as Executive Dean of the Faculty of Medicine, Nursing and Health Sciences.

Christina's research delivers impact in discovery science, together with her leadership in building research capacity and excellence at Monash University. She leads a preeminent phosphoinositide signalling research group. She pioneered the phosphoinositide phosphatase field, discovering and characterising enzymes that mediated interconversion of phosphoinositides. This membrane signalling pathway influences all aspects of cell biology, and plays a prominent role in human development. Christina has co-authored more than 170 publications. She has played a major role in training the next generation of scientists, directly supervising more than 40 PhD students to completion. She has been awarded more than $30 million in competitive grants and received the ASBMB Lemberg Medal in 2015. Christina was made an Officer of the Order of Australia in 2019

Christina has played a pivotal role in building Monash's major infrastructure assets and growing research capacity and excellence, supporting the development of the Biodiscovery Institute, the Australian Regenerative Medicine Institute and the Victorian Heart Hospital. She has also supported successful bids to establish the National Centre for Healthy Ageing and the Moderna mRNA manufacturing facility, Australia's first. Christina is known for her strategic and inclusive leadership.

Tony Weiss. © University of Sydney/ Michael Amendola

Professor Tony Weiss AM FAA FTSE FAHMS is the McCaughey Chair in Biochemistry, NHMRC Leadership Fellow, and Professor of Biochemistry and Molecular Biotechnology in the School of Life and Environmental Sciences and the Charles Perkins Centre at the University of Sydney.

In 2024, Tony was awarded the ASBMB Lemberg Medal. He is the leader in molecular studies of human tropoelastin, the protein building block that gives tissue its elasticity, and its assembly to make three-dimensional elastin protein biomaterials. Tony has taken his discoveries beyond the lab. He is an awarded innovator and inventor, whose recognition includes the Prime Minister's Prize for Innovation, NSW Premier's Prize for Science and Engineering Leadership in Innovation, Eureka Prize for Innovation in Medical Research, Ian Wark Medal (Australian Academy of Science), Clunies Ross Award (Australian Academy of Technological Sciences and Engineering), Entrepreneurship Award (Federation of Asian and Oceanian Biochemists and Molecular Biologists), Applied Research Medal (Royal Australian Chemical Institute) and Weickhardt Medal (Royal Australian Chemical Institute).

Tony is a Fellow of the Royal Society of NSW, Royal Society of Chemistry; Royal Australian Chemical Institute, US National Academy of Inventors, American Institute for Medical and Biological Engineering, Tissue Engineering and Regenerative Medicine, and Biomaterials Science and Engineering. He is Chair of the International Fellows of Tissue Engineering and Regenerative Medicine. He was President of the Tissue Engineering and Regenerative Medicine International Society and President of the Matrix Biology Society of Australia and New Zealand.

Tony serves on 14 editorial boards and is an inventor on 174 granted international patents covering the use of human tropoelastin, focusing on tissue elasticity and enhancing the repair of scars and wounds. He founded the clinical stage company Elastagen Pty Ltd, which was spun off from the University of Sydney to commercialise tropoelastin. Benefitting from a remarkable executive and board, Elastagen was acquired in one of the largest transactions completed in the Australian life science sector.

Australian Academy of Science Honour for ASBMB Member

On 8 April 2025, the Australian Academy of Science awarded 22 Australian researchers for their contributions to the advancement of science, including ASBMB member, Jane Visvader, who was awarded the Ruby Payne-Scott Medal and Lecture.

Professor Visvader is Joint Head of the Breast Cancer Laboratory and the Division of Cancer Biology and Stem Cells at the Walter and Eliza Hall Institute of Medical Research (WEHI) and holds a professorial appointment at the University of Melbourne. She carried out PhD studies at the University of Adelaide and held postdoctoral positions at the Salk Institute, San Diego, and the Children's Hospital/Harvard Medical School, Boston.

