Australian Biochemist

The Magazine of the Australian Society for Biochemistry and Molecular Biology Inc.

April 2025, Volume 56, Number 1

ISSN 1443-0193

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According to Professor Danny Liu of the University of Sydney, without a clear model of best practice, teaching and assessment in the generative artificial intelligence (GenAI) era are akin to "building the plane while flying it." Image courtesy of Dr Matthew Clemson, University of Sydney. Created with Adobe Firefly, an app that uses GenAI to create images, audio and video.

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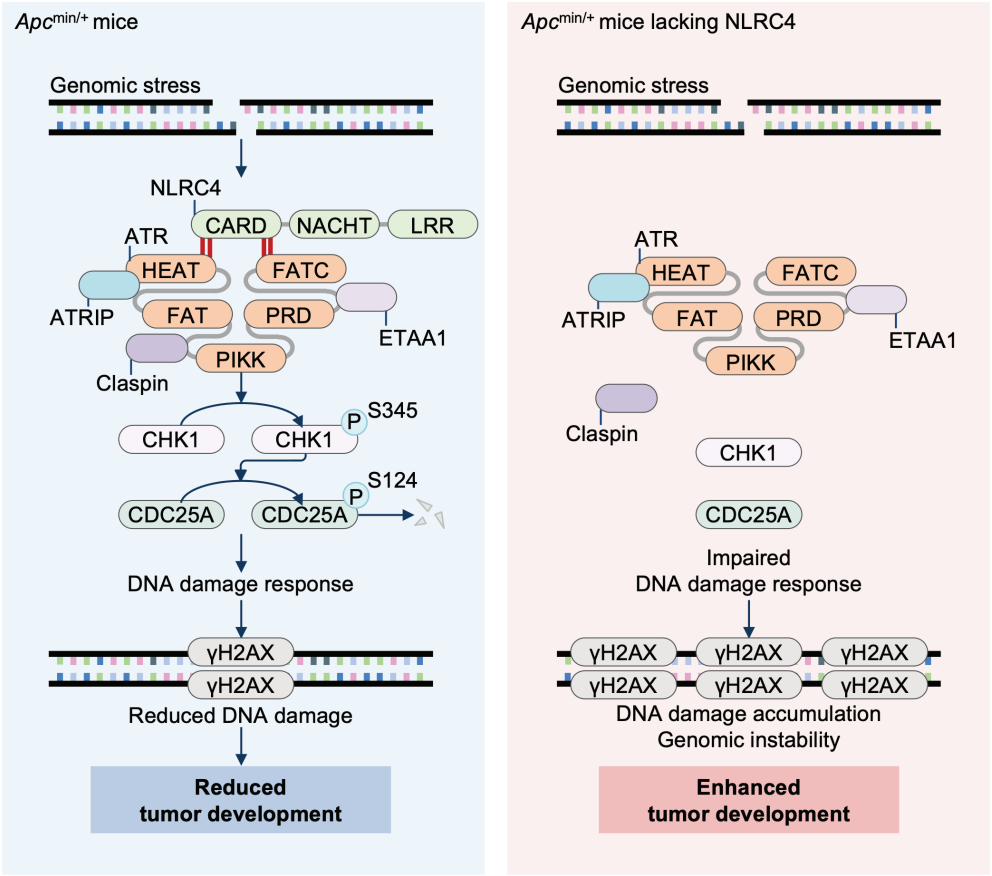
A Nod to Cancer Destruction

Shen C, Pandey A, Enosi Tuipulotu D, Mathur A, Liu L, Yang H, Adikari NK, Ngo C, Jing W, Feng S, Hao Y, Zhao A, Kirkby M, Kurera M, Zhang J, Venkataraman S, Liu C, Song R, Wong JJ, Schumann U, Natoli R, Wen J, Zhang L, Kaakoush NO, Man SM.* Inflammasome protein scaffolds the DNA damage complex during tumor development. *Nat Immunol* 2024;25(11):2085–2096. *Corresponding author: siming.man@anu.edu.au

Bowel (colorectal) cancer is the second deadliest cancer in Australia: it kills more than 100 Australians every week. The development of many types of cancer is inhibited by the immune system, whilst accelerated by pathological and chronic inflammation. Innate immune proteins are one such example, with the Nod-like receptor NLRP3 attenuating inflammation-associated colorectal cancer and driving the secretion of the inflammatory cytokine IL-1β to promote the development lung cancer and cancer of the thymus.

We wondered whether Nod-like receptors had a role in controlling cancer development in a context that was independent of inflammation. To answer this question, we genetically crossed mice lacking Nod-like receptors with mice carrying a genetic mutation in the tumour suppressor APC that would spontaneously develop intestinal cancer without inflammatory triggers. This mouse model is crucial because colorectal cancer develops with a 100% penetrance in humans who have APC mutations inherited or accumulated from the exposure to harmful chemicals. In addition, more than 60% of patients with colorectal cancer carry mutations in APC. We found that mice lacking the Nod-like receptor called NLRC4 developed more tumours in the small intestine. Mice lacking other related receptors, such as NLRP3 and NLRP6, had no effects, suggesting that NLRC4 may have a unique cancer-inhibitory role in this model.



NLRC4 scaffolds around damaged DNA to assemble the NLRC4-ATR complex, promote DNA repair, inhibit the cell division process, and maintain genomic stability. Figure from Nat Immunol *2024;25(11):2085–2096 (CC BY-NC-ND 4.0 license).*

Publications with Impact

The Nod-like receptors are a family of cytoplasmic proteins that sense pathogens and danger signals. Traditionally, previous studies have shown that NLRC4 is a sensor of bacteria that have invaded the cytoplasm of cells, with NLRC4 partnering with receptors that bind bacterial flagellin or certain proteins of the bacterial type III secretion systems. NLRC4 then activates the inflammasome to kill mammalian cells, acting as the Grim Reaper.

In the small intestine of mice carrying an APC mutation, however, NLRC4 does not control inflammasome functions. Instead, we noticed that NLRC4 is found within the nucleus, where it interacts with a DNA-damage controller called ATR. Further biochemical experiments revealed that the NLRC4-ATR complex also contains other DNA-damage response proteins, including ATRIP, ETAA1 and Claspin, forming a protein scaffold. Together, this newly identified NLRC4 protein complex activates the DNA-damage response pathway via the checkpoint protein CHK1, promoting DNA repair, inhibiting the cell division process and maintaining genomic stability.

Unlike the Grim Reaper (NLRC4 that kills infected cells), we have identified Bob the Builder (NLRC4 that is constructive). We believe that the protein scaffold put up by NLRC4 around damaged DNA stops less healthy cells from growing and dividing during the repair process. This function is important to prevent healthy cells from turning into cancer cells, or cells that are becoming cancerous from turning into a tumour.

Future studies that develop new drugs that turn NLRC4 from the Grim Reaper to Bob the Builder might help fight colorectal cancer. Importantly, we also found that people with colorectal cancer carry less amount of NLRC4 than healthy people, suggesting that NLRC4 might be a good biomarker for colorectal cancer and could be used to guide the frequency of colorectal cancer screening. Thankfully, almost 99% of colorectal cancer cases can be treated successfully if detected early. We believe our research into the fundamental biochemistry and molecular biology of cell signalling processes helps raise awareness of cancer prevention, detection and treatment.

Si Ming Man and Cheng Shen
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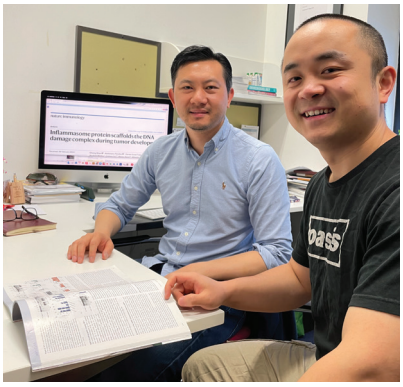
Australian National University



Si Ming Man (left) and Cheng Shen.

Mitochondrial DNA 6mA Modifications Drive Ageing and the Inheritance of Deleterious Mutations

Hahn A, Hung GCC, Ahier A, Dai CY, Kirmes I, Forde BM, Campbell D, Lee RSY, Sucic J, Onraet T, Zuryn S*. Misregulation of mitochondrial 6mA promotes the propagation of mutant mtDNA and causes aging in *C. elegans*. *Cell Metab* 2024;36(12):2528–2541.e11.
***Corresponding author: s.zuryn@uq.edu.au**

Mitochondrial defects are linked to age-associated diseases, such as neurodegeneration, but also the ageing process itself. Crucial for mitochondrial function is the small, circular mitochondrial genome (mtDNA) that encodes key subunits of the electron transport chain. Its replication and transcription machinery are distinct from that of the nucleus and their regulation is not entirely understood.

We investigated an epigenetic modification of the mtDNA, N6-methyl adenosine (6mA), that reflects its bacterial ancestry. When we were able to detect mtDNA 6mA in various eukaryote species, we reasoned that this mark might be a common mitochondrial feature, passed down from the bacterial endosymbiont that gave rise to mitochondria.

Among the species that harboured mtDNA 6mA was the nematode *C. elegans*, which we used to further characterise the role of this epigenetic mark. We screened for potential mitochondrial methyltransferases and demethylases that altered mtDNA 6mA levels when overexpressed. The enzymes we identified, the demethylase ALKB-1 and methyltransferase DAMT-1, are highly conserved in higher eukaryotes, supporting the idea that this mitoepigenetic mark is an ancient trait of mitochondria.

By enhancing the activity of DAMT-1 or ALKB-1, we were able to modulate mtDNA 6mA levels to study the role of the methyl mark. We found that 6mA methylation impacted mtDNA transcript levels. Misregulating mtDNA 6mA levels enhanced ageing, while also inducing markers of oxidative stress.

Publications with Impact

We hypothesise that transcriptional changes within mitochondria, caused by altered 6mA levels, tip the stoichiometric balance between nuclear- and mitochondrial-encoded protein subunits that together make up the electron transport chain and ATP synthase. Consequently, the protein complexes cannot be assembled properly, leading to malfunction and leaking of reactive oxygen species that accelerate ageing.

Remarkably, we discovered an additional factor by which low mtDNA 6mA levels could drive ageing, tied to pathogenic mutations that promote mitochondrial dysfunction and a unique aspect of mitochondrial genetics: while there are hundreds to thousands of mtDNA copies per cell, a mutation will usually affect only a fraction of the copies, making it 'heteroplasmic'. Over time, and independent of cell division, the exact heteroplasmy percentage can fluctuate, and certain mutations, specifically mtDNA deletions, could expand in the pool of mtDNAs because smaller mutant genomes complete replication faster than wild-type copies. In animals with reduced mtDNA 6mA levels, we found higher mtDNA copy numbers than in control samples, indicating increased replication. This alone heightens the risk of acquiring pathogenic mtDNA mutations through replication errors, but we also discovered that a large deletion in the mtDNA expanded dramatically from generation to generation in populations with low mtDNA 6mA. Eventually, these populations turned sterile.

Our results suggest that there is a mitoepigenetic mark, 6mA methylation, that has the potential to alter the mtDNA genetic makeup of future generations and, through various mechanisms, influence the ageing process. Considering the strong conservation of mtDNA 6mA, this epigenetic mark is hypothesised to play an important role in human health and disease.

Anne Hahn and Steven Zuryn
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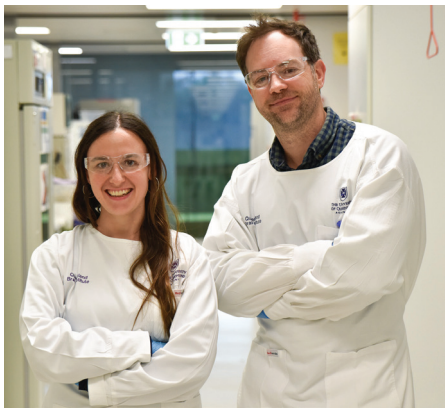
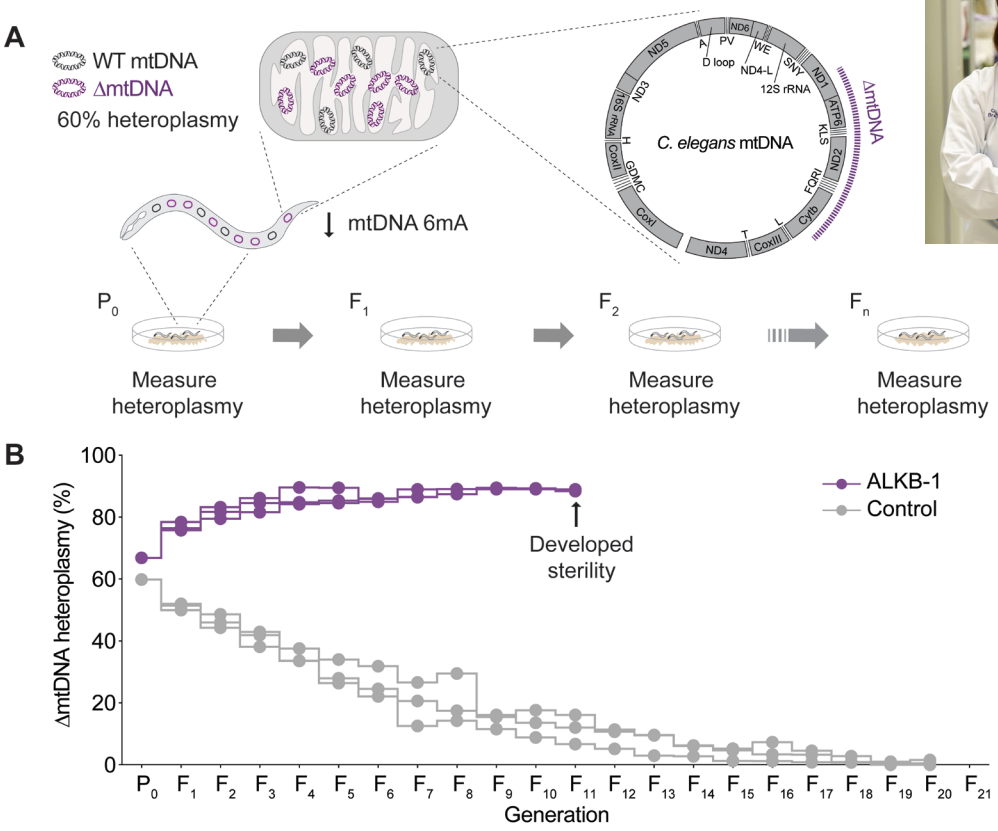


Anne Hahn and Steven Zuryn. Photo credit: Angus Brien.



(**A**) *Experimental design to follow heteroplasmy levels of a large mtDNA deletion across generations in* C. elegans. *The dashed line shows the location of the mutation within the mtDNA.*
(**B**) *Heteroplasmy levels across successive generations in animals with enhanced ALKB-1 activity, compared to control animals.*
Figure adapted from Cell Metab *2024;36(12):2528–2541.e11 (CC BY-NC-ND 4.0 license).*

Publications with Impact

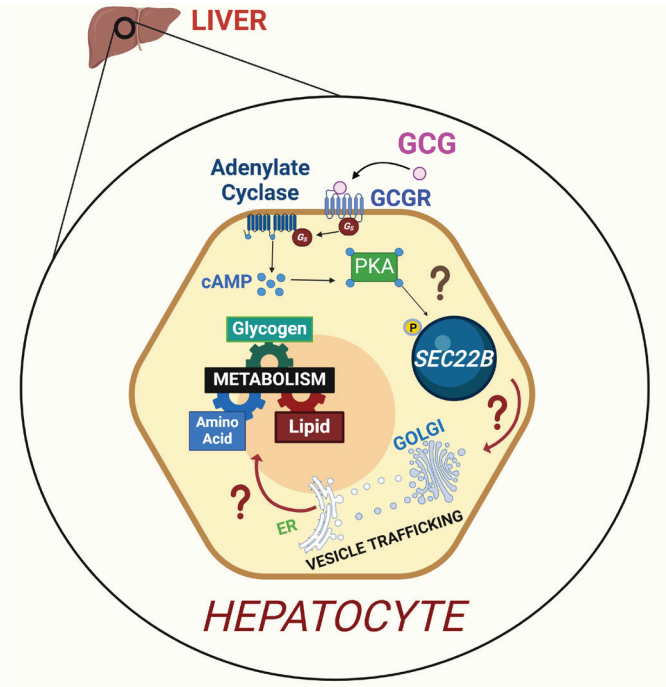
Shining a Light into a Black Box: an Unanticipated Role for Intracellular Trafficking in Glucagon Signalling

Wu Y, Foollee A, Chan AY, Hille S, Hauke J, Challis MP, Johnson JL, Yaron TM, Mynard V, Aung OH, Cleofe MAS, Huang C, Lim Kam Sian TCC, Rahbari M, Gallage S, Heikenwalder M, Cantley LC, Schittenhelm RB, Formosa LE, Smith GC, Okun JG, Müller OJ, Rusu PM, Rose AJ*.
Phosphoproteomics-directed manipulation reveals SEC22B as a hepatocellular signaling node governing metabolic actions of glucagon. *Nat Commun* 2024;15:8390.
***Corresponding author: *adam.rose@monash.edu**

Everyone knows about the star metabolic peptide hormone: insulin. It is the epitome of why hormonal control of metabolism is important, as life without insulin leads to hyperglycaemia and diabetes. The importance of this hormone has seen a burst of knowledge about hormone signalling within cells. Indeed, we now know how insulin signals within the cell, producing a multitude of downstream actions. However, despite its discovery over 100 years ago at about the same time, insulin's counterpart hormone, glucagon, has received far less attention. Indeed, aside from its receptor, a dedicated G-protein coupled receptor, G proteins, and some downstream events like cAMP-activated protein kinase, very little is known about how glucagon signals within its target tissues. This knowledge is important, as glucagon is clearly part of the aetiology of type 2 diabetes, and more recently drugs containing glucagon-receptor agonist activity have been shown to be the best in class for treating people with obesity, type 2 diabetes and fatty liver disease – even outperforming drugs like Ozempic!

