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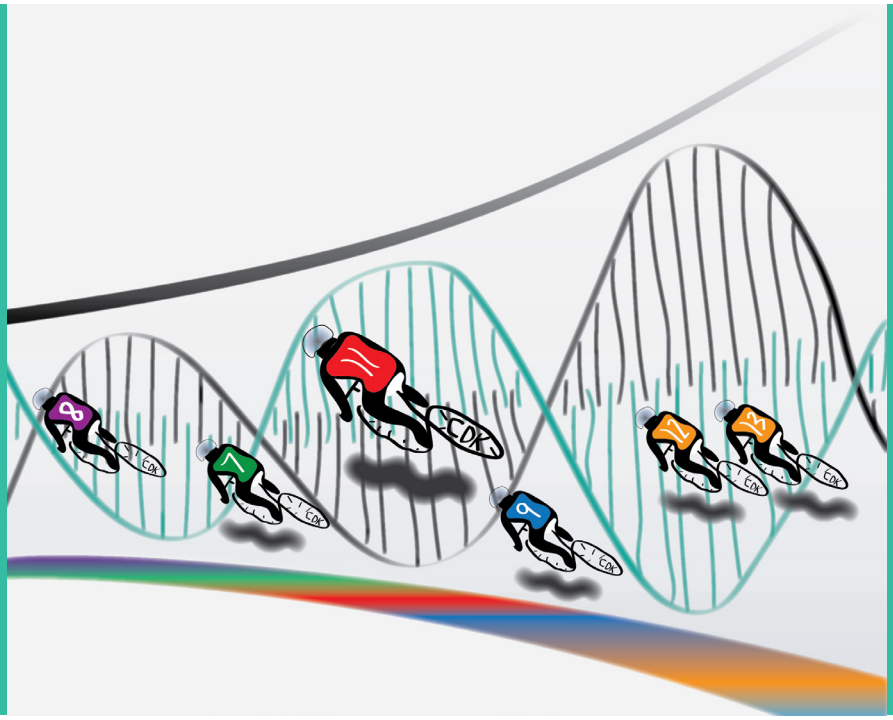

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CDK11 regulates Pol II pausing within the transcription cycle at a checkpoint upstream and independent of CDK9. Transcriptional CDKs are depicted as cyclists racing around a DNA velodrome in the order in which they promote Pol II progression through transcription cycle phases.

Image created by Jennifer Devlin using Adobe Illustrator, based on a publicly available photograph (https://alpinecols.com/top-five-reasons-to-ride-the-velodrome/). Image courtesy of Jennifer Devlin and Ricky Johnstone.

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ComBio 2026 Education Day, Tuesday 29 September 2026, promises an inspiring and energising program for anyone passionate about advancing teaching and learning in the molecular and biological sciences.

We will celebrate excellence in discipline-based education research with a dedicated session showcasing the **2026 Education Award winners** from the **Australian Society for Biochemistry and Molecular Biology (ASBMB), New Zealand Society for Biochemistry and Molecular Biology (NZSBMB)** and **Australian Society of Plant Scientists (ASPS)**. These presentations will highlight the innovative, evidence-based approaches that are transforming learning experiences across our higher education communities.

The day will include a thought-provoking **plenary** from Professor Danny Liu, whose work spans artificial intelligence, student engagement, educational technology and professional development – driving innovation in how we understand and enhance teaching and learning in the biosciences.

The program also includes a **GenAI in Molecular Biosciences Education session** that will explore practical strategies, challenges and opportunities arising from the integration of generative AI into higher education. To round out the day, an open session will include a collection of **lightning talks** offering snapshots of diverse projects, classroom innovations and emerging ideas from educators across Australasia.

If you are an educator interested in sharing your innovations, insights or classroom practice, we warmly encourage you to **submit an abstract for either an oral or poster presentation**. Whether you're an experienced education researcher, a mid-career educator or presenting for the first time, the Education Session is an ideal forum to engage with colleagues, spark new collaborations and contribute to a vibrant community of practice.

We look forward to seeing you there!