In 1998, she was appointed as a Laboratory Head at WEHI along with Professor Geoff Lindeman to lead studies on mammary gland development and breast cancer. Her primary research interests are directed towards understanding the breast epithelial hierarchy and elucidating cells susceptible to breast oncogenesis. Her laboratory's contributions to the mammary gland field include: identification of mouse and human breast stem cells and lineage tracing of mouse stem cells *in situ*; definition of master regulators of mammary lineage commitment and differentiation; identification of distinct luminal progenitor subsets as the 'cells of origin' in *BRCA1* and *BRCA2* mutation carriers. Professor Visvader is a Fellow of the Australian Academy of Science, the Australian Academy of Health and Medical Sciences, the Royal Society (London) and the American Association for Cancer Research.

Jane Visvader.

Our Sustaining Members

bio-strategy
delivering technology

Beyond the Limits of Single-Cell RNA Sequencing

By dissecting cellular heterogeneity, single-cell RNA sequencing has revolutionized biomedical research. However, it first requires dissociating a tissue into individual cells. Fragile and tightly packed cells are typically lost, as is all spatial organization. In contrast, the CosMx Spatial Molecular Imager (SMI) from Bruker Spatial Biology maps individual RNA transcripts directly in the tissue with subcellular resolution, preserving tissue architecture and all cells in their native position. This allows deep exploration of tissue architecture, cell-to-cell interactions, microenvironmental gradients, and tissue anatomy. To fulfill the promise of hypothesis-free discovery science, Bruker have now released their CosMx® Spatial Biology Whole Transcriptome (WTx) Panel. The WTx Panel surveys the whole protein-coding transcriptome in every cell, targeting over 19,000 genes and a full range of engineered assay controls important to QC and analysis. Note WTx chemistry targets individual genes, and is not random-primed, enabling the top 10 expressors to be purposely ignored as they are non-informative and add only noise. WTx chemistry is robust, using only two simple and fundamental processes – hybridisation and photocleavage. No enzymes or exotic chemicals are deployed. For the first time you can now access whole transcriptome profiling in all the millions of cells typically arrayed in a mounted tissue section.

For more information, please contact **Bio-Strategy**, Part of DKSH Group
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W: www.bio-strategy.com

Our Sustaining Members

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EXODUS Quickly Isolates High-quality, Intact Exosomes With Excellent Yield and Purity

Exosome isolation has been the artistic dance of filtration and ultracentrifugation for decades and whilst it can only be described as less than stellar there have been little to no other choices… until 2021. A Nature Methods Article described Exosome detection via the ultrafast-isolation system: EXODUS https://doi.org/10.1038/s41592-020-01034-x

EXODUS is an automatic, label-free, and highly efficient exosome isolation system. With EXODUS, you can easily and quickly isolate high-quality, intact exosomes with excellent yield and purity from a variety of bio-fluids and sample volumes.

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Bioprinting and Organ-on-a-Chip: AXT's Integrated Approach to Biomedical Innovation

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- CELLINK's user-friendly and highly evolved extrusion and DLP systems
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These technologies allow for the fabrication of complex, multicellular structures that closely mimic native human tissues.

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FcZero Recombinant Antibodies for Flow Cytometry

Proteintech have designed recombinant antibodies featuring their all-new FcZero™ backbone engineered to silence the Fc domain for the cleanest flow cytometry data yet.

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For further information, please contact United Bioresearch Products who distribute the full range of Proteintech products in Australia.

https://www.ptglab.com/products/flow-cytometry-antibodies/recombinant-antibodies-for-flow-cytometry/fc-silenced-antibodies/

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Grants of **up to USD 100,000** will be awarded to projects demonstrating strong scientific merit, innovation and strategic alignment with GenScript's focus areas. Funding must be used for GenScript reagents and services, enabling researchers to tap into GenScript's integrated platforms and world-class capabilities to drive their projects forward.

Open to universities, research institutes and biotech companies worldwide, this program offers two application cycles in 2025 to support projects at various development stages. Selected projects should commence within six months of award and conclude within one year.

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