To shed light on glucagon signalling, we conducted a time-resolved glucagon regulated phosphoproteomics analysis of the perfused rat liver model in collaboration with Professor Greg Smith from UNSW. We chose this model as there are very few glucagon responsive cells lines, and most of these would not recapitulate signalling and fully differentiated cells *in vivo*. In addition, we chose to examine phosphoproteomics due to the robustness of these methods as well as the well-known influence of protein phosphorylation on cellular metabolism. To our surprise, metabolic enzymes were not the big hits, but rather proteins involved in intracellular trafficking were robustly affected. PhD student, Yuqin, chose to examine one of these proteins that was substantially (approximately 30-fold!) regulated – the vesicle trafficking protein SEC22 homologue B (SEC22B).

Through collaborations with Dr Yuqin Wu, Ashish Foollee and Patricia Rusu, as well as Dr Susanne Hille and Professor Oliver Mueller Kiel University, Germany, we cloned and made AAVs to selectively silence and express SEC22B (and mutants) in hepatocytes *in vivo*, and could demonstrate a clear role for SEC22B in glycogen, lipid and amino acid metabolic control; particularly in response to glucagon treatment. Using IP-proteomics experiments conducted with Dr Matt Challis and Dr Luke Formosa at Monash University, we showed that SEC22B binds a multitude of vesicle trafficking proteins and is particularly enriched in the ER–Golgi interface. For the first time, together these experiments showed that not only does a proximal step of glucagon signalling control multiple aspects of metabolism, but also a distal signalling event.



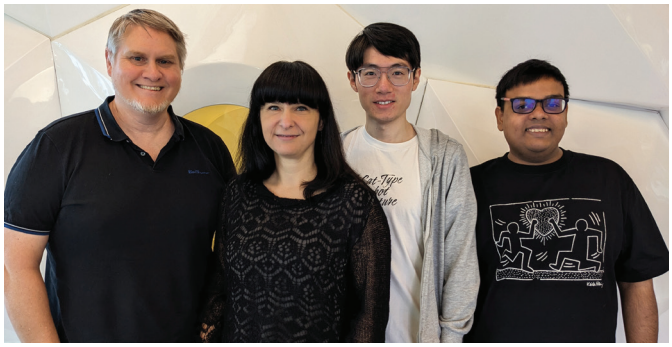
Graphical summary of the findings. We discovered that SEC22B and SEC222B phosphorylation was a key downstream signalling node in glucagon signalling in the liver hepatocytes. It is downstream of canonical glucagon signalling, and regulates most aspects of metabolism, but the precise regulatory events remain unknown. Created by Ashish Foollee in BioRender. https://BioRender.com/u13s975

However, we have only just scratched the surface of how and why SEC22B affects metabolism, and our future experiments are focused on the molecular mechanisms of how it controls metabolism, its role in metabolic

pathophysiology such as fatty liver and type 2 diabetes, and whether it modulates the beneficial effects of glucagon-based pharmacotherapies for obesity, diabetes and fatty liver disease. Here's hoping funding agencies see the value in our future applications as there is still many more glucagon signalling mysteries to uncover!

This work would not have been possible without critical seed funding from the Endocrine Society of Australia and a Project Grant from Diabetes Australia.

Adam Rose, Patricia Rusu,
Yuqin Wu and Ashish Foollee
Monash Biomedicine Discovery Institute
Monash University



From left: Adam Rose, Patricia Rusu, Yuqin Wu and Ashish Foollee.

Plant Tropism May Hold the Secret to Putting Cancer on a Diet

Bayly-Jones C#, Lupton CJ#, Keen AC, Dong S, Mastos C, Luo W, Qian C, Jones GD, Venugopal H, Chang YG, Clarke RJ, Halls ML*, Ellisdon AM*. LYCHOS is a human hybrid of a plant-like PIN transporter and a GPCR. *Nature* 2024;634(8036):1238–1244.
#Co-first authors
***Corresponding authors: michelle.halls@monash.edu, andrew.ellisdon@monash.edu**

To respond to their environment, our cells have evolved complex mechanisms. These processes are carefully regulated and must be strictly controlled to maintain our health and wellbeing. Dysregulation of these controlling mechanisms is frequently observed in metabolic and neurodegenerative diseases. Indeed, excessive cell growth is a major hallmark of cancer.

At the lysosome, a network of proteins sense and respond to nutrient and energy changes, switching metabolism on or off to regulate cell growth. In eukaryotes, this extensively conserved pathway is known as the AKT/mechanistic target of rapamycin (mTOR) axis.

Cholesterol is an essential nutrient required for lipid bilayer synthesis. In 2022, a lysosomal transmembrane protein, LYCHOS, was discovered to facilitate the cholesterol-dependent activation of the master protein kinase mTOR complex 1 (mTORC1). LYCHOS is the only known cholesterol sensor for the mTOR/Akt pathway. Yet the structure of LYCHOS remained unknown and several questions were raised about its precise mechanism of action.

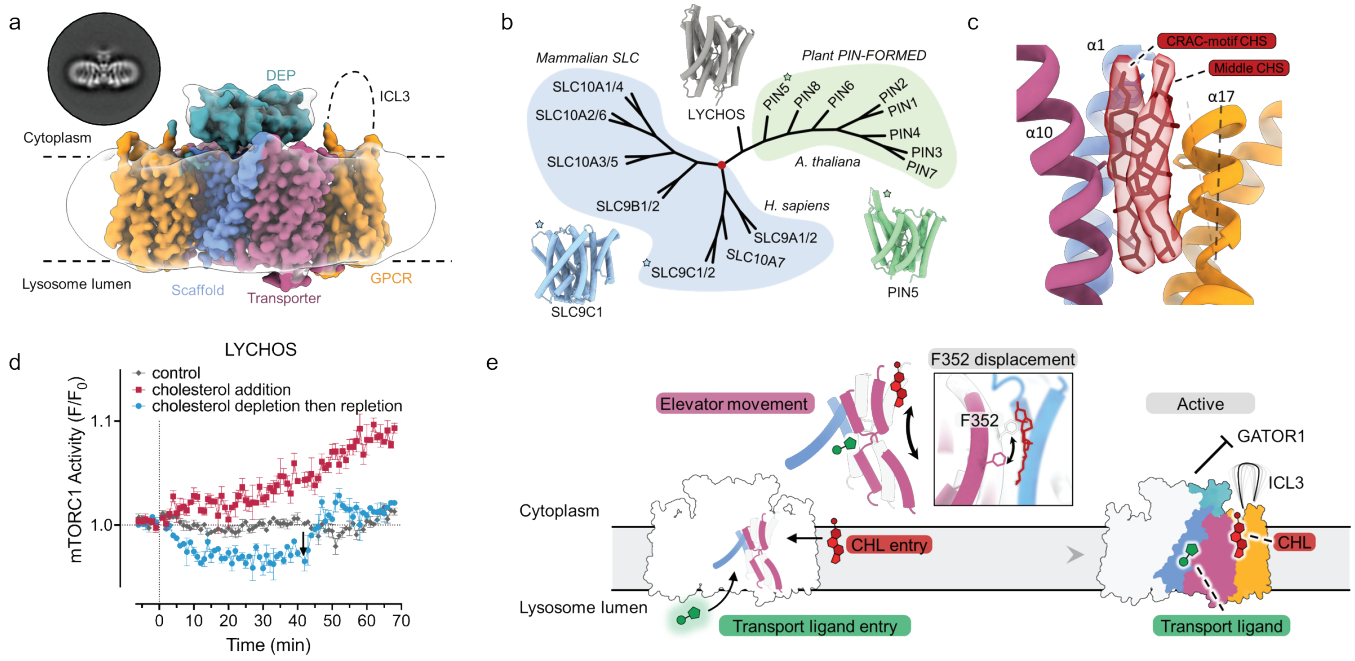
To address this problem, our team used cryo-electron microscopy (cryo-EM) to capture structural snapshots of LYCHOS at high spatial resolution. In addition to the overall architecture, these structures revealed key mechanistic details that govern LYCHOS regulation, providing new understanding and insight into LYCHOS function. The study used a variety of biosensors and structural observations to pinpoint key residues involved in cholesterol recognition.

We discovered that LYCHOS is a hybrid composed of a G protein-coupled receptor (GPCR) and a PIN-FORMED transporter. Our structure revealed LYCHOS as the first and only known member of the PIN-FORMED transporter family in mammals. PIN-FORMED transporters are typically found in plants, where they regulate various tropisms. The substrate of PIN-FORMED transporters is a plant hormone known as auxin. Remarkably, surface plasmon resonance and cryo-EM revealed that LYCHOS retains the ability to bind and recognise auxin through a conserved substrate channel.

The LYCHOS GPCR domain is most closely related to the class B2 family of adhesion GPCRs, normally involved in cell–cell contacts and sensing mechanical forces. The GPCR domain was captured in the apo state where it packs against the PIN-FORMED transporter. This provided a highly unusual example of a GPCR functioning as a domain in a larger transmembrane assembly.

Through the combined use of genetically encoded biosensors and cryo-EM, we pinpointed the location of cholesterol recognition to the interface of the GPCR and PIN-FORMED domains. Site-directed mutagenesis was able to inactivate or constitutively activate LYCHOS by blocking or opening the cholesterol recognition pocket, respectively. Further, we determined the structure of LYCHOS bound to a cholesterol analogue, defining the whole recognition pocket and providing a biophysical basis to explain cholesterol coordination at the residue level.

Publications with Impact



LYCHOS is a hybrid of a plant PIN-FORMED transporter and a GPCR. *(**a**) High resolution cryo-electron microscopy reconstruction, and 2D class average (inset), of LYCHOS. (**b**) LYCHOS is more closely related to the plant hormone PIN-FORMED transporter family than the mammalian solute carrier (SLC) family. (**c**) Cholesterol hemisuccinate density is visible in the high resolution LYCHOS reconstruction, positioned between the GPCR (orange) and transporter (purple) domains. (**d**) Cholesterol-dependent mTORC1 activation or inactivation can be observed in response to LYCHOS overexpression in conditions of cholesterol addition or depletion. (**e**) LYCHOS is proposed to undergo an elevator mechanism akin to the PIN-FORMED transporters of plants. This lateral translation of the transporter domain is hypothesised to open and close a distally located cholesterol entry site. Cholesterol entry triggers LYCHOS signalling through an unknown mechanism, ultimately inhibiting the GATOR1 complex and in turn releasing the inhibition of mTORC1.*
Figure adapted from Nature *2024;634(8036):1238–1244 (CC BY-NC-ND 4.0 license).*

Next, we asked what role the PIN-FORMED transporter played in cholesterol sensing. We again leveraged our live-cell biosensors and site-directed mutagenesis approaches, this time to target conserved residues necessary for auxin recognition. This inhibited LYCHOS from sensing cholesterol and prevented mTORC1 activation. PIN-FORMED transporters typically undergo a transport cycle involving a lateral conformational rearrangement. We noticed this conformational rearrangement would open the distally located cholesterol recognition site.

We therefore proposed a model where coordinated action of both the PIN-FORMED transporter and the GPCR domain work to sense cholesterol and activate mTORC1. Several questions remain to be answered. How are signals relayed to mTORC1? Can the GPCR domain signal through canonical G protein or β-arrestin pathways? Since auxin is not a major human metabolite, what is the nature of the endogenous substrate recognised by the PIN-FORMED transporter, if any?

Ultimately it seems that evolution has repurposed the plant hormone machinery to detect cholesterol in mammals. We believe that the development of new drugs to switch off LYCHOS, analogous to the herbicides that switch off PIN-FORMED transporters, might just be key to putting cancer on a diet.

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Monash Biomedicine Discovery Institute
Monash University

From left: Andrew Ellisdon, Michelle Halls, Charles Bayly-Jones and Christopher Lupton.

Publications with Impact

In Vivo Imaging Reveals a Novel Biomarker of Vascular Damage

Atkin-Smith GK*, Santavanond JP, Light A, Rimes JS, Samson AL, Er J, Liu J, Johnson DN, Le Page M, Rajasekhar P, Yip RKH, Geoghegan ND, Rogers KL, Chang C, Bryant VL, Margetts M, Keightley MC, Kilpatrick TJ, Binder MD, Tran S, Lee EF, Fairlie WD, Ozkocak DC, Wei AH, Hawkins ED#*, Poon IKH#*. *In situ* visualization of endothelial cell-derived extracellular vesicle formation in steady state and malignant conditions. *Nat Commun* 2024;15:8802.

#Co-senior authors

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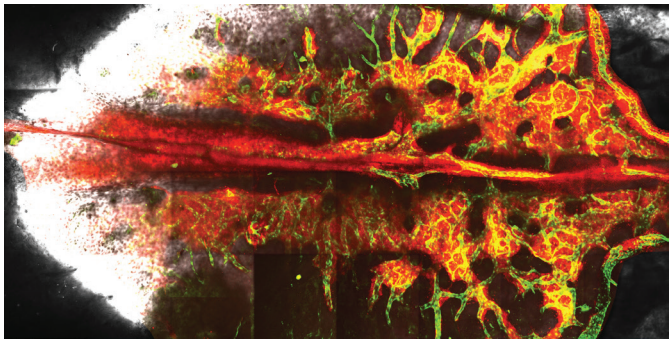
Endothelial cells (ECs) are key barrier cells that line the entire vascular system. They play vital roles in regulating vascular permeability, angiogenesis and embryogenesis. As ECs are located on the inside of the blood vessel wall, they are frequently exposed to a variety of molecular factors and shear force that can induce cell stress. Surprisingly, endothelial cells have an extremely low turnover rate, and it is unclear how unhealthy ECs are removed or how they eliminate unwanted waste.

One way cells can remove unwanted waste is through the formation of subcellular membrane-bound cargo known as extracellular vesicles (EVs). Specifically, the generation of large EVs, ~1-5 μm in diameter, provides effective vehicles to package and dispose of unwanted contents. For example, cardiomyocytes and neuronal cells can generate a large EV subset known as exophers, which harbour dysfunctional mitochondria and protein aggregates. Under stressed settings, migrating cells can package damaged mitochondria into a large EV subset known as migrasomes. Moreover, the disassembly of apoptotic cells into discrete vesicles known as apoptotic bodies also provides an effective route to package cellular debris for clearance. Despite the rapid expansion of EV research, the formation of large EVs by ECs, especially *in vivo*, is largely unclear.

To investigate the formation of large EC-derived EVs *in vivo*, we exploited the EC-specific reporter mouse model Flk1-GFP whereby all VEGR2$^+$ ECs express GFP. We identified a population of large, mitochondria-rich GFP$^+$ particles found in the blood and tissues such as the bone marrow. We performed extensive *in vivo* imaging of the calvarium to monitor the ECs within the bone marrow microenvironment. For the first time, we captured and characterised the formation of EC-derived EVs *in vivo* in mice. EVs were released either directly into the blood stream and on occasion, into the bone marrow space. Extrapolation of our intravital imaging quantification predicts that ECs release thousands of EVs every day. Notably, *in vivo* imaging of zebrafish embryos revealed an abundance of EC EVs within the zebrafish vasculature, and mitochondria-rich EC EVs could also be detected in human blood.

Mitochondrial content such as mtDNA is a potent damage-associated molecular pattern, which, when detected, can trigger inflammation. Therefore, we hypothesised that EC EVs (which are mitochondria-rich), must be cleared efficiently to prevent the accumulation of mitochondria-containing particles. Through both conventional and imaging flow cytometry approaches, we revealed a series of immune cell subsets that could bind to and engulf EC EVs. This interaction and clearance of EVs was in part due to the exposure of the 'eat me' signal, phosphatidylserine, on the EVs.



Tile scan maximum intensity projection of the bone marrow calvarium captured by intravital imaging.
Red – acute myeloid leukemia
Green – Flk1-GFP (endothelial cells)
Grey – second generation harmonic (bone)

Finally, we investigated the formation of EC EVs under the condition of vascular stress by using a model of acute myeloid leukemia (AML). Intravital imaging of AML-burdened mice at late-stage disease demonstrated an approximate threefold increase in EV formation. EVs were released through both a budding-like event as well as cell fragmentation. Consistently, multiphoton imaging of cleared long bones demonstrated that AML resulted in significant degradation of the bone marrow vasculature. We also assessed two additional blood cancer models including T-ALL and EμMyc lymphoma, which further revealed a correlation between vascular damage and elevated numbers of EC-derived EVs found in circulation.

This study has revealed a novel subset of large,

EC-derived EVs and has provided the first *in vivo* characterisation of EC EV formation in mice. Excitingly, it demonstrates that the levels of EC EVs found in circulation correlates with vasculature degradation. Thus, EC EVs represent a novel biomarker that can predict the extent of vascular damage during blood cancer.