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Associate Professor Amber Willems-Jones | ASBMB Education Committee

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A New Model for Conformational Switching in Estrogen Receptor α

McDougal DP#, Pederick JL#, Novick SJ, Jovcevski B, Warrender AK, Pascal BD, Griffin PR, Bruning JB*. A ternary switch model governing ERα ligand binding domain conformation. *Nat Commun* 2025;16(1):10363.
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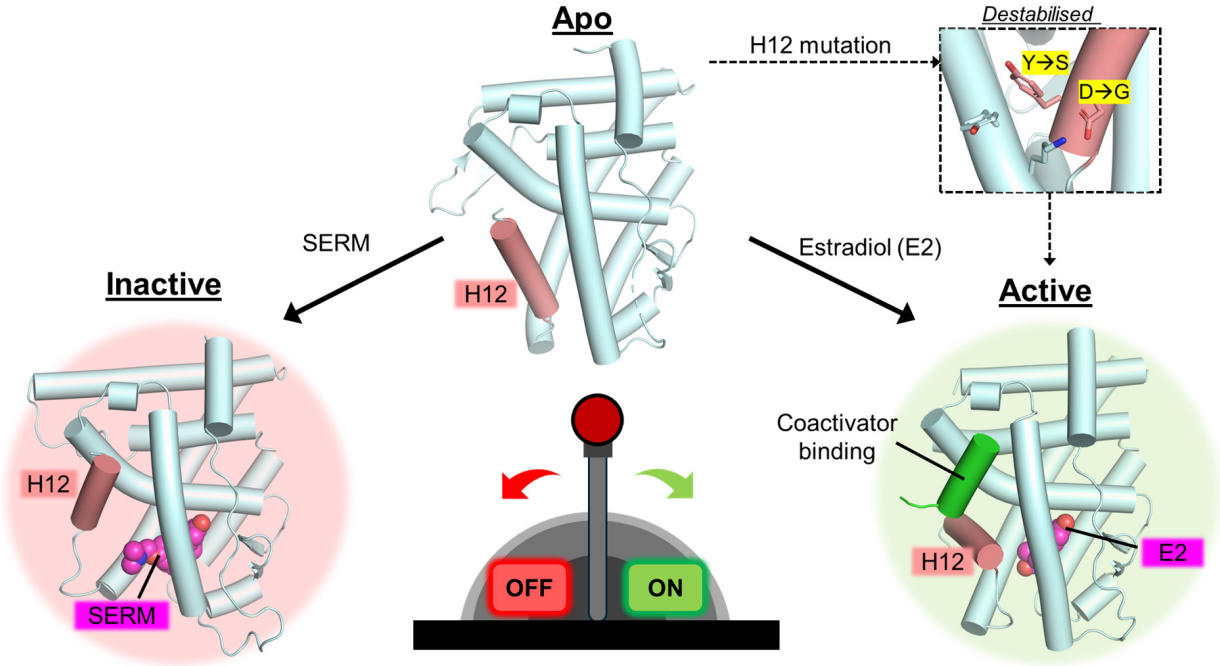
Estrogen receptor α (ERα) is one of the most intensively studied nuclear receptors, a superfamily of transcription factors, having critical roles in reproduction, development, metabolism and hormone-driven cancers. ERα function is largely directed by ligands engaging its ligand binding domain (LBD), which determines the conformation of a critical structural element, helix 12 (H12). Structural biology has provided a comprehensive understanding of how ligands control ERα activity through H12; activating ligands such as the sex hormone estradiol (E2) stabilise H12 in a conformation that enables transcriptional co-activators to be recruited, whereas synthetic modulatory ligands – selective estrogen receptor modulators (SERMs) – displace H12, blocking co-activator recruitment. These outcomes result in changes to gene expression. Despite this knowledge a fundamental question remained unsolved: what does the ERα LBD look like in the absence of ligand? For many nuclear receptors, the unliganded (apo) state is considered flexible and dynamic, only becoming ordered upon ligand binding. However, hydrogen–deuterium exchange studies have shown minimal change in deuterium uptake in the critical H12 region upon ligand binding, hinting that the unliganded receptor might already adopt a defined