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Walter and Eliza Hall Institute of Medical Research
Ivan Poon
La Trobe Institute for Molecular Science
La Trobe University

From left: Ivan Poon, Georgia Atkin-Smith and Edwin Hawkins.

Aiming to Kill: Rhs Toxin Delivery by the Type VI Secretion System

Hayes BK#, Harper M#, Venugopal H, Lewis JM, Wright A, Lee HC, Steele JR, Steer DL, Schittenhelm RB, Boyce JD*, McGowan S*. Structure of a Rhs effector clade domain provides mechanistic insights into type VI secretion system toxin delivery. *Nat Commun* 2024;15:8709.
#Co-first authors
***Corresponding authors: john.boyce@monash.edu, sheena.mcgowan@monash.edu**

Acinetobacter baumannii can use a type VI secretion system

Bacteria live in complex polymicrobial environments where they are constantly competing for space and resources. To help them dominate in these environments, around 25% of all Gram-negative bacteria use a potent nano-weapon termed the type VI secretion system (T6SS). Akin to an inverted bacteriophage tail, the T6SS physically injects deadly toxins directly into adjacent cells, often causing target cell death. The bacterial pathogen *Acinetobacter baumannii* is known to utilise a T6SS system for bacterial competition. Currently, treatment of *A. baumannii* infections is challenging due to extensive and widespread drug resistance. Often infecting critically ill patients, *A. baumannii* is a major cause of hospital-acquired infections in intensive care units. As such, the WHO has designated *A. baumannii* as a priority one critical pathogen, and therefore new approaches to infection control are urgently required.

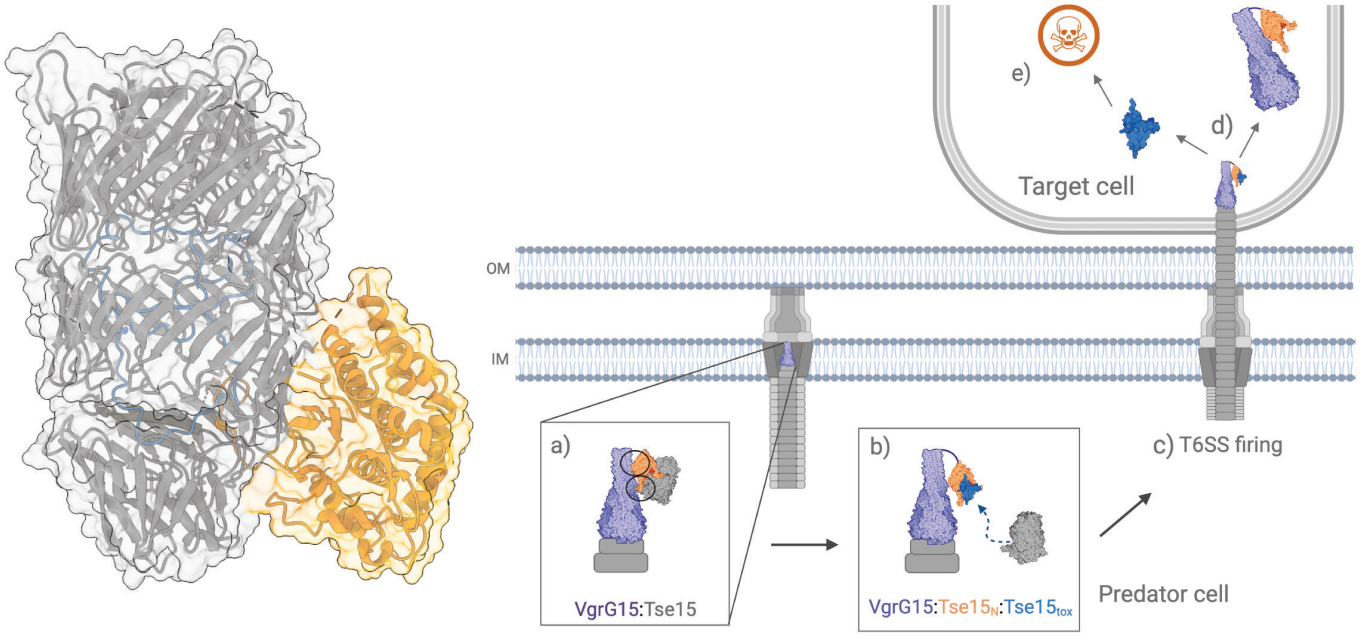
Rhs effectors auto-process and form a triple layered β-cocoon structure

We characterised a novel T6SS toxin, Tse15, from a clinical *A. baumannii* strain. Tse15 belongs to a class of T6SS toxins called rearrangement hotspot (Rhs) effectors. Rhs effectors interact with the T6SS structural machinery for delivery, but the precise interactions and how the toxins are activated are poorly defined. We showed that prior to delivery, Tse15 undergoes auto-processing into three separate domains, N-terminal, central Rhs and C-terminal toxin, but these remain associated in solution. We demonstrated that this separation occurs through two independent auto-cleavage events involving aspartyl protease activity for toxin self-cleavage and a nucleophilic glutamic acid for self-cleavage of the N-terminal domain. The 1.8 Å cryoEM structure of Tse15 showed the central Rhs domain forms a triple layered β-cocoon with an N-terminal α-helical domain that sits outside the cocoon. The unfolded C-terminal toxin domain is located inside the β-cocoon, which physically protects the host cell from self-intoxication. Notably, we observed a 10 Å cleft in the otherwise sealed Rhs β-cocoon between the first and second substructures. Inside the cleft, the N-terminal and C-terminal domains are in proximity to each other – suggesting an interaction may be necessary for delivery. This is the first structure of a T6SS effector from *A. baumannii*, and the only Rhs effector structure that has the full-length protein resolved.

Rhs effector delivery mechanism

Adopting biochemical techniques, we mapped the regions of interaction between Tse15 and its cognate T6SS delivery protein, VgrG15. These data showed that the N-terminal and Rhs domains of Tse15 interact with the VgrG15 C-terminal. To further understand the Tse15 delivery mechanism, we assessed what components of Tse15 were delivered into the target cell via proteomic analyses. We showed that the N-terminal and C-terminal toxin domains, but not the Rhs β-cocoon, are delivered outside of the host cell. This finding contrasts with all previous hypotheses that propose the entire Rhs effector is delivered into the prey cell, and hence suggests a novel mechanism for Rhs toxin delivery and activation.

Publications with Impact



Rhs effector, Tse15, structure and delivery mechanism.
Left: *structure of Tse15 resolved using cryoEM. Tse15 is shown as a cartoon with surface representation. Orange indicates N-terminal domain, grey Rhs domain and inside the Rhs domain, the toxin is shown in blue.* ***Right:*** *Tse15 delivery schematic. Tse15 colours are as left, VgrG15 model is shown in purple: (**a**) Initial VgrG15 and Tse15 interaction, (**b**) the Tse15 N-terminal ($Tse15_N$) and toxin domains interact ($Tse15_{tox}$), allowing the Rhs domain to dissociate, (**c**) the T6SS fires into the target cell, (**d**) the toxin domain is released from the delivery apparatus and (**e**) the toxin mediates death of the target cell.*

Taken together, our findings suggest that Rhs toxin delivery requires an interaction between the N-terminal domain and the C-terminal toxin domain, where the N-terminal domain acts as an internal chaperone to mediate tethering of the toxin to the T6SS machinery. Following these initial interactions, the Rhs domain is no longer required for delivery into the target cell and dissociates prior to, or during, T6SS firing. Strikingly, conservation of the N-terminal domain in other Gram-negative bacteria suggests this may represent a common mechanism for T6SS toxin delivery.

Manipulating the type VI secretion system

Our findings help to elucidate the complex molecular mechanisms by which toxic effectors are delivered by the T6SS and therefore identify potential targets for disrupting effector delivery by VgrG-bound cargo effectors. Further, defining T6SS toxin delivery may allow for anti-T6SS therapeutics, or for artificial payloads to be delivered by this nanomachine. Allowing delivery of chosen molecules to manipulate select bacteria or bacterial niches, may aid in the future control of life-threatening multidrug resistant pathogens like *A. baumannii.*

Brooke Hayes
Monash Biomedicine Discovery Institute
Monash University

From left: Brooke Hayes, Marina Harper, John Boyce and Sheena McGowan.

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Two Lanes Forward: the Concept of Trust and the University of Sydney's Response to Generative AI and Assessment

Matthew Clemson

School of Life and Environmental Sciences and Office of PVC (Educational Innovation), University of Sydney

The landscape within which we teach and assess our students has changed significantly since the widespread release of generative artificial intelligence (GenAI) tools, such as ChatGPT.

At the core of the issue, and institutional responses to the risks imposed by GenAI, is *trust*. Students need to *trust* that their university education is something that will be valued and recognised. Employers and the public need to *trust* that graduates have gained the necessary disciplinary knowledge, skills and experience required to navigate future complex professional environments. And finally, educators must *trust* that their work remains relevant and impactful, by developing assessment practices that promote learning, are valid, fair, transparent and regularly reviewed.

The University of Sydney has introduced a 'two-lane approach' to assessment, addressing the challenges and opportunities presented by GenAI in higher education. The approach is intentionally binary, making it clear to students that they can use GenAI tools for all tasks unless they are completing a secure, in-person, supervised assessment. For these 'open' or 'unsecured' assessment tasks, students need to be assisted and guided by their educators in how they should use GenAI and other technologies, with their use fully allowed. This approach is designed to ensure that graduates are equipped for a future where GenAI is ubiquitous.

The first lane, secured assessments, validates students' attainment of program learning outcomes (PLOs) through in-person, supervised tasks like exams and practical tests, where GenAI use is either controlled or completely restricted. This ensures assessments rigorously measure individual competencies. Secured assessments can be considered as summative tasks, or *assessment of learning*.

The second lane, open assessments, focuses on fostering learning and preparing students for AI-integrated workplaces by allowing and guiding the use of GenAI tools in assignments like case studies and creative projects. Open assessments can be considered as formative tasks, or *assessment for learning*.

Students will have more confidence, more *trust*, in an assessment schedule that either permits or prohibits the use of GenAI for specific tasks. Educators and institutions should not set assessments with rules that are likely to be broken by students, such as prohibiting the use of GenAI for take home assignments or unsupervised tasks. Doing so damages student *trust* and undermines the validity of the assessment, as judgements of student performance are made with the incorrect assumption that the rules were obeyed by every student (1).

At this juncture, it is critical that we revisit the concepts of assessment validity and constructive alignment.

Assessment validity: educators must ensure that an assessment task measures what it was intended to measure. A task designed to measure students' understanding of a concept will require a secure, in-person activity. Open assessment tasks serve to motivate students and drive learning, but educators must be mindful that their validity is limited to measuring student achievement working with the available technology, including GenAI. It requires equitable access to the latest models, student training and guidance in their responsible and ethical use.

Constructive alignment: Educators may need to reconsider their intended learning outcomes (ILOs) in terms of a GenAI-assisted cohort, and design assessment tasks that permit a valid judgement of student performance within this context. For example, in an AI-enabled world, does a perfectly scripted laboratory report demonstrate that the student has mastered the experimental process, data analysis, interpretation of results and formation of conclusions? Can the task be redesigned to measure these intended learning outcomes? Or are these ILOs no longer relevant *with the help of AI?*

Many current assessments need to be entirely redesigned to ensure their relevance and validity within this new AI-enabled world. At the University of Sydney, this process is underway through the adoption of the two-lane approach to assessment. Without any clear existing model of best practice, the journey in 2025 has been described by Professor Danny Liu as

"building the plane while flying it" (**Fig. 1**).

Finally, learning is achieved through the activities that students undertake, and the cognitive processes elicited. Humans will take shortcuts where there is little or no perceived benefit in taking the long road. As educators, we may need to refocus on the human elements of learning – inspiration, curiosity, belonging, community, empathy, self-determination, growth and motivation. After all, none of us applied to get into university to collect marks or grades; we went there to learn.

Fig. 1. *Building the plane while flying it. Image created with Adobe Firefly.*

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Additional references of interest

- Student-developed resource site to help students and educators use AI responsibly
- How we aim to align our assessments for generative AI
- White paper setting out the landscape and pathways to success

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The Challenges Students Experience When Applying Quantitative Literacy Skills in a Practical Biochemistry Context

Amber Willems-Jones[1], Thi Thu Giang Tran[2] and Jan van Driel[2]

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[2]Faculty of Education, University of Melbourne

Quantitative literacy skills (QLS) are crucial in biomedical science education and have been linked to academic achievement in this field (1), with students who excel in these skills generally achieving higher academic success as their confidence boosts their belief in success (2).

Despite the critical role QLS plays in education, competence and confidence in this area have been declining for some time, exacerbated by maths anxiety and a lack of basic foundational knowledge in mathematics (3,4). In science courses, a key barrier students encounter when applying QLS is their lack of foundational QLS (4). Furthermore, students' abilities to transfer their mathematical knowledge and skill beyond secondary education are also lacking (5), though research suggests that students with strong QLS are better equipped to transfer these skills effectively (6). Additional challenges to successfully apply mathematics knowledge include language barriers (7) and the presumption by science educators that students are adequately prepared in QLS.

The aim of our mixed methods research study was to identify the key challenges students perceive associated with their application of QLS, and to thereby provide suggestions for curriculum revision and targeted educational support. We explored the

challenges experienced by students in Techniques in Molecular Science, BCMB20005, a second-year practical biochemistry and molecular biology elective in the Science and Biomedicine Bachelor degrees at the University of Melbourne.

Students in BCMB20005 were invited to participate in a concise online quick-poll and a semi-structured interview. The quick-poll was a preliminary tool to identify specific areas in quantitative literacy that students found challenging or difficult, and to obtain a measure of perceived confidence in QLS, drawing on the link between self-confidence and mathematical competence. Next, semi-structured interviews were conducted which were informed by insights from the quick-poll. The study design was approved by the Faculty of MDHS HREC (#30171).

A total of 110 students completed the quick-poll, while 12 students also took part in the interview. In the quick-poll, students were asked, "How confident are you in your quantitative literacy abilities?" **Fig. 1** indicates the predominant confidence level among the students is 'moderately confident', as reported by 50.91% of respondents, with 29.09% rating their confidence less than this. Notably, this reduced level in confidence is larger than those who express higher levels of confidence (very confident plus extremely confident, totaling 20%).

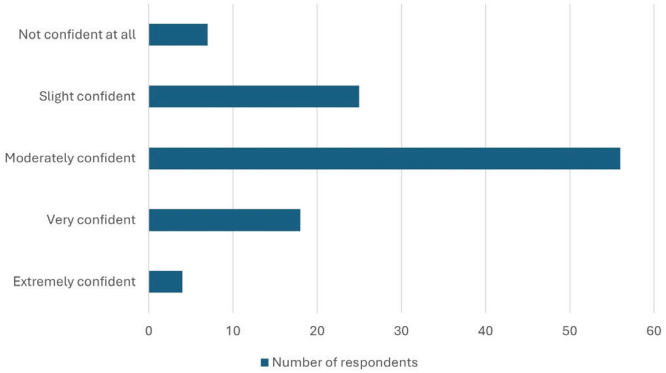

Fig. 1. *Confidence levels in quantitative literacy skills (QLS) of students in BCMB20005 in response to the question, "How confident are you in your quantitative literacy abilities" (n=110 from 171 enrolled students).*

In the quick-poll, students identified four specific areas of quantitative literacy that they found difficult/challenging, with each achieving ≥30% respondent selection, including (1) Explaining simple statistical measurements such as p values, means, medians, standard deviations: 38%, (2) Converting units of measurement: 37%, (3) Calculating dilution factors: 32%, and (4) Stoichiometry measurements: 30%. Interestingly, only 8% students selected the 'I don't find any of these areas difficult' option for the 13 areas presented.

When asked in interview, "What aspects of quantitative literacy do you find most challenging and why?", students highlighted five main challenges associated with application, knowledge retention and confidence. These included performing unit conversion and stoichiometry calculations, applying theoretical mathematical knowledge in practical situations due to the significant gap between theory and practice, encountering complex calculations where understanding the theoretical basis is crucial for application (yet lacking), forgetting past mathematics knowledge, and a decrease in confidence in their mathematical abilities attributed to the gap in time between high school and university. Furthermore, the interview participants elaborated on the reasons for their perceived difficulties including: (i) the fast-paced nature of the practical class environment leading to errors not reflective of actual capabilities, (ii) lack of specific resources outlining how to perform specific calculations (despite students being provided with such resources in the form of a lab manual and online resources), and (iii) a lack of adequate contextualisation of mathematical concepts in biomedical science, along with (iv) finding it difficult to see the relevance and application of the mathematics they learned in high school. In addition, students identified reasons for their difficulties including having English as a second language, not actually having the assumed prior knowledge of QLS, and the cognitive load involved in understanding and applying molar relationships.

Strategies students developed and put into place to overcome the challenges they experienced when using QLS were also shared by participants (**Fig. 2**).

In addition, interviewed students proposed valuable suggestions to further enhance a student's proficiency in QLS that could be adopted by subject coordinators, including:

- Additional text-based resources to provide a better understanding of how to work through calculation-based problems independently.
- Additional supportive teaching methods, including drop-in sessions where students can ask questions and clarify their understanding in person.
- Introductory sessions (either online or in-person) on basic quantitative concepts at the start of semester for those transitioning from a purely biological background into quantitative fields, to help bridge any gaps in understanding and provide a smoother transition into the mathematical demands of biomedical studies.

In summary, the study illustrates that the challenges students face in applying QLS to university-level biomedical science subjects arise from adapting to new teaching methods, their ability to integrate interdisciplinary (i.e. maths and science) knowledge, and rebuilding confidence in a new context – all of which are a natural part of the educational journey. Recognising these challenges allows educators to provide appropriate support, helping students to further develop their skills and succeed in their studies. If

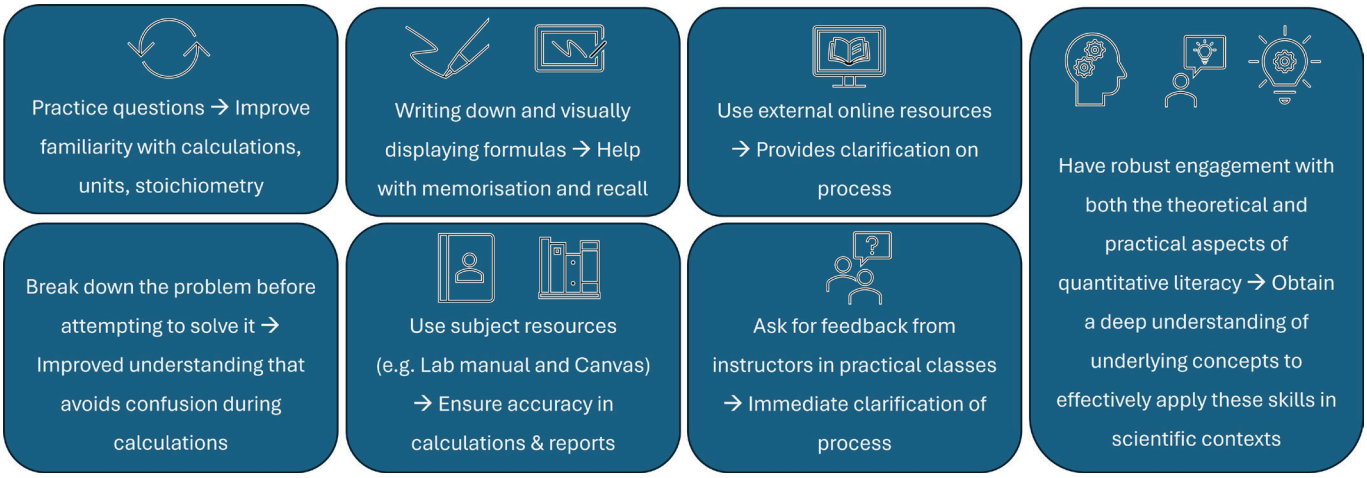

Fig. 2. *Student-developed strategies used to overcome the quantitative literacy skills (QLS) challenges (n=12).*

students are given access to *targeted resources* and clear direct instruction on how to *transfer and apply* their mathematics knowledge to university subjects, they will be better equipped to apply their quantitative literacy skills, reinforcing the foundations laid during their secondary education.

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ASBMB Education Feature

Crossing the Pacific: an Academic's Experience of Transnational Education

Alyssa Van Dreumel

School of Molecular Sciences, University of Western Australia

Alyssa Van Dreumel, Senior Lecturer and International Program Coordinator in the School of Molecular Sciences, University of Western Australia (UWA), shares her experience of transnational education (TNE) as part of the Biotechnology/Biochemistry program at Westa College, Southwest University, Chongqing, China. Founded in 2016, Westa College is a tripartite partnership of UWA, University of Tasmania and Southwest University to educate high achieving Chinese students who receive undergraduate degrees from both China and Australia.

My TNE experience has played an important part in my professional development as an educator. My position at UWA is a unique education-focused role which involves teaching undergraduate students in Australia and coordinating a TNE programme and teaching students at our partner university in China. Our agreement requires 24 hours of contact (32 x 45-minute classes) per subject.

In my first year in the role (2018–2019), I was a fly-in-fly-out (FIFO) lecturer, and in a single trip would typically spend two intense weeks delivering approximately 18 lectures in blocks of two to three classes, to cohorts of 30–60 students. My journey to our partner university took approximately 16–20 hours (ten hours total flight time, plus layover/transit), travelling four times for teaching visits and once for an Open Day event.

My suitcase is usually filled with a diverse mix of personal and professional items, such as the essentials: business attire, a range of black teas, Cadbury chocolate block, long-life lactose-free milk, collapsible camping bowls, plastic cutlery, as well as the laptop, a flash drive and laser pointer!

I usually have a day to settle in (thankfully, there is no time difference between China and Western Australia), to ensure my learning materials are ready before I start delivering classes. In between classes and meals at on-campus canteens, I mainly prepare for subsequent classes; some of my Australian colleagues use this time to write research manuscripts undisturbed!

From the beginning of 2020 to mid-2023, as the situation required, we taught our Chinese students online utilising a flipped classroom model. We supplied lecture recordings via an external learning management system and assumed students were engaging with these for study. Hosting online workshops was incredibly challenging, with students only engaging via the chat function, resulting in long silent pauses and very little feedback overall on how the cohort was grasping the content.

Academic mobility resumed in the Autumn semester in September 2023. However, it wasn't until December 2024, after four and a half years, that I finally made it back on campus in China! (**Fig. 1**). Our teaching model continued using a flipped approach with a series of workshops delivered online, as well as a series taught face-to-face during on-campus visits spread throughout the semester (**Fig. 2**). In my most recent visit, as I walked around my classrooms observing, listening to and speaking with my Chinese students… what did I learn? I learned that the students were primarily relying on the PDF lecture notes as their study resource, that they were not engaged with lecture recordings, and they were expectant that the 'teacher' would tell them exactly what parts of the curriculum they needed to know for the examination.

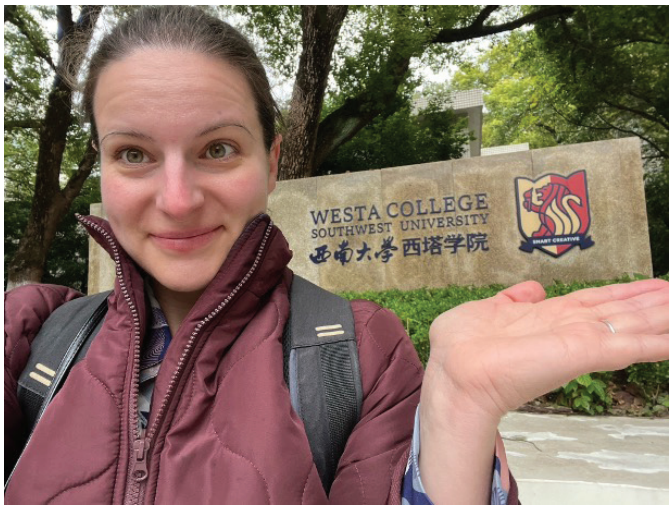

Fig. 1. *Alyssa Van Dreumel visits Westa College, Southwest University campus in Chongqing, China, in December 2024 after a 4.5-year travel hiatus.*

I observed students reviewing lecture notes from previous topics during our classes or completing tasks set for other subjects entirely. Some students commented they were apprehensive they would learn all the material using a flipped learning model due to limited private study time. This is understandable as our Chinese students study five to ten subjects per semester, requiring anywhere between 5–20 hours of study per week; subjects include compulsory Physical Education, Political and English Language subjects, as well as our – exclusively taught in English – discipline-specific Biochemistry subjects. A common challenge encountered by educators using a flipped approach is a lack of students' motivation to watch the recorded lectures or to

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Fig. 2. *Alyssa Van Dreumel facilitates learning activities during a workshop session for a cohort of approximately 55 juniors (third year) biochemistry students at Westa College.*

study content outside of class time (1), however I believe 'study load pressure' is a prominent factor preventing some of my Chinese students' preparation for class. As we race towards the Spring semester 2025, I am considering reducing the volume of pre-class content, as well as the implementation of gamified learning strategy for the review the pre-class materials and peer competition during in-class activities (e.g. a polling tool with leaderboard) as suggested by Zainuddin *et al.* (2019). I'll be monitoring student engagement analytics within the polling tool and be seeking student feedback regarding the adjusted study load.

Being a transnational educator continues to influence my teaching practise in both my Chinese and Australian classrooms. It reminds me to constantly put my students first when considering teaching pedagogy and ask – what is this experience like for them? – from their perspective, and how is it influenced by their culture and context. While demanding on time, being physically in the classroom on campus enables me to foster positive relationships with my students and Chinese colleagues. Switching focus between my Australian and Chinese classrooms encourages my engagement in regular critical reflection to enhance my practise, and the need to be creative, resourceful and most importantly, adaptable. Ultimately, this experience has enabled me to continue to become a better facilitator of learning. Smith (2) argues a powerful professional development opportunity is gained by a novel experience that transforms one's perspective, such as in TNE – I agree. Though my experience working within a different cultural context as a transnational educator has been challenging in numerous ways – both professionally and personally – the reward is ultimately improving my teaching practise, not just for students in my international classroom but also in Australia.

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In Memoriam

John Wallace 1939–2024

John Wallace at the University of Adelaide, 1978.

John Campbell Wallace was born in Sydney in 1939. He attended North Sydney Boys High and then obtained a scholarship to study Agricultural Science at the University of Sydney, where he discovered a lifelong interest in protein chemistry. He completed his PhD at the University of Sydney where he met his future wife Pat. Subsequently, both John and Pat were awarded fellowships through the Royal Commission for the Exhibition of 1851 to work in the laboratory of Sir Hans Krebs in Oxford. John then spent some time at Case Western Reserve University, Cleveland, Ohio, in the laboratory of Merton Utter, where he met Bruce Keech, who was there on sabbatical leave from the University

of Adelaide. Utter and Keech had published two papers in the *Journal of Biological Chemistry* in 1963 describing the reaction catalysed by pyruvate carboxylase (PC) and the enzyme's properties. It was in Cleveland that John developed his lifelong interest in PC and his friendship with Bruce. John joined the University of Adelaide in 1969, became a member of faculty in 1970 and published his first paper on PC in 1971 (1).

John became a highly valued member of the Department of Biochemistry, University of Adelaide, contributing to teaching and running two very successful research programs in the PC and insulin-like growth factor (IGF) fields. He remained there until his retirement in 2011, after which he became Emeritus Professor. Here, we present some reflections on his research career by representatives of the many students and researchers he mentored and supported over the years.

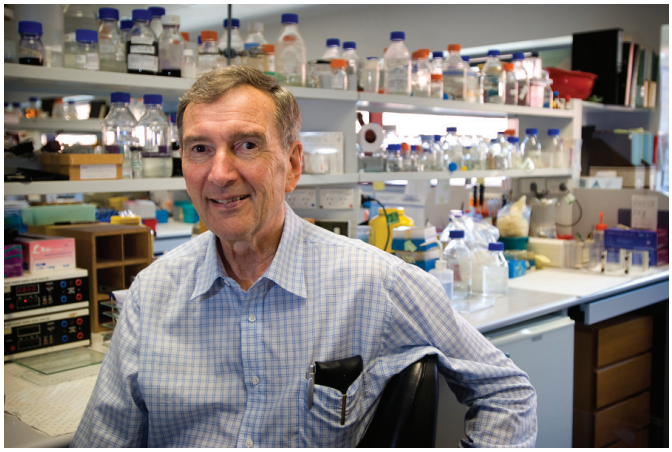
The Pyruvate Carboxylase Story

Paul Attwood: *"I first met John when I was working on my PhD on the mechanisms of visual transduction in Freddie Gutfreund's laboratory at the University of Bristol. John had come over to do some fluorescence measurements on PC and I was familiar with the photon-counting fluorometer, so helped him out. After one of these work sessions, I took John for an Indian curry and then a pub crawl across Bristol. I was very impressed with John's stamina and enthusiasm for socialising. As I neared the end of my PhD, John offered me a Senior Teaching Fellowship in his and Bruce's lab in Adelaide (he assured me that it did not involve much teaching!). I made a decision that was to shape the rest of my life.*

"My wife and I arrived in Adelaide on a hot November day in 1980. The second day after I arrived, the lab group took me on a winery tour of McLaren Vale, I knew then that I had found my spiritual home! The next four years were some of the most exciting times for me scientifically. John gave me a lot of freedom to explore various aspects of the structure and mechanism of PC. Not only did John give me this freedom and his unwavering support, he encouraged me to collaborate with as many other scientists as possible.

"One of the main problems at this time was the interpretation of the biophysical and kinetic results that the lab (including Greg Goodall, Yee-Sim Khew Goodall, Anne Chapman Smith and Nelson Phillips) was generating because there were no 3D structures of PC available and indeed, the gene had not been cloned and sequenced. John was well aware that our understanding of how PC worked and was regulated, both at the protein level and expression level, would not progress until we had the sequence of the gene and the 3D structure of the enzyme. So, John set in motion work in his lab by Filip Lim, Ian Cassady, Philip Morris, Michelle Walker, Grant Booker and Sarawut Jitrapakdee that led to the cloning and sequencing of the PC genes in yeast, rat and chicken. John's lab also set about developing expression systems for the yeast and human PCs.

"John and I collaborated, along with Sarawut, on using site-directed mutagenesis to investigate structure–function relationships in PC, but always in the back of our minds was the need to obtain a structure of PC. So, we decided to establish a collaboration with someone overseas who had access to substantial funding and crystallographic expertise. Consequently, John and I visited Madison and persuaded Mo Cleland to form a collaboration with us, Sarawut and the crystallographer, Ivan Rayment, in whose lab Martin St. Maurice worked. Between 2005 and 2012, we obtained about $3.5 million in NIH funding, and the crowning achievement of this collaboration was the determination of the first structure of a PC (Rhizobium etli) *in 2007 (2). This structure completely changed our understanding of the mechanism of action and regulation of PC as it demonstrated that PC exhibited inter-subunit catalysis and half-of-the-sites-reactivity, and showed the effects of the major physiological regulator, acetyl CoA, on the structure of the enzyme."*



John Wallace at the University of Adelaide, 2008.

Sarawut Jitrapakdee: *"I had the great privilege of joining John's research team as a PhD student in 1994. At that time, John's PC team, which included Michelle Walker, Neil Brewster, and Dale Vale, was exploring the regulation of yeast PC isozymes, PYC1 and PYC2. I was fortunate to contribute to this work by focusing on the regulation of PC in mammalian cells. We became the first group to identify that mammalian PC employs two alternative promoters to control its expression in a tissue-specific manner under varying physiological conditions. This discovery not only enhanced our understanding of PC regulation but also opened avenues for further exploration into its metabolic roles.*

"Our research extended through an inspiring collaboration with Michael MacDonald (University of Wisconsin-Madison, USA). This work unraveled the metabolic role of PC in regulating glucose-induced insulin secretion in pancreatic islets. Using the Zucker fatty rat as a model, we discovered that PC

is overexpressed in the adipose tissue of these rats. These findings underscored the influence of nutritional and hormonal factors on PC expression, paving the way for further research into its regulatory mechanisms. We continued to understand what factors controls PC overexpression in adipose tissue by collaboration with Antonio Vidal-Puig and Stephen O'Rahilly at the University of Cambridge. We demonstrated that PC is regulated by peroxisome proliferator-activated receptor gamma (PPARγ), a master regulator of adipocyte differentiation and insulin sensitivity. This discovery bridged a critical connection between PC and insulin, another protein central to John's research interests.

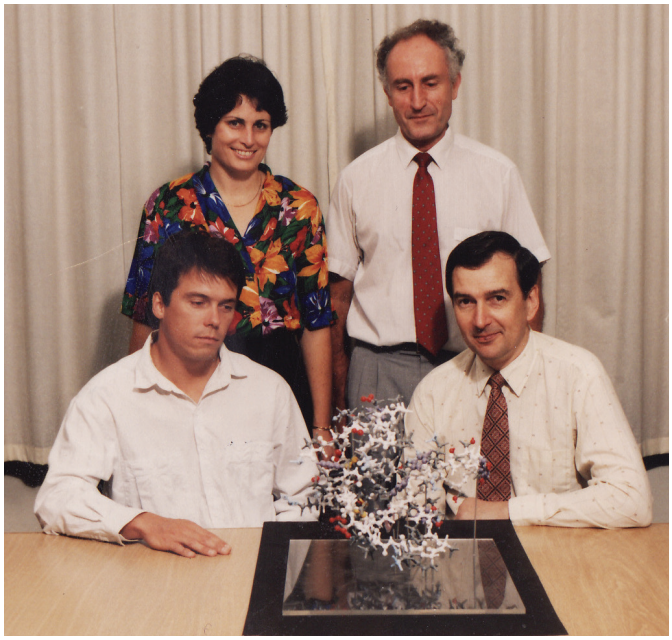
"John's mentorship and collaborative spirit have been pivotal to my academic journey and have left an indelible mark on the field of metabolic biochemistry."

As time went by, John's interests further broadened to understanding the mechanisms regulating PC action by biotin protein ligase (BPL). Again, the approach involved molecular biology, biochemistry, structural biology, chemical synthesis and enzyme kinetics, culminating in several BPL structures and development of inhibitors with an eye towards application as novel antibiotics.