Overview of the ternary switch model controlling ERα activity via the LBD. The apo state (centre) can be shifted into the active conformation (right) by binding of the hormone ligand estradiol (E2) or through mutations in H12; both modify the H12 position and allow transcriptional co-activators to be recruited, resulting in increased expression of target genes. Conversely, the apo state can be shifted into the inactive state (left) by binding a synthetic modulatory ligand (selective estrogen receptor modulator; SERM) which displaces H12 such that it blocks co-activator recruitment, inhibiting ERα-dependent transcription. Image generated by Jordan Pederick.

structure. Our investigation addressed this question directly, using both human ERα and a highly conserved fish ERα as complementary models to capture and characterise this elusive state.

To do this, we used a combination of X-ray crystallography and molecular dynamics (MD) simulations. While human ERα proved resistant to crystallisation, apo crystals of the fish ERα LBD were obtained and a high-resolution crystal structure of the apo ERα LBD was successfully resolved. This revealed a third state, distinct from the previously defined on and off conformations, where H12 is neither fully active nor repressive. MD simulations reinforced this finding, demonstrating that this apo conformation of H12 is energetically stable. Together, this discovery supports that ERα exists in a defined apo state that serves as a structural baseline of a ternary switch. In this model, ligand binding does not impose order on a disordered receptor but instead shifts ERα between pre-existing conformational states.

This ternary switch model also provides new molecular insight into cancer-associated ERα mutations (Y537S and D538G) and the mechanisms of ERα-targeting therapies such as SERMs. Mapping of Y537S and D538G mutations onto the apo structure reveals that these likely destabilise the apo conformation of H12 due to loss of interactions with the receptor core. This would shift the conformational equilibrium of ERα, bypassing the apo state and locking H12 into an active conformation. In contrast, the model suggests that SERMs act by actively excluding the apo conformation. Their bulky or extended chemical substituents sterically clash with the apo positioning of H12, redirecting it into alternative conformations that block co-activator binding. In the context of the ternary switch model, both mutations and ERα therapeutics exert their effects not by creating entirely new receptor states, but by selectively destabilising or stabilising pre-existing conformations.

Taken together, this work reframes our understanding of ERα regulation. Rather than functioning as a binary molecular switch, ERα operates through a ternary system in which the apo state plays an active and previously underappreciated role. By defining this long-elusive unliganded conformation, our study provides a unifying model for ligand action, mutation-driven activation and therapeutic intervention. It also highlights a broader principle to consider for other nuclear receptors: regulation may emerge not only from disorder, but from controlled switching between well-defined structural states.

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Daniel McDougal (third from left) and Jordan Pederick (third from right) led the project under the supervision of John Bruning (head of the table).

Placing CDK11 at the Pausing Checkpoint of Pol II Transcription Cycles

Devlin JR, Martin B, Bartonicek N, Ting K, Fan Z, Todorovski I, Bjelosevic F, Verschoor S, Cicconne A, Trapani JA, Horvath A, Tinsley E, Fraser P, Newbold A, Sandow JJ, Muscat A, Simpson KJ, Geyer M, Vervoort SJ, Johnstone JW*. A CDK11-dependent RNA polymerase II checkpoint precedes CDK9-mediated transition to transcriptional elongation. *Mol Cell* 2025; 85(17):3256–3274. *Corresponding author: ricky.johnstone@petermac.org

Normal cellular functions depend upon controlled gene expression facilitated by the exquisite regulation of RNA Polymerase II (Pol II)-dependent transcription. Pol II's journey from gene promoters, and through transcription-start-sites (TSS) and gene-body regions to termination cues, is best thought of as a 'cycle' consisting of distinct checkpoints rather than an unobstructed linear pathway. Analogous to the cell-cycle, for Pol II to proceed through each transcription cycle checkpoint, distinct transcriptional-cyclin-dependent-kinases (tCDKs) are required to phosphorylate key substrates (including Pol II itself). Roles at key checkpoints had been well established for CDK8 (Pol II promoter recruitment), CDK7 (transcription initiation), CDK9 (promoter-proximal pause-release) and CDK12/CDK13 (gene-body elongation), but it was still unknown if and how CDK11 contributed to transcription cycle checkpoint(s) control. This, in contrast to other tCDKs, was largely due to the unavailability (prior to 2019) of selective inhibitors of CDK11 and the limitations of 48-hour plus RNA-

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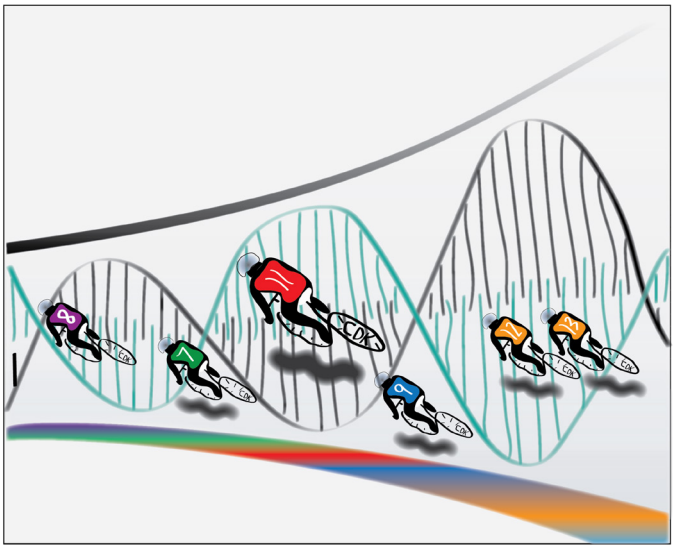

CDK11 regulates Pol II pausing within the transcription cycle at a checkpoint upstream and independent of CDK9. Transcriptional CDKs are depicted as cyclists racing around a DNA velodrome in the order in which they promote Pol II progression through transcription cycle phases.

interference- and CRISPR-based genetic approaches to investigate acute (within minutes) molecular impacts of CDK11 disruption on Pol II transcription cycles.

To address this issue, we took advantage of a previously mischaracterised small-molecule identified to selectively inhibit CDK11 called OTS964, and generated cell-line based chemical-genetic systems to enable rapid inducible degradation (auxin-inducible-degron) or ATP analog-sensitive kinase-inhibition of CDK11. Our study focused on aggressive haematological malignancies, primarily acute-myeloid-leukaemias with Mixed-Lineage-Leukaemia gene rearrangements (*MLL*r-AML) that are well known to exhibit transcriptional dysregulation. These have responded favourably to CDK7, CDK9 and CDK12/CDK13 inhibitors in previous studies published by us and others. With these tools, we achieved rapid and selective ablation of CDK11 activity and then used a diverse range of DNA- and RNA-next-generation-sequencing, global proteomics, recombinant kinase biochemistry and flow-cytometry applications to characterise acute molecular phenotypes and assess biological/therapeutic impacts including *in vivo* with syngeneic mouse models.

Using complementary approaches coupling nascent-RNA metabolic labelling with next-generation-sequencing, we determined that CDK11 kinase activity is essential for Pol II-dependent mRNA production. While CDK11 is important transcriptome-wide, by comparing impacts of CDK11 inhibition at shorter genes versus longer genes we found that Pol II activity is most dependent on CDK11 near the beginning of transcription cycles, close to the TSS and promoter-proximal region. This is where the molecular phenomenon termed 'pausing' occurs, in which Pol II briefly stalls prior to entering the gene-body and is 'released' by the kinase activity of CDK9. Our chromatin-immunoprecipitation (ChIP)-seq experiments revealed a similar accumulation of Pol II at promoter-proximal regions in response to CDK11 versus CDK9 inhibition, suggesting a requirement for CDK11 in facilitating pause-release. To dissect CDK11- vs CDK9-dependent roles at this checkpoint we used two approaches: 1) high-resolution λ exonuclease-based ChIP Nexus-seq to pinpoint sites of paused Pol II accumulation; and 2) precision-nuclear-run-on (PRO)-seq to map the location of active transcription through biotin-nucleotide labelling of Pol II-engaged nascent RNA molecules. These experiments revealed that CDK11 inhibition induces Pol II pausing closer to TSSs than CDK9 inhibition and that CDK11 activity is necessary for Pol II release upstream, but not downstream, of the CDK9-dependent checkpoint. Our proteomics studies highlighted disengagement of CDK11 from Pol II upon its inhibition, qPCR experiments revealed the necessity of CDK11 for gene expression in response to external stimulation (e.g., heatshock), and *in vitro* assays using in-house generated recombinant CDK11 complexes demonstrated its ability to directly phosphorylate Pol II.