Steven Polyak: *"I contributed to the BPL project first as a PhD student and subsequently as a postdoctoral researcher. The BPL project was first established through a collaboration involving John, Anne Chapman-Smith and John Cronan (University of Illinois), who visited Adelaide on a 12-month sabbatical. The team cloned the gene for BPL from the prototypical yeast* Saccharomyces cerevisiae, *which enabled protein structure and function studies to be performed to better understand the enzyme's role in the activation of PC (and other biotin-dependent enzymes) through the attachment of the biotin cofactor. BPL became a focus of interest for the pharmaceutical company Pfizer that wanted to pursue the enzyme as a drug target for new antifungal therapies. At the completion of that collaboration, I and John's team continued to pursue BPL as target for anti-infective drugs (3), this time with a focus on new antibacterials. The project was significantly enhanced with the collaborative contributions of medicinal chemist Andrew Abell (Adelaide University) and structural biologists, Grant Booker (Adelaide University) and Matthew Wilce (Monash University). Our team pursued this project for over a decade, and successfully published many papers in the field, as well as several patent applications."*

The IGF Story

Whilst John's first passion was PC, remarkably he developed an equally strong growth factor research program. This was initially based on a collaboration with John Ballard and Leanna Read to characterise the growth factors present in colostrum, which subsequently led to his long-term interest in insulin-like growth factors (IGFs). Purification, sequencing and cloning of human, cow, rat, pig and chicken IGFs with Geoff Francis, Chris Bagley and Zee Upton culminated in identification of the super potent IGF, des(1–3)IGF-I. John, John Ballard, Leanna Read and Julian Wells (Department of Biochemistry, University of Adelaide) quickly realised the translatable potential of des(1–3)IGF-I. Subsequent patents supported the formation of Gropep Pty Ltd and the highly successful Cooperative Research Centre for Tissue Growth and Repair, which served as training grounds for many students and postdocs.



Clockwise from top left: Leanna Read, John Ballard, John Wallace and Rob King in 1991 with a model of IGF-I.

John's approach and key to success was to attract and nurture top students and postdocs to both research programs and to provide them with a lab family in which to pursue their studies and interests. Part of the family atmosphere was generated through the many cherished lab curry nights. These were always highly anticipated, as were Friday nights at the staff club. John also encouraged external collaboration and attendance at local (Lorne Proteins, in particular) and overseas meetings. He saw the importance of networking and making connections with both researchers and industry.

Briony Forbes: *"I was fortunate to be one of those trained under John and I subsequently spent many years working alongside him. He gave me and other team members freedom to pursue our passions whilst quietly keeping us on track to success. He was continually looking for the latest innovations that would help us push the boundaries in our research. John was an early adopter of BIAcore technology, influenced by a bright Swedish postdoc from Pharmacia (Goran Forsberg) and I quickly realised its potential for understanding the IGF system. This was particularly useful as we characterised IGFs' molecular interactions with IGFBPs that had been*

cloned and purified in the lab, and interactions with the IGF-1R and IGF2R. Through the generation of around 100 IGF analogues, we contributed significantly to the body of knowledge describing the mechanisms of IGF action. The group built an understanding of how IGFs were bound and released by the IGFBPs during pregnancy (Sharon Gargosky) and cancer (Cher Soh and myself), forming the basis of the idea to generate an IGF 'molecular sponge' as a cancer treatment, an approach that is still being pursued by others in the field. John forged lifelong friendships and collaborations in the IGF field, including Ray Norton, Leon Bach, Grant Booker, John Carver and Leah Cosgrove, as we sought to understand the structure and function of IGFs. Together we were the first to determine the structure of IGF-II (4) and solved structures of IGF-I, IGFBP N- and C-terminal domains."

The ARIIA Prize ceremony in 2007. From left: Briony Forbes (runner-up), Paul Tolstoshev (joint winner), John Wallace (joint winner) and Pat Wallace.

Contributions to Science

John was always a strong supporter of the ASBMB and was involved with the organisation of the Society as the State Representative for South Australia between 1977 and 1979. He was awarded the Society's LKB Medal in 1986. In 2000, John was awarded the Society's most prestigious award, the Lemberg Medal. John was elected President of the Society in 2003 and became an Honorary Member in 2009. He was a member of the Society for more than 50 years.

In 2004, John was awarded the Leach Medal by the Lorne Protein Conference, a conference he looked forward to attending every year. In 2007, John was awarded the ARIIA Prize by Adelaide Research & Innovation for 'demonstrating entrepreneurship and/or innovation in his work with measurable impact in the community'. John further served the field of biochemistry by being a Member of the National Committee for Biomedical Sciences 2003–2005, a Member of the Expert Advisory Committee for Biological Sciences & Biotechnology of the Australian Research Council 2001–2003, and a Member of the NHMRC Grant Review Panel (Biochemistry).

Personal Interests and Family Life

As a young man, John enjoyed an active life, as did his sweetheart Pat. It must have been a great blow to discover he was afflicted with rheumatoid arthritis, which limited his movement and provided much pain and suffering over the years. Thankfully, his passion for research, good food and wine, and travel provided other interests, and swimming in a warm pool provided some relief to his aching joints. Some of his happiest times were sipping a good red wine in the company of his fellow researchers. John touched so many in his academic life and he enjoyed nothing more than seeing past students and postdocs go onto their own careers. He always kept in touch over the years, with many overseas past lab members enjoying and looking forward to his annual Christmas and birthday wishes.

Although John's 'research family' provided much enjoyment, his wife, Pat, and sons, Rob and Chris, were most important to him, and he was delighted when his two granddaughters, Orla and Charlotte, came along. Pat and John enjoyed 60 years of marriage and were devoted to one another. Sadly, Pat passed away in 2022. John will be greatly missed by us all.

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University of Western Australia
Sarawut Jitrapakdee
Mahidol University, Thailand
Steven Polyak
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Briony Forbes
Flinders Health and Medical Research Institute

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Off the Beaten Track

Written by former researchers who have now established careers outside of research, Off the Beaten Track is intended to give the readers insights into the range of alternative careers available to them. Authors describe the paths they have taken to arrive at their present career and provide a detailed description of exactly what the job entails on a day-to-day basis.

The Shift From Papers to Patients: Transforming Into a Clinical Research Associate

Shaun Gaskin
Senior Clinical Research Associate, IQVIA

"Academia is not for me." "I want something different." These were the phrases floating around my mind as I progressed into the final year of my PhD in biochemistry/cancer cell biology. Bench research had been a lot of things to me; exciting, laborious, motivating, frustrating and many more emotions. I always knew that I wanted to work in the development of novel therapeutics and really loved lab work throughout my studies. Entering the last year of my PhD research though, I knew that my time at the bench had come to an end. I began to think about how else I could involve myself in this rewarding field. I enjoyed being hands on and at the forefront of research, so clinical trials stood out to me as an interesting option. Taking a look at the different types of roles that exist in the clinical trials world, there were so many options, but how many were (a) something I could move into without having to undertake further study, and (b) didn't have a long pathway to reach the position (I needed that achievable goal)? The position that jumped out to me was a Clinical Research Associate (CRA). As a CRA, you oversee the conduct of clinical trials at research sites (hospitals and clinics), ensuring that studies are done according to established protocols, regulatory requirements and ethical standards. You act as a bridge between the sponsor drug company and the clinical trial sites to guarantee the smooth and compliant execution of research studies.

The CRA role excited me because (1) there were a lot of advertisements for CRAs and senior CRAs, meaning that there were plenty of positions available and room for growth, (2) the only qualification required for the role was a life sciences degree (tick!), (3) you are required to be an 'expert' in the protocols you are working on, just like your PhD project, (4) you interacted with actual people throughout your day, instead of Eppendorf tubes and cultured cells, and (5) domestic travel was a requirement, something which I enjoyed doing at that stage of my life. The unfortunate thing about the advertisements I was reading was that they required two years CRA experience, meaning it wasn't really an entry level position that I could comfortably move into directly from my PhD. Armed with this knowledge, I attended an industry career information and chatted with a CRA guest speaker about my goal. They indicated that their company ran a competitive training program to become CRAs, and that preference was often given to people with experience working as a Study Coordinator (SC) at a site. To help obtain a job as a SC, I took a free online course in Good Clinical Practice; the fundamental principles that govern trials worldwide. Securing a SC position, I was able get my first experience in the trials industry. While the role and company itself wasn't what I could see myself doing for a long time, I always knew it was my foot in the door. After about a year in the role, I applied for the CRA training program. Although I was unsuccessful in entering the program, I was offered a side-step into the company with the plan to put me into the next round of the training program. Six months later, I was accepted into the CRA training program and I haven't looked back since! It's now been five years since I completed the program and I have worked my way up to become a senior member of our team, developing a great understanding of the ins and outs of the role, and being able to drive progress to improve the CRA role in the ever-evolving world of clinical trials, gaining the respect of colleagues and management globally.

Shaun Gaskin.

I have described in general terms the role of a CRA, but this doesn't really tell you much about what I do every day. This role is very dynamic, where your plan for the day can change in the space of a phone call, having to switch priorities quickly to deal with urgent situations that arise. Maybe there are unexpected changes to a patient's dosing requiring your immediate attention. Maybe there is important safety information you need to obtain from the site to ensure patient safety is not compromised. Maybe you need to change your scheduled visit to a site to the next day instead of next week. All of these can throw the best laid plans out the window. But as mentioned above,

Off the Beaten Track

you are the main connection between the site running the trial, and the drug company, so in these situations, you're the first responder. Building and maintaining strong relationships between the trial stakeholders will help you succeed as a CRA. You are the go-to person for the site. As questions flow from the site to the sponsor through you, the reverse is also true. Your study team will reach out to you to gather information from the site, to have site capture data missing from databases, to discuss particular patients, etc. Domestic travel is required for pretty much all CRA roles, so you'll have some long days catching 6 am flights to go to site, landing back at home at maybe 7 pm. While emails will make up most of your communications, phone calls and face to face conversations play pivotal roles in executing your job.

As a CRA, you'll meet some amazing SCs and Investigators who build strong connections with their patients and enjoy offering the latest in treatments to their patients. You'll work on studies where just by looking at the data (as you have no interaction with patients), you'll see improvements in the patient's health, lifestyle and overall wellbeing. You will be a part of that positive change, bringing improved outcomes to patients.

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Moving the Goalposts: Key Factors Shaping the Scope of Patent Claims

Dr Harriet Keenan (Associate) from FPA Patent Attorneys describes the factors to consider when determining claim scope.

Harriet Keenan.

Introduction

It will come as no surprise that patent claims are crucial – they define the scope of the invention and the resulting monopoly granted by the patent.

Throughout the journey from patent application to granted patent, claim scope is influenced by a variety of internal and external factors including:

- **Internal** – the data and disclosure available within the patent application; previous inventor disclosures; drafting and commercial strategy to maximise value
- **External** – prior art from other parties; the patent examination process; and competitor activity (patent landscape and freedom-to-operate)

Understanding the nuances of claim scope, and how to effectively navigate the trade-offs between broad and narrow claims, is essential for patent applicants seeking to maximise the commercial impact of their inventions.

This article will explore the key principles and considerations surrounding claim scope and explain why it is such a vital aspect of developing a successful patent strategy.

What is claim scope and why is it important?

The **claims** of a patent application define the invention; and their scope ultimately define the scope of the granted patent's monopoly. Understanding claim breadth is therefore an essential aspect of obtaining commercially-valuable patent protection.

The **description** of a patent application provides evidence to demonstrate that the invention works and describe the invention with enough information that a person in the field would be able to perform the invention. This is the quid pro quo of patents – in exchange for obtaining a monopoly to use the invention defined in the granted patent, the patentee must provide sufficient information for others to readily work the invention once the monopoly expires. The information included within the patent specification directly influences how narrow or broad the claims can be. In turn, this impacts the scope of the protection/monopoly provided by the granted patent.

How claims are written, such as what features are included or which language/terms are used, directly contributes to whether the claims are interpreted as broadly or narrowly defining the invention (see **Table 1**).

Claim **broadening** is a defensive technique: to avoid failing to encompass straightforward "design-arounds", and to therefore strengthen protection against potential infringers. In other words, if the scope of a patent is too limited, then third parties may be able to design-around a patent claim which reduces the commercial value of the patent. However, claim **narrowing** is also a technique to avoid problematic prior art or potential issues with establishing support for the claimed invention.

Moving the Goalposts: Key Factors Shaping the Scope of Patent Claims

Table 1. *Claim features that impact claim breadth.*

Broader	Narrower
Less elements/steps required	More elements/steps required (e.g. a biomarker assay requires all six biomarkers to be detected instead of one out of the six; a method requires two steps instead of three)
More variation (e.g. greater sequence variation for protein or nucleic acids)	Less variation (e.g. no or minimal sequence variation)
Less specific terms/elements required	More specific terms/elements required (e.g. an exact component, sequence and/or combination must be included in the claim)
Molecule or composition is for use in a less specific context	Molecule or composition is for use in a more specific context (e.g. defining disease to be treated as liver cancer, not *any* cancer; defining the cancer to be treated as expressing a specific tumour antigen, not treating *any* cancer)

What factors influence claim scope?

Drafting

Drafting claims with the appropriate breadth is a critical aspect of obtaining commercially-valuable patent protection. When writing (drafting) a patent application, various strategies may be employed to draft the claims broader or narrower depending upon the prior art and the data available.

To assist in establishing that the claimed invention is novel and inventive over the prior art, claims may be narrowed to include additional features that distinguish the invention from previous disclosures. This may include previous disclosures from the inventors themselves.

The experimental data and information that is available to support the invention will directly influence the scope of the claims. Claims may be broadened to encompass other similar ways of performing or achieving an invention, which have not been experimentally exemplified by the inventors, but that the skilled person would reasonably expect to work based on their understanding of the field.

Additional experimental examples can help more firmly establish proof of a general principle; broadening the scope of a patent application by making it more plausible that the skilled person would extrapolate from the data of the patent application to other versions/formats/iterations/diseases (see **Fig. 1**). Conversely, if insufficient information is available to include within the patent application, then the scope of the claims may be narrowed to correspond with the information that is available (and a strategy may be developed to capture other claim positions in other patent filings).

Examination

The claims in your freshly drafted patent application are unlikely to be what you have at the end of the patent examination process in your granted patent.

Before a patent application is granted, the application undergoes examination (also referred to as patent prosecution). An examiner at a patent office assesses whether the application (including the description and claims) meets the legal requirements to constitute a valid patent.

During examination, claims can be amended to address objections raised by the examiner, to increase the chances of the patent application being granted. These amendments often result in a change in claim scope compared to what was originally drafted.

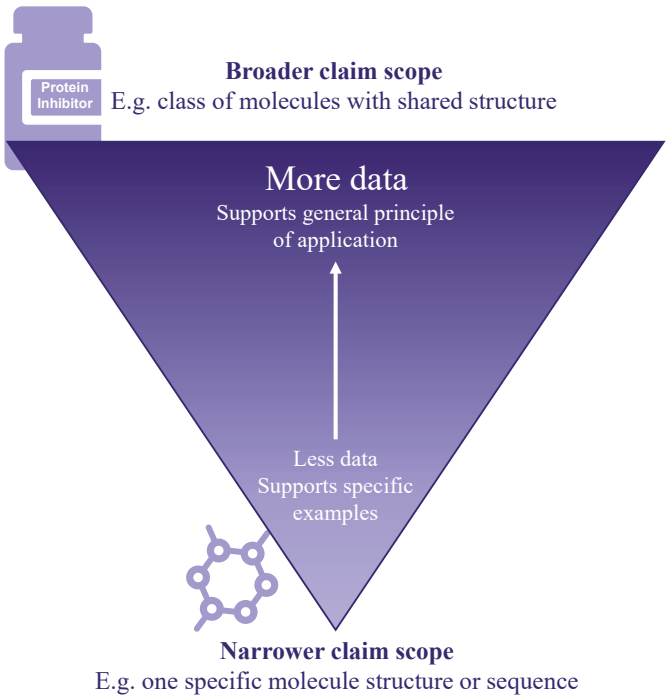

Fig. 1. *In life sciences, the experimental data included in a patent application directly impact the claim scope.*

Moving the Goalposts: Key Factors Shaping the Scope of Patent Claims

Jurisdiction

Patent examination process differs from jurisdiction to jurisdiction, as do the legal requirements that must be met for a patent to be granted. This can often result in the claims being pursued in one jurisdiction (e.g. Australia) being different from those in another jurisdiction (e.g. the US, Europe). In particular, some jurisdictions have stricter requirements for support, meaning claims are usually amended to have narrower scope, and some jurisdictions do not permit claims to particular subject matter (e.g. Europe will not permit claims directed to methods of medical treatment). Across a patent portfolio, these differences often result in the obtained claim scope being different in different jurisdictions.

Strategy

Strategic choices also come into play when drafting and prosecuting patent applications, which often impact claim scope. These choices to narrow or broaden claim scope factor in the considerations discussed above: existing prior art; supporting data; potential challenges during examination; and jurisdictional differences. But patent strategy may additionally take into account commercial aspects such as: known or predicted competitor activity; the patent landscape; freedom-to-operate; avenues to extend patent term; and building a portfolio that is attractive to potential investors. You patent attorney can advise how to maximise the value of your patent protection.

Is broader claim scope always better?

Broad claim scope improves the scope of patent protection. However, narrow claims can still provide valuable protection for a key commercial product. For example, if you know that certain modifications to the product cause it to work poorly, then narrowing the claim scope to exclude those modifications is unlikely to be detrimental to your protection.

And in some instances, it may be commercially beneficial to pursue narrower patent protection first, to ensure that a patented position is obtained. Having patent 'runs on the board' can help progress funding applications and investor interactions – see our previous article in the August 2024 issue of the *Australian Biochemist*.

Take-home messages

- Understanding claim scope is essential for ensuring the value of protection achieved by a patent.
- Multiple factors influence claim scope throughout the patenting process, including drafting, examination and commercial considerations.
- Drafting and claim amendments during examination are levers that can be strategically pulled to improve patent protection.
- Broader claims are not always better – narrow claims can still provide valuable protection for key commercial products. Narrow claim protection can also fit into an overarching strategy for obtaining a commercially attractive patent portfolio.

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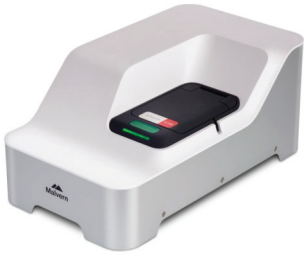

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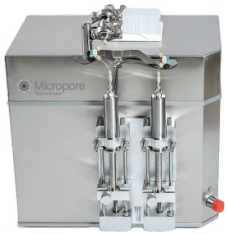

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ASBMB Medallist and Awardee Profiles

The Lemberg Medal is awarded to a distinguished Australian biochemist or molecular biologist who will present the Lemberg Lecture at the annual ASBMB conference. The Medal is presented in memory of Emeritus Professor MR Lemberg, who was the Society's first President and Honorary Member. Nominees must have been members of the Society for at least five years before the year in which the Medal nomination is to be considered. An honorarium is provided by the ASBMB.

The Lemberg Medal
Michelle Haber

Michelle Haber is Executive Director of the Children's Cancer Institute, Co-Head of the Institute's Experimental Therapeutics and Molecular Oncology Group, and Conjoint Professor at the UNSW Sydney. She is recognised internationally as a leading childhood cancer researcher, who has made pioneering breakthroughs that have greatly advanced our understanding of childhood cancer. Through a career focussed on identifying novel targets and developing therapeutic and diagnostic approaches to improving outcomes of children with aggressive childhood malignancies, Michelle has contributed fundamental advances in knowledge and changed clinical practice, improving survival and quality of life for children with these cancers.

Michelle has pioneered three novel therapeutic approaches for high-risk child cancers (polyamine inhibition, NAMPT inhibition and chromatin modifier therapies), which have since been adopted into five national/international clinical trials. She played a key role in developing PCR-based technology to detect minimal residual disease (MRD) in children with Acute Lymphoblastic Leukaemia (ALL), which resulted in doubling of the cure rate for high-risk patients with ALL. This led to MRD testing being made standard of care for patients with ALL, and subsequent government funding to make this test reimbursable through Medicare. Michelle has also changed clinical practice for Australian children with cancer through her establishment and leadership of ZERO, Australia's first child cancer personalised medicine program, which is enabling every child with cancer to have tailored therapy, targeting the specific genetic and biological characteristics of their individual tumour.

Michelle has received numerous awards (Order of Australia; NSW Scientist of Year; NHMRC Ten of the Best; Premier's Awards for Excellence in Translational Research, Cancer Researcher of Year) and is a Fellow of both the Australian Academy of Science, and the Australian Academy of Health and Medical Science. She was featured in *Cancer Cell* as one of ten international child cancer research experts. Most recently, Michelle was awarded the Sidney Sax Medal for outstanding health leadership from the Australian Healthcare and Hospitals Association, and received Lifetime Achievement Awards from both the Advances in Neuroblastoma Research Association and *CEO Magazine*. She was also a 2024 finalist for NSW Senior Australian of the Year.

Michelle has served on the Steering Committee of the International Advances in Neuroblastoma Research Association; Director of Association of Australian Medical Research Institutes; board member for Kids Cancer Alliance, Luminesce Alliance and South Australian immunoGENomics Cancer Institute; and is Co-Chair of the ACRF Medical Research Advisory Committee. She has also secured $300 million to build Australia's first Children's Comprehensive Cancer Centre to house up to 900 research staff and clinical partners, opening in late-2025.

ASBMB Medallist and Awardee Profiles

The Shimadzu Research Medal is awarded to an outstanding Australian biochemist or molecular biologist with less than 15 years postdoctoral experience. The successful candidate will present the Shimadzu Medal Lecture at the ASBMB annual conference. Nominees must have been members of the Society for at least two years before the year in which the Medal nomination is to be considered. An honorarium is provided through the courtesy of Shimadzu.

The Shimadzu Research Medal
Si Ming Man

Si Ming Man completed a Bachelor of Medical Science (Hons I, University Medal) at UNSW Sydney. His interests in host–pathogen interaction inspired his move to the UK, where he completed his PhD at the University of Cambridge in 2013 under the supervision of Professor Clare Bryant. During his PhD, he studied macrophage responses to the foodborne pathogen *Salmonella*, generating two first-author publications in *PNAS*. With the support of an NHMRC RG Menzies Early Career Fellowship, Si Ming moved to Memphis Tennessee, USA, where he completed his postdoctoral training at St. Jude Children's Research Hospital under the mentorship of Dr Thirumala-Devi Kanneganti. During this time, Si Ming and his colleagues identified a role for innate immune proteins in liberating microbial ligands to drive activation of innate immunity and unexpected roles of immune receptors in cancer, generating first-author publications in *Cell* (2015, 2016), *Nature* (2016) and *Nature Immunology* (2015).

Si Ming returned to Australia in 2017 to establish his lab at the John Curtin School of Medical Research, Australian National University. He is now a Professor, CSL Centenary Fellow and NHMRC Leader Fellow. His more recent research is focused on the molecular and biochemical mechanisms of inflammation, including how antimicrobial killer proteins destroy bacteria and reduce antimicrobial resistance (*Nature Communications* 2022 and *EMBO Journal* 2023), anti-cancer capabilities of immune proteins (*Nature Immunology* 2024, *Science Advances* 2024 and *Nature Communications* 2024), and immunity to toxins (*Nature Microbiology* 2019, *Nature Communications* 2020 and *EMBO Reports* 2023). Si Ming was named a Clarivate Highly Cited Researcher in 2020, 2022, 2023 and 2024. His research has been recognised with 27 prizes, including the Australian Academy of Science Gottschalk Medal in 2023, Frank Fenner Prize for Life Scientist of the Year in 2022, Prime Minister's Prizes for Science in 2022 and the ASBMB Eppendorf Edman ECR Award in 2020.

ASBMB Medallist and Awardee Profiles

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 (in Australia or overseas) 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 conference. Applicants must have been members of the Society for at least two years before the year in which the Award application is to be considered. The contribution to travel expenses is provided through the courtesy of SDR Scientific.

The SDR Scientific Education Award
Amber Willems-Jones

I am an education-focused academic in the Department of Biochemistry and Pharmacology at the University of Melbourne. Two decades ago, I began my biochemistry journey by embarking on a Bachelor of Science (Honours) degree at the University of Melbourne and then completing my PhD investigating the 'Molecular Interactions of the TyrR Bacterial Regulatory Protein' in the then Department of Biochemistry and Molecular Biology, University of Melbourne.

For my first (and only, as it turned out) postdoctoral position, I worked as a molecular biologist research fellow with the familial breast cancer consortium, kConFab at the Peter MacCallum Cancer Centre. During the seven years in this role, I had the amazing opportunity to meet my science hero, Professor Joe Sambrook, who became a most valuable mentor, giving me sage advice on all things research, from analysing data to preparing manuscripts. We also spent a lot of time talking footy as he too was a Carlton Blues fan.

In 2012, I returned to the University of Melbourne to assume the role of subject coordinator for the second-year practical biochemistry subject, Techniques in Molecular Science. It is in this role that I found my true calling and my passion for education. I have had the joy of guiding and inspiring students towards building a foundation of laboratory-based biochemistry and molecular biology skills from which to pursue *their* biochemistry journey. As coordinator, I have introduced inquiry-based learning modules to develop troubleshooting skills and critical thinking, and I also foster skill development in scientific writing. More recently, I have been privileged to be part of the teaching team for the first-year Bachelor of Biomedicine core subjects, Discovering Biomedicine and Exploring Biomedicine, working and sharing expertise with amazing colleagues.

My research interests lie in the Scholarship of Teaching and Learning. I am passionate about ensuring students acquire the requisite skills and understanding of key concepts that lay at the foundation of practical biochemistry and molecular biology. My research is directed at improving student understanding, as well as promoting the importance of self-regulated learning processes and strategies, alongside the development of skills in academic literacy and academic judgement. I also have a keen interest in exploring the quantitative literacy skills of university students, inspired by research from the 2024 ASBMB SDR Scientific Education Award recipient, Dr Julian Pakay.

I am a life-long learner who regularly reflects on my teaching practice and incorporates new approaches to continue to stay curious and to integrate the latest advancements to my teaching. I apply my own research findings to make improvements to my craft and relish opportunities to learning through peer collaborations.

I am honoured to have been recognised for the 2025 ASBMB SDR Scientific Education Award by my peers and will continue to work to inspire budding young biochemists of the future.

ASBMB Medallist and Awardee Profiles

The Eppendorf Edman ECR Award is awarded to an ASBMB member with no more than seven 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 present a lecture within a symposium at the ASBMB annual conference. Applicants must have been members of the Society for at least two years before the year in which the application is to be considered, or must have taken out a three year membership in the year of the application. The contribution to travel expenses is provided through the courtesy of Eppendorf South Pacific.

The Eppendorf Edman ECR Award
Dimitra Chatzileontiadou

Dimitra Chatzileontiadou was awarded her PhD with Distinction in Biochemistry and Molecular Biology from the University of Thessaly, Greece, in November 2016. Immediately after completing her PhD, she was awarded a competitive international IKY Fellowship for excellence in her postgraduate studies, that supported her postdoctoral research for one year. Both her PhD and one-year postdoctoral research project were very successful, evidenced by an outstanding publication record.

In late-2017, Dimitra moved to Australia as a postdoctoral research fellow in the laboratory of Professor Jamie Rossjohn, at Monash University. In 2019, she joined Professor Gras' newly established group at Monash University, and, in 2021, the group relocated to La Trobe University. Since her PhD, she has driven multiple successful projects resulting in a deeper understanding of host–pathogen recognition. Dimitra was recently awarded an NHMRC Emerging Leadership 1 Investigator Grant commencing in 2026 to investigate the protective nature of human leukocyte antigens in fighting against viruses. She has been awarded many competitive research grants and awards, including an Australian Institute of Nuclear Science and Engineering Early Career Research Grant for her leading work in collaboration with the Australian Synchrotron (2020), an Australian Society for Medical Research Small Research Grant (2021) and a La Trobe University Large Collaboration Internal Investment Scheme Grant (2021), for her leading work on COVID-19 research. Moreover, she was awarded a La Trobe Institute for Molecular Science Miller Postdoctoral Travel Fellowship (2022), the Australian and New Zealand Society for Immunology Career Advancement Award (2022) as well as a La Trobe University Excellence in Research: Engagement and Impact Award (2023).

The key aim of Dimitra's research is to elucidate the molecular mechanisms that are involved in the immune system actions when faced with viral infections. In total, Dimitra's work has thus far resulted in 34 publications in top-tier journals in their respective fields, with more than 50% lead authored including the high impact publications in the journals *Nature* (2023), *Immunity* (2021) and *Cell Reports* (2024). Her publications have drawn wide international attention, with the recent one in *Nature* being ranked in the top 1% of most cited articles by media in history, with an Altmetric Attention score of 2959. Dimitra is familiar with research dissemination in the media via podcasts, social media and blogs, as evidenced by personal invitations for several interviews, including in *The Guardian, ABC News, Neos Kosmos, Kathimerini* and *Proto Thema.*

ASBMB Medallist and Awardee Profiles

The Boomerang Award is offered to an outstanding expatriate Australian biochemist or molecular biologist to provide an opportunity to return to Australia to present their work in a Symposium at the annual ASBMB conference and to give seminars at universities or research institutes in at least one other Australian city. The Award is intended to provide the awardee with exposure in Australia and to facilitate interactions with local researchers. Applicants must have been a member of a recognised Australian scientific society for at least two years, or must have taken out a three year membership in the year of the application, and awarded their PhD not more than ten years prior to the closing date (or equivalent taking any career disruption into account). The contribution to travel expenses is provided by ASBMB.

The Boomerang Award
Alexander Knights

Alexander Knights grew up in Sydney and completed his undergraduate studies and graduate training at UNSW Sydney. Alex had his first taste of laboratory research as an undergrad, when he received a Summer Vacation Research Scholarship to study gene regulation with Professor Merlin Crossley. Alex then undertook his Honours year in Professor Crossley's lab, focusing on the transcription factor KLF3 and its role in metabolic and immune regulation. Alex graduated with a BA (Hispanic Studies), a BSc Adv (Biochemistry) with First Class Honours and was awarded the University Medal, given to the highest performer in a degree program.

Alex received an Australian Postgraduate Award and Research Excellence Award, allowing him to pursue his doctoral studies under the mentorship of Professor Crossley and Professor Kate Quinlan. During his PhD, Alex uncovered roles for KLF3 as a regulator of galectin-3 (*Journal of Biological Chemistry* 2016) and as a transcriptional guardrail against NF-κB-mediated systemic inflammation (*Journal of Biological Chemistry* 2020). Alex also sought out new research directions during his PhD, with a focus on adipose immunology. This led him to discover novel functions of fat-resident eosinophils (*Nature Communications* 2020), and he performed the first transcriptomic characterisation of these cells (*Journal of Leukocyte Biology* 2023).

Alex then moved abroad for his postdoctoral studies to the University of Michigan. Here, he was awarded a Michigan Life Sciences Fellowship to study immunometabolic crosstalk in adipose tissue and liver under the supervision of Dr Jun Wu. During the year he spent with Dr Wu, Alex discovered a subpopulation of fat-resident macrophages that secrete acetylcholine to regulate adipose function and thermogenesis (*EMBO Journal* 2021).

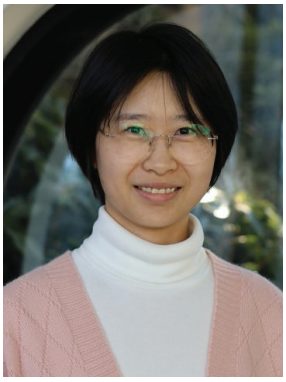
One year into his postdoctoral studies, Alex was the recipient of a Pioneer Fellowship that prompted him towards new interdisciplinary pursuits. He joined Michigan's Department of Orthopaedic Surgery to team up with veterinarian-scientist Dr Kurt Hankenson, and biomedical engineer Dr Tristan Maerz, to understand pathological Wnt signaling in osteoarthritis. Since then, Alex's work has shed light on the diversity and functions of synovial fibroblasts in osteoarthritis disease progression (*Annals of the Rheumatic Diseases* 2023), plus he has characterised the recruited and resident macrophages of synovial tissue (*eLife* 2023). In 2023, he received a prestigious K99/R00 NIH Pathway to Independence Award to complete his postdoctoral studies and fund the start of his independent career. In March 2025, Alex launched his own laboratory studying crosstalk in joint health and disease at Washington University in St Louis.

ASBMB Fellowship Profiles

The ASBMB Fellowships are awarded annually to biochemists or molecular biologists, in their early career and 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 briefly visit a research laboratory in Australia or elsewhere to access specialised equipment or to learn new research techniques. Applicants must be at least in the second year of PhD training and not more than two years subsequent to the award of their PhD degree. Applicants must have been members of the Society for at least one year immediately prior to application or must have taken out a three year membership in the year of the application.

The Collins family kindly established the Fred Collins Award to honour the role that Fred Collins played in the establishment of the Australian Biochemical Society.

Shouya Feng – recipient of the Fred Collins Award for the most outstanding ASBMB Fellowship applicant



Shouya Feng completed her Bachelor of Science in Biology in 2018 at Wuhan University, China. She commenced her PhD studies at the John Curtin School of Medical Research at the Australian National University under the supervision of Professor Si Ming Man. During her PhD, Shouya investigated how antimicrobial proteins trigger the release of pathogen-associated molecular patterns and lead to the activation of innate immune pathways. Upon completion of her PhD, Shouya transitioned to a postdoctoral position with Professor Seth Masters at the Walter and Eliza Hall Institute of Medical Research and then at the Hudson Institute of Medical Research. She now focuses on the molecular mechanisms of innate immune signalling in autoinflammatory diseases.

Shouya has published 16 articles (six first/co-first author articles in *Nature Immunology, Nature Communications, EMBO Journal, Trends in Cell Biology* and *Journal of Molecular Biology*). In 2024, Shouya received an Early Career Research Grant from the Jack Brockhoff Foundation, an Australian and New Zealand Society for Immunology postdoctoral travel award and an EMCR oral presentation prize from the ImmuMon symposium. She has previously received student travel awards from the International Cytokine and Interferon Society (2022), the Australian Society for Microbiology NSW–ACT branch (2022), the Biotron Founders Award (2022) and three early career grants from the Bootes Medical Research Foundation as CIB (2019, 2020 and 2021).

This ASBMB Fellowship will support Shouya's travel to the 13th Meeting of the International Society of Systemic Autoinflammatory Diseases (ISSAID) and a short laboratory visit to the Institute Cochin in Paris, France.

Daniel Fox

Daniel Fox completed a Bachelor of Medical Science (First Class Honours) at the Australian National University in 2018, where his research focussed on innate immunity, inflammasomes and host–pathogen interactions. Currently, he is in his final year of his PhD under the supervision of Dr Rhys Grinter and Dr Gavin Knott at the Bio21 Institute at the University of Melbourne, and Monash University. His current research focusses on the structure and function of transporters responsible for iron piracy in Gram-negative pathogens, where he leverages state of the art advances in machine learning to design *de novo* protein binders that can potently inhibit bacterial growth.

His research has been published in *Nature Communications, Nature Microbiology, Journal of Molecular Biology, FEBS Letters, Cell Research, Science Advances* and *EMBO Journal*.

He has presented his work at Cold Spring Harbor Asia in Suzhou, China, at the Bacterial Infection and Host Defense conference, and Queenstown Research Week in New Zealand. He has been awarded an EMBL Australia Travel Grant, a Royal Society of New South Wales Scholarship, ICIS Milstein Travel Award, two grants from the Bootes Medical Research Foundation, and has won poster prizes at Lorne Proteins, Melbourne Protein Group Student Symposium, CCeMMP Research Symposium and SCANZ Crystal34.

This ASBMB Fellowship will allow Daniel to travel to Busan, South Korea, to participate in the Young Scientist Program as a part of the 2025 meeting of the Federation of Asian and Oceanian Biochemists and Molecular Biologists.

ASBMB Fellowship Profiles

Cynthia Turnbull

Cynthia Turnbull is a postdoctoral researcher at the John Curtin School of Medical Research (JCSMR) within the Australian National University (ANU). Her PhD, conferred in 2023, with Professor Carola Vinuesa explored the role of genetic variants in the development of autoimmune disease. She discovered that the anti-fungal protein DECTIN-1 is a novel regulator of the immune system and can exacerbate the severity of autoimmune disease. Currently, she works in the molecular biology laboratory of Professor Si Ming Man and hopes to identify more regulators of the immune system to improve the diagnosis and treatment of diseases such as autoimmunity and cancer.

Her research has been recognised by several awards including the Royal Society of New South Wales Bicentennial Early Career Research and Service Citations Award (2024), Australian and New Zealand Society of Immunology (ASI) BD Science Communication Award (2023), ASI Postdoctoral Travel Award (2024), ANU Early Career Travel Award (2024) and the Biotron Founders Grant International Travel Award (2023).

Outside of the lab, Cynthia has a passion for teaching and science communication. She has provided guest lectures at ANU, been invited to present at Australian and international research institutes and conferences, and has featured in several media articles and radio talk shows.

This ASBMB Fellowship will allow Cynthia to attend the 19th International Congress of Immunology in Vienna, Austria, in August 2025.

Xuan Ling Hilary Yong

Hilary Yong completed a PhD in neuroscience and is passionate about uncovering novel molecular pathways underlying synaptic plasticity and memory formation. Under the mentorship of Associate Professor Victor Anggono at the Queensland Brain Institute, University of Queensland, she identified key molecular pathways regulating presynaptic and synaptic plasticity with implications for neurological disorders. Her scientific contributions have led to 12 publications, including two first-author articles in *Cell Reports*, as well as co-authored studies published in leading journals such as *Nature Communications* and the *Journal of Neuroscience*.

Hilary has been recognised for her scientific accomplishments, receiving the Ian Lindenmayer PhD Top-Up Scholarship and Dean's Award for Outstanding Thesis, and international travel fellowships from the Society for Neuroscience and the Young Scientist Program. She also contributed to securing an NHMRC Ideas Grant, further supporting her research into synaptic function. Hilary is now a postdoctoral researcher under the continued guidance of Associate Professor Anggono.

This ASBMB Fellowship will provide Hilary with the opportunity to attend the Gordon Research Conference on the Cell Biology of the Neuron in Tuscany, Italy, where she will present her latest findings.

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SDS Page: Short Discussions for Students Page

Supporting Diverse Scientists: the Role of Inclusive Workplaces in Contributing to Career Success for LGBTQIA+ Early Career Researchers

Benjamin Broomfield and Jin Ng

In an academic career where large experiments and heavy workloads can result in weeks with long and unusual working hours, we all sometimes find ourselves spending a lot of time at work. It's therefore no surprise that the workplace environments we find ourselves in have an outsized impact on our wellbeing and productivity. This is particularly true for minority groups, including the LGBTQIA+ community, where at all stages of career, but particularly early on, there can be a lot of anxiety around how much of ourselves we bring to the workplace and how to interact with colleagues when conversations turn to our personal lives. With the recent discussion around, and rollback of, diversity initiatives in global corporations, we look at some perspectives on how a supportive workplace environment and effective allyship contributes to success for postgraduate and early career LGBTQIA+ scientists.

WE-Pride, the WEHI LGBTQIA+ network, at an all-staff director's seminar highlighting the lived experience of LGBTQIA+ individuals working in medical research.

How has your identity as an LGBTQIA+ person affected your career progression and satisfaction at work?

Benjamin – I have been incredibly fortunate to find a lab where I feel safe and supported in sharing my queer identity. Being in an environment that encourages authenticity allows me to fully engage with my research without the burden of hiding aspects of who I am or maintaining a facade with colleagues. This sense of belonging has not only enhanced my career satisfaction but has also reinforced the importance of inclusive spaces in academia, where everyone can thrive as their true selves.

Jin – As a queer person of colour cis-gender male, I feel immense pride in being able to be myself at work, especially when WEHI's values align with my own. Beyond WEHI, the medical research industry in Australia as a whole is welcoming of queer identities. The importance of LGBTQIA+ representation at WEHI led me to volunteer as co-Chair of our LGBTQIA+ network, WE-Pride, and this helped with my career progression and personal development.

What have you found to be supportive while pursuing a scientific career?

Benjamin – Connecting with other queer students, scientists and colleagues has been a game changer for me. When I joined WEHI as an Honours student in 2019, I became part of WE-Pride, WEHI's queer staff, student and ally network. Being involved in a collective that actively drives policy and societal change within the WEHI community has reinforced the strong support from both queer and ally staff and students. These networks have provided invaluable support, both professionally and personally, throughout my journey.

Jin – The celebration and acknowledgement of LGBTQIA+ associated days of observations (i.e., Wear It Purple Day, IDAHOBIT, Transgender Awareness Week) by WEHI and other medical research institutes in the Parkville Precinct, and beyond, is a beacon of support for me. This messaging tells me that our community is visible and there is a safe space to be yourself and do the best science you can.

Do you have any queer role models in science?

Benjamin – Absolutely! Representation has been incredibly important to me – it's empowering to see other queer scientists excelling in their fields while creating a path for younger scientists to feel safe and confident in being their authentic selves. As a late-stage PhD student, I find inspiration in my queer peers, both other PhD students and postdocs, who achieve incredible things while bringing their full, authentic selves to work. Their success and visibility reinforce the importance of inclusivity in STEMM and motivate me to do the same.

Jin – I have met some of my closest friends through my work and they are my role models. I aspire to be as kind and giving as them.

SDS Page: Short Discussions for Students Page

What does being affirmed as a queer person at work look like to you?

Benjamin – Being affirmed as a queer person in STEMM means existing in a space where I don't have to choose between my identity and my work. A place of genuine inclusion where I can share aspects of my life with colleagues without hesitation, see queer representation at all career stages, and know that institutional policies actively support LGBTQIA+ people. It's being part of networks like WE-Pride, where both queer and ally colleagues work together to create meaningful change. Ultimately, affirmation means feeling valued not just for my contributions as a scientist, but as my authentic self.

Jin – It manifests in a number of ways. People ask you what your pronoun is, check in about how the current sentiments against trans individuals are affecting the LGBTQIA+ community, use gender-neutral pronouns when asking you to invite your partner to social events, and differentiate between sex and gender in scientific talks. All these encounters and experiences make me feel affirmed as a queer person in STEMM.

How can STEMM academic environments do better for queer people?

Benjamin – With public discourse around accessible safe spaces and affirming care for LGBTQIA+ people feeling ever present and at times regressive, it often feels like our path of progressive change is being stalled and even reversed. This makes it more critical than ever for STEMM environments, such as universities and research institutions, to actively foster and expand safe and inclusive spaces for queer individuals. These institutions must not only promote equality and equity but also take a leading role in upholding, strengthening and advancing queer rights. By committing to meaningful action and policy change, STEMM can set the standard for true inclusivity and support.

Jin – We as scientists need to do better in engaging with queer people in the general public. Our research has the potential to benefit everyone, but we seem to lack diversity in consumer engagement.

How can we be better allies for queer people at work?

Benjamin – This prompt perfectly carries on from the previous question – while organisations play a crucial role in maintaining safe environments for queer people, individual allies can have an equally significant impact. Creating an open, inclusive and understanding workplace, regardless of whether someone is openly queer, helps foster a culture where everyone feels valued. When safe spaces are maintained, we feel empowered to be ourselves, leading to a more supportive environment where us scientists can thrive and reach our full potential.

Jin – Don't be afraid to ask questions. Being inquisitive, wanting to improve your understanding and being accommodating of difference is always well received in my book. Just be sensible about asking questions at work and consider how appropriate they are (e.g., "What does being gender non-conforming mean?" is OK, whereas, "Who wears the pants in the relationship?" is not OK). We are all allowed to make honest mistakes, and we all have the capacity to learn and be kinder to everyone.

Benjamin Broomfield (he/him) is a third year PhD candidate in the Groom laboratory of the Immunology Division at WEHI. His research focuses on revealing factors that direct CD8⁺ T cell differentiation within the lymph node, which can be targeted to skew effector or stem-like memory T cell generation for immunotherapeutic applications. Ben is co-Chair of the WEHI LGBTQIA+ network, WE-Pride, advocating for a more inclusive, safe and welcoming workplace for all through policy consultation, seminars and pride events.

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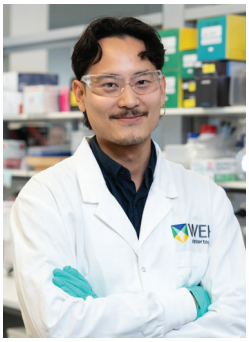
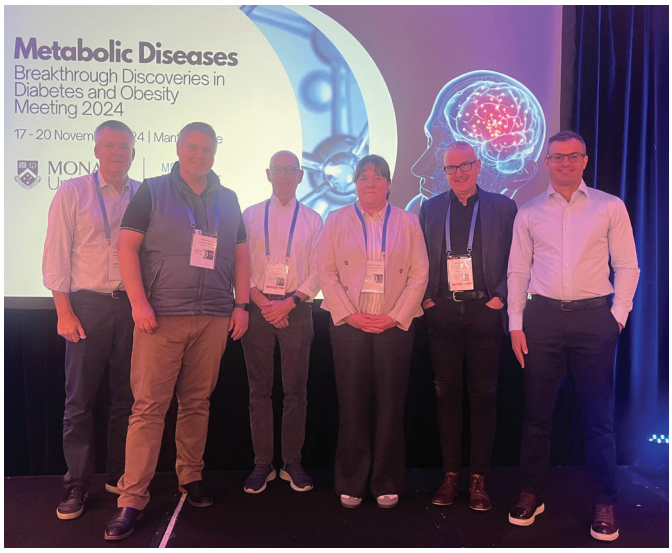


Dr Jin Ng (he/him) received his PhD from the University of Auckland, New Zealand, and is a Senior Research Officer in Professor Kate Sutherland's laboratory at WEHI. His research centres on understanding tumour and immune cell heterogeneity in lung cancer using single cell sequencing. He has served three terms as co-Chair of the WEHI LGBTQIA+ network, WE-Pride, where he organises educational seminars and advises on institutional policies to support and accommodate LGBTQIA+ individuals. In the future, Jin hopes to start his own independent research program exploring tumour-immune cell interactions that can be modulated using de novo *protein design.*

ng.ji@wehi.edu.au

Metabolism and Molecular Medicine: an ASBMB Special Interest Group

I recently was elected and took over as Chair of the Metabolism and Molecular Medicine Special Interest Group (SIG) from Sean McGee and Nigel Turner. I thank Sean and Nigel, as well as Kate Quinlan and Dominic Ng, for the relatively smooth transition and guidance for this new role. Since this time, I have recruited Simon Bond (Baker Institute) and Kristen Brown and Andrew Cox (both Peter MacCallum Cancer Centre) as committee members of our group. The Metabolism and Molecular Medicine SIG of the ASBMB comprises 181 ASBMB members and hence represents a substantial interest for our Society, and as such, it is our primary goal to bring us together to discuss and collaborate on this important facet of biochemistry.



Chairs and speakers of the Exercise and Metabolic Health Symposium at the 4th Metabolic Diseases: Breakthrough Discoveries in Diabetes & Obesity. From left: Mark Hargreaves, Adam Rose, Erik Richter, Meagan McGrath, Mark Febbraio and Nir Eynon.

We supported an important symposium within the 4th Metabolic Diseases: Breakthrough Discoveries in Diabetes & Obesity meeting held in Lorne in November 2024. This meeting brought together international and national experts in metabolism and metabolic disease as well as industry scientists (i.e. Pfizer, Eli-Lilly, Regeneron) and was well attended with approximately 120 participants. The Metabolism and Molecular Medicine SIG supported the Exercise and Metabolic Health Symposium, featuring Professor Erik Richter from the University of Copenhagen, Denmark. Erik is an international leader on exercise biochemistry and conducts studies in humans as well as rodent models to discover molecular physiological mechanisms governing the adaptive biology of physical activity. I co-chaired this session with Professor Mark Hargreaves (University of Melbourne) and together with local experts such a Professor Mark Febbraio, Professor Nir Eynon and Dr Meagan McGrath (all Monash University), Erik shared the latest developments on skeletal muscle and whole-body adaptive processes that confer improved health with exercise including REDOX biology, extracellular vesicles, glycogen metabolism, and epigenomic control. The symposium was certainly well received and the discussion around these issues was lively.

Going forward, the MMM committee will run a symposium on Measuring Metabolism this year. The goal of this mini-symposium will be to bring together key experts to discuss cutting-edge methods for metabolic measurement from whole-room indirect calorimetry of humans, *in vivo* and cellular metabolic tracing of flux and fates, and spatial metabolomics. Stay tuned for details via the ASBMB. We hope to see you there!

Adam Rose (Monash University)
Chair of the Metabolism & Molecular Medicine Special Interest Group
adam.rose@monash.edu

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 SDR Scientific Education Award Report

A Meeting of Open Minds

Julian Pakay.

I attended the Open Education (OE) Global Conference, held in Brisbane from 13–15 November 2024. OE Global is an international non-profit organisation and is uniquely positioned as the global steward for open education. OE Global's goal is to increase access to high-quality education in line with UNESCO's recommendation on open education. This annual conference was first held in 2005, and 2024 was the first time it has been hosted in Australia. The conference was co-hosted by the University of Southern Queensland, Queensland University of Technology (QUT) and the State Library of Queensland.

Most people associate open education with the sharing of educational resources to make them more affordable and accessible. However, the goals of open education are becoming broader and now encompass increasing inclusivity, access to research data and methodology, the sharing of assessment practices and new pedagogical approaches. This was captured by the theme of the conference, 'Open is Everyone's Business', and was reflected in the diversity of attendees, which included around 200 open education practitioners, research and teaching academics, students, librarians, education designers, policy makers, Indigenous open education leaders and education technologists from over 21 countries.

There were 112 sessions and included presentations, workshops, lightning talks and panel discussions. This was the highest ratio of participation to attendance for any conference I have attended and certainly contributed to a strong sense of camaraderie. Although a relative newcomer to the open education community, I was made to feel very welcome. I was also finally able to meet in person many people who I had collaborated with online or by correspondence.

The standard of the presentations was excellent, and it is difficult to choose standouts. However, there were three particular highlights for me:

- A deeply inspired and moving plenary presentation from Robert dhurwain McLellan (University of Queensland and Program Manager for the Language Data Commons of Australia) on how to reconcile open policies with Indigenous self-determination and custodianship of Indigenous data/cultural heritage.
- A though-provoking invited presentation from Martin Dougiamas (founder and CEO of Moodle, and founder of the non-profit organisation, OpenEdTech) on the future of education. Martin presented a refreshingly optimistic scenario where education will be far more immersive and personalised, integrating augmented and virtual realities and powered by open-source collaboration.
- A presentation from my La Trobe University colleague, Steven Chang, Wicked problems and bold solutions – lessons distilled from a decade of open education at La Trobe University. Steven discussed how institutions can better align academic reward and recognition with open education practice. This talk resonated with education-focused academics in particular who often struggle to find support for scholarship of learning and teaching in general.

I was fortunate enough to be able to present twice. I presented a paper with the mildly provocative title, What can open educational resources do that AI and traditional textbooks cannot?, where I was able to speak about how my own open education projects with the La Trobe eBureau incorporate teacher presence, help foster professional identity and have brought in students as content creators.

I was also very excited to be part of a panel discussion (as one of the authors) for the launch of the openly licensed anthology, *Open Education Down UndOER: Australasian Case Studies*. This showcases open educational practices of teaching academics, curriculum developers, learning designers and information specialists from across

Some Open Education Down UndOER: Australasian Case Studies editorial team members at the book launch and panel discussion at OE Global 2024. From left: Sarah McQuillen (University of South Australia), Mais Fatayer (University of Technology Sydney), Debrorah King (James Cook University), Angie Williamson (Deakin University), Alice Luetchford (James Cook University) and Ash Barber (University of South Australia).

ASBMB SDR Scientific Education Award Report

Australia. The resource contains succinct case studies intended for use by learning and teaching communities in higher education. I highly recommend that anyone interested in developing open education resources look through the practical examples provided which are often transferable across disciplines and/or institutions.

I would like to congratulate OE Global and the local organising team, Adrian Stagg and Carmel O'Sullivan from the University of Southern Queensland, Sarah Howard from the QUT Library, and Anna Raunik from the State Library of Queensland, who put on a fantastic conference. For those interested in attending the OE Global conference, a venue and format has not yet been decided for 2025, but the conference will return to Massachusetts, USA, in 2026 to be co-hosted by MIT OpenCourseWare. Just enough time to publish that nascent open education project!

This trip would not have been possible if not for the generous ASBMB Education Award sponsored by SDR Scientific. As an open education author, this represented an invaluable opportunity for me to obtain feedback from other open education authors and education designers and to discuss potential collaboration opportunities with like-minded academics.

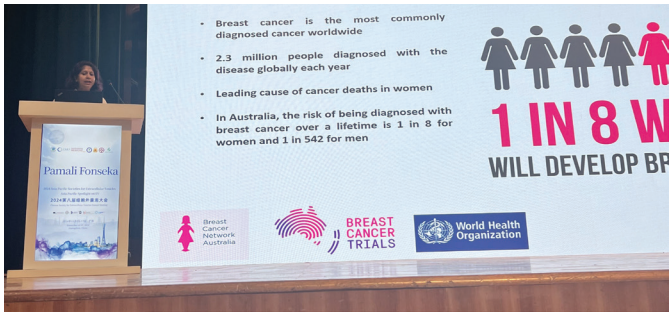
As you might expect with a conference dedicated to open education, much of the conference content is freely available online! I encourage you to peruse the pre-conference program of open education-related podcasts, the OE Global YouTube playlist which includes the keynote speakers, the sessions collected as audio and the library of abstracts.

Dr Julian Pakay is a teaching-focused academic in the Department of Biochemistry and Chemistry at La Trobe University.

ASBMB Fellowship Report

Yum Cha, Dim Sums and Extracellular Vesicles

I was honoured to be awarded the ASBMB Fred Collins Award, which supported my travel to attend the 2024 Asia Pacific Societies for Extracellular Vesicles (APSEV) meeting that was held in the vibrant city of Guangzhou, China. Although I received the ASBMB Fred Collins Award in 2021, the COVID pandemic and maternity leave delayed my travel plans. I am grateful that I was able to attend the APSEV meeting in November 2024.



Pamali's presentation at APSEV 2024.

APSEV 2024 had a fantastic combination of researchers and clinicians showcasing the latest developments in the field of extracellular vesicles (EVs). The meeting had a rich agenda of presentations ranging from the role of EVs in disease diagnostics to therapeutic applications. The 15 plenary talks captured the essence of how far the EV field has come and what a powerful tool EVs can be in treating diseases including cardiac fibrosis, cancer, diseased gut and atopic dermatitis. The organising committee also gave opportunities to junior researchers to present their research via impactful short talks. One of the things that I really appreciated was that the organising committee had arranged special seats, name tags, bottled water and stationery for all the speakers regardless of their research career stage. This kind gesture made all the junior researchers feel equally important.

Representatives of the Australia and New Zealand Society for Extracellular Vesicles at the APSEV meeting.

Highlights of the meeting for me were the networking and poster presentation events. It was nice to indulge in authentic Chinese food and catch up with collaborators during these events. There was an interesting collection of very informative poster presentations that sparked many collaborations and ideas.

I presented my latest work on the role of plasma EVs derived from mice and humans with metastatic breast cancer, who were subjected to high-intensity interval training exercise. I was nervous at the beginning of my talk as APSEV 2024 was a huge platform with many experienced researchers. However, my talk was well received, and I was asked many questions after the presentation. More importantly, I received very constructive comments from the Editor-in-Chief of *Journal of Extracellular Vesicles* (impact factor: 15.5), which has helped improve my research project.

I was so happy that I was able to catch up with my friend, Kenning Zhao, after many years. Kenning finished her PhD with me at La Trobe University in 2018 and is now a researcher in Guangzhou. She was a member of the APSEV 2024 organising committee. It was very interesting to gain a perspective on her life, career prospects and the work culture in Guangzhou.

The trip was close to my heart as I was able to experience the traditions, culture and food of my in-laws who are originally from Guangzhou. Guangzhou is one of the oldest cities in China and was formerly known as Canton. It is the birthplace of Cantonese cuisine and is famous for delicious dim sums. However, global influences on Guangzhou have made it a gastronomic hub with many international cuisines. I had the opportunity to experience many flavourful foods while listening to local stories and the meaning behind certain dishes during my travel.

I had an amazing and memorable trip. I am extremely grateful to the ASBMB for awarding me the Fred Collins Award that made this very fruitful trip possible.

Dr Pamali Fonseka is an NHMRC Emerging Leadership Fellow and a new Group Leader at the La Trobe Institute for Molecular Science, La Trobe University. She is also the Deputy Director of the La Trobe Research Centre for Extracellular Vesicles.

Enjoying a meal in Guangzhou with family.

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Researchers use nucleic acid extraction for studies ranging from basic research to biomarker discovery, cell-free diagnostics, epidemiology and microbiome studies. Robotic liquid handling technology in automated nucleic acid purification (aNAP) systems streamlines tasks like serial dilution and cherry picking. Automated systems offer sample mixing, temperature control and bead washing, reducing errors from manual handling, pipetting bias and protocol deviations, crucial for fragile nucleic acids like RNA. These systems help circumvent the risks associated with manual sample processing and ensure better overall data quality.

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Key Benefits:

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The MPure™ aNAP System is compatible with MagBeads Purification Kits for cost-effective, flexible workflows. Contact us to discuss your research requirements at www.mpbio.com/au/

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).

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Fisher Biotec stands out as a premier supplier of high-quality laboratory equipment in Australia. With decades of experience backed by JAS-ANZ ISO 9001:2015 certification for the sale and supply of laboratory equipment, you can depend on us to provide the scientific community with reliable, cost-effective, and timely solutions for your laboratory operations.

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The new Eppendorf BioBased pipette epT.I.P.S.® are available in Bulk Bags, Biopur, ep Dualfilter, and SealMax® formats. Eppendorf Tubes® BioBased, Sterile, with screw caps^ are available in volumes of 5 mL, 15 mL, 25 mL and 50 mL. Eppendorf twin.tec® PCR Plates BioBased are available in 96 well and 384 well formats and also in LoBind.

More information about the BioBased range:
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^These tubes are made with at least 90% BioBased polypropylene. The screw caps are currently fossil-based material but will soon switch to BioBased.

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bioaustralis fine chemicals

BioAustralis is an Australian manufacturer, marketing over 5,000 microbial metabolites and related semi-synthetic and synthetic small molecules, covering rare and common metabolites for use in discovery, structure-activity and mode-of-action research, and as reference standards for synthetic biology and other purposes. Our specialty is rare metabolites.

Our most recent catalogue (August 2024) features microbial pesticides for agrochemical research, including many rare and first-to-market antifungals (ilicicolin H, sporminarins A and B, hymeglusin), antiinsectans (leporin A, haenamindole), plant growth regulators (scytalone, neovasinin, ferulic acids and esters) and nematicides (4-hydroxyscytalone). Other metabolites of high interest are stromemycin, an MMP inhibitor; and the antitumor actives, sambutoxin and N-hydroxyapiosporamide. For these and other research fine chemicals, go to www.bioaustralis.com.

Microbial Screening Technologies, the parent company of BioAustralis, continues to support laboratory research. In November, we sponsored the RACI Natural Products Chemistry and Biology conference in Sydney. Most recently, we exhibited at the January 2025 SIMB meeting in San Diego for Natural Product Discovery and Development in the Genomic Era. The calibre of presentations and posters was exceptional and highlighted the most recent research into natural product discovery in the USA and globally.

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mexec is an Executive Search Recruitment firm that also supports individuals seeking to transition to a new role. We specialise in the science, health and innovation sectors.

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SBMB

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CreoptixWAVE for Label-free Binding Kinetics and Affinity Analysis

Conventional bioassays like ELISA have relied on enzyme or fluorescent labels to detect and monitor biomolecular interactions, however, these labels can introduce artifacts, complicating data interpretation. Such assays are also incapable of providing kinetic insights, such as binding speed or duration. While surface plasmon resonance (SPR) offers label-free analysis, it often captures only a snapshot in time and is prone to issues like clogging and non-specific binding, which can compromise results.

Malvern Panalytical's Creoptix® WAVEsystem overcomes these limitations by delivering a robust, label-free technology for real-time analysis of biomolecular interactions. The system delivers deeper insight into previously undetectable interactions and provides detailed kinetic rate parameters and affinity constants (ka, kd, KD), as well as binding specificity, even for challenging samples and complex biological matrices.

The power behind the Creoptix® WAVEsystem is in its patented Grating-Coupled Interferometry (GCI) technology, paired with the innovative, non-clogging WAVEchip microfluidics system. GCI measures the evanescent wave across the entire sensor surface, offering exceptional sensitivity. The kinetics of weakly binding fragments and large molecules with high affinity and slow dissociation can be measured simply (even native proteins in complex matrices) without purification.

For applications requiring higher throughput, the system's waveRAPID method enables faster screening by generating a pulsating concentration profile, streamlining workflows for screening studies. Additionally, Calibration-Free Concentration Analysis (CFCA) provides a quick and reliable approach for quantifying active protein concentration.

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www.atascientific.com.au

Tomocube HT-X1™ Plus Holotomography System

The HT-X1™ Plus Holotomography system takes bioimaging to the next level and extends the reach of Holotomography to an even broader array of challenging specimens, including dense organoids, tissue sections and fast-moving microorganisms. This state-of-the-art imaging platform is designed to empower researchers with the precision, efficiency and reliability needed for applications in 3D biology, immunology, regenerative medicine and cell biology.

Equipped with a high-spec sCMOS camera featuring a 4x larger field of view and significantly reduced acquisition time, the HT-X1™ Plus is perfect for high-throughput phenotypic screening of cells and organoids without the need for stitching. Its upgraded correlative imaging capabilities – incorporating an sCMOS-based fluorescence module – enable seamless integration of molecular studies with single-cell-resolution 3D images. Experience clearer, more detailed imaging of multi-layered specimens with improved illumination optics and advanced image reconstruction algorithms. Imaging can be customised with three wavelength options to enhance contrast or improve penetration.

Benefits of the HT-X1™ Plus include high content screening of live cells and organoids making it highly suitable for high-content, image-based drug screening research. High resolution imaging of 3D biological samples is especially advantageous for research involving 3D cultures, enabling the detailed investigation of dense organoids and intact tissue sections. Enhanced correlative fluorescence imaging is possible with the fluorescence module (FLX™) featuring an sCMOS camera designed specifically for precise signal intensity measurements. With the new color brightfield imaging modality and wide preview scan features, researchers can gain deeper insights into histological tissue section studies.

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Cayman Chemical Natural Products Screening Library

Cayman Chemical's Natural Products Screening Library (catalogue #20897) is suitable for screening a variety of natural products. The screening library consists of 22 plates and contains ~1,640 natural products in a 96-well Matrix™ tube rack format as 2 mM or 2 mg/mL stock solutions in DMSO. This library includes compounds from a variety of natural product classes, including alkaloids, flavonoids, glycosides, terpenes, saponins and polyphenols that have anti-inflammatory, antioxidative and anticancer activities, among others. Stability data is not available for individual compounds as supplied in the screening library. Panels are routinely re-evaluated to include new catalogue introductions as the research evolves.

Cayman Chemical Natural Products Screening Library is distributed in Australia and New Zealand by Sapphire Bioscience.

For more information, please contact:
Sapphire Bioscience Pty Ltd
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sales@sapphirebioscience.com
www.sapphirebioscience.com
www.caymanchem.com/product/20897/natural-products-screening-library

Our Sustaining Members

Tissue Motion Stabiliser for Intravital Microscopy

Intravital imaging (IVIM) is essential for cellular level studies in live animal research, but capturing high-resolution images of deep tissues is challenging due to organ pulsation and animal movement, which can displace imaging areas. Consequently, IVIM Technology have developed a Tissue Motion Stabiliser (TMS) to combat micron-level movements which can obstruct the clear imaging of dynamic organ behaviour.

TMS works by applying negative pressure to securely hold pumping organs in place, ensuring stable imaging conditions and minimising motion artifacts. This restrains motion enabling high-quality imaging, thus mitigating the impact of pulsations, making it ideal for studying organs such as the heart, lungs, thymus and uterus in live subjects.

The lung imaging chamber features fine adjustment controls for precise tissue sample positioning, optimising conditions for accurate imaging. This setup enables detailed observation of blood flow and immune cell mobility in live lung imaging. This setup enables detailed observation of blood flow and immune cell mobility in live lung imaging.

The introduction of vacuum-suction chambers with IVIM-TMS marks a significant advancement in intravital imaging technology. By overcoming inherent challenges in visualising dynamic organs *in vivo*, this innovation opens new frontiers in physiological research and biomedical imaging, promising groundbreaking discoveries.

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SDR Scientific Expands Offerings with Astoria Pacific and Global FIA

SDR Scientific is proud to announce our appointment as the exclusive distributor for **Astoria Pacific** and **Global FIA** in Australia and New Zealand. These partnerships expand our range of innovative flow-based analytical solutions, providing laboratories with cutting-edge technology backed by SDR Scientific's trusted local expertise and support.

Astoria Pacific is renowned for high-performance flow analysis systems, delivering precise and efficient nutrient, environmental and other industrial testing. Global FIA is highly regarded in presenting a broad range of componentry related to fluid handling at the microlitre scale and linear motion systems to automate laboratory units of operation.

For researchers and laboratory professionals, this means enhanced access to reliable, high-quality instrumentation tailored to diverse analytical needs. Whether you require a robust solution for high-throughput analysis or a flexible system for specialised research, these partnerships provide a broader selection of options to meet your requirements.

Complementing our existing **Hoefer** range, these additions further strengthen our commitment to delivering efficient, user-friendly solutions that empower laboratories to achieve their goals with confidence and accuracy.

With a strong focus on education, plans are already underway here at SDR Scientific for an industry event in 2025. As always, we are also dedicated to providing exceptional service, including local expertise, training, and after-sales support.

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Kuhner Orbital Shaken Bioreactors – Scale Up Without Compromising Quality

Kuhner's Orbital Shaken Bioreactors (OSB) are solutions for cultivating mammalian, human, insect and plant cell cultures. Available in four sizes with flexible working volumes, they cater to a variety of research and production needs: 4–12 L (SB10-X), 15–50 L (SB50-X), 50–200 L (SB200-X) and 500–2500 L (SB2500-Z).

The cylindrical vessels of Kuhner's OSB employ single-use, gamma sterilised 3D bags and are equipped with ports for inoculation, aeration, feeding, sampling and harvesting. Depending on the bag type, they support online measurement via built in chemo-optical sensors and active control of pH and DO. They also facilitate alternating tangential flow filtration (ATF) and tangential flow filtration (TFF) perfusion.

For high throughput applications, microtitre plates are available in 12, 24, 48 and 96 well plate formats. For process development bioreactor tubes (5–35 mL) and disposable shake flasks (10 mL–4 L) are used. The consistent orbital mixing provided by these vessels ensure scale-up from microtitre plates to larger systems. Smaller bioreactors like the SB10-X can serve as an inoculum for larger models such as the SB50-X and SB200-X, enabling seamless scalability up to 2500 L, ensuring smooth transition from pilot to production.

For more information, contact **Capella Science** on (02) 9575 7512 or email sales@capellascience.com.au

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Tecan's advanced automation solutions are tailored to address the complexities of proteomics sample preparation. Our recently launched Resolvex® i300 module, an integrated component of the Fluent® automation workstation, consolidates sample preparation, cleanup, evaporation and resuspension tasks into one seamless operation.

Complemented by our innovative AffinEx™ affinity purification columns and digital tools like Introspect™ and LabNavigator™, we empower your transition to a fully automated, error-reduced and ROI-driven lab environment.

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Interested in learning more or want to arrange a demonstration? Visit https://www.tecan.com/proteomics-automation, call us on 1300 808 403 or email info-aus@tecan.com

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Palmtop Raman Spectrometer from JASCO

The PR-1w Palmtop Raman spectrometer is an innovative instrument from JASCO that is compact, has easy-to-use software and produces unrivalled data quality. A step away from microscope-based Raman systems, the simplicity of the PR-1w is perfect for undergraduate teaching labs, research labs or even commercial labs that require quick data analysis and sampling.

The various attachments further enhance the PR-1w's flexibility, allowing the instrument to measure sample matrices ranging from solids to powders, liquids & even gases. The PR-1w can also be attached to JASCO's FTIR-ATR accessory for complimentary IR and Raman sample measurement, giving users the benefit of two different instruments for the footprint of one.

The simplified software user-interface is perfect for beginners. With the capability to perform real time data correction, there is no need to spend time post-processing already acquired data. With the instrument comes 1-year complimentary subscription to the Wiley online Raman database and spectra search functionality. Being able to match to commercially available data saves you time from compiling your own reference library.

For more information, please contact **Bio-Strategy**, Part of DKSH Group
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Monday 2 June 2025

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