Transcriptional perturbation upon acute CDK11 inhibition/degradation was detrimental to the viability of MLLr-AML and other haematological cancer cells resulting in cell cycle arrest and cell death. Importantly, the CDK11 inhibitor OTS964 is orally bioavailable and exhibited robust anti-cancer effects *in vivo* after delivery of only a single dose to mice with established leukaemia or MYC-driven B-cell lymphoma. Overall, our study has advanced our fundamental understanding of Pol II transcription cycles and how gene expression is controlled, for the first time placing CDK11 at a new transcriptional checkpoint that is upstream and independent of CDK9, essential for steady-state and stimulus-triggered gene expression, and critical for the normal functioning and survival of cancer cells.

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From left: Attila Horvath, Ben Martin, Ricky Johnstone, Jennifer Devlin and Nenad Bartonicek.

Publications With Impact

Along Came a Spider: Nuclear Filamentous Actin Helps Telomerase Find Telomeres

Harman A, Kartawinata M, Maroun NM, Nguyen DR, Rahman S, Hughes WE, Winardi K, Cohen SB, Cesare AJ, Lamm N, Bryan TM*. Nuclear actin and DNA replication stress regulate telomere maintenance by telomerase. *Nat Commun* 2025;16:10193.
***Corresponding author: tbryan@cmri.org.au**

Telomeres cap the ends of linear chromosomes and are essential for the protection of genome integrity and cellular survival. In somatic cells, telomeres normally shorten slightly with each round of cell division; however, this shortening does not occur in cells which proliferate indefinitely, such as stem and germline cells, and also cancer cells. In approximately 85% of cancers, telomere length is maintained by the ribonucleoprotein complex telomerase. While a large body of work has investigated the mechanism by which telomerase extends telomeres, exactly how telomerase gets to those telomeres when it is needed, a process known as 'telomerase recruitment', has been less well studied. In this study, we have discovered a regulatory system in which a network of nuclear actin fibres tethers damaged telomeres in place, helping telomerase find them.

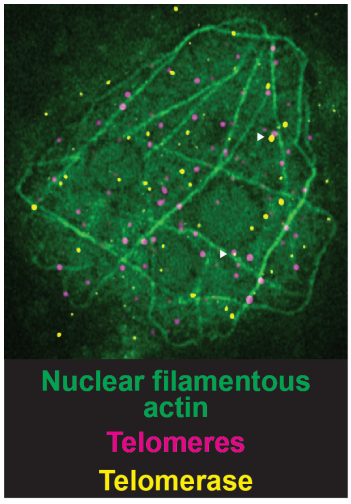
Roughly a decade ago, we identified that the DNA damage response (DDR) is important for successful telomerase recruitment (Tong *et al.*, *Cell Reports* 2015), particularly during replication stress (any process which stalls or stops the DNA replication machinery). Since then, there have been an increasing number of studies implicating a role for actin in the DDR and demonstrating that actin (traditionally considered cytoplasmic) is present in the nucleus, where it can polymerise into filamentous actin (F-actin). This facilitates the resolution of DNA damage, including that caused by replication stress, as shown by our collaborator Dr Noa Lamm (Lamm *et al.*, *Nature Cell Biol* 2020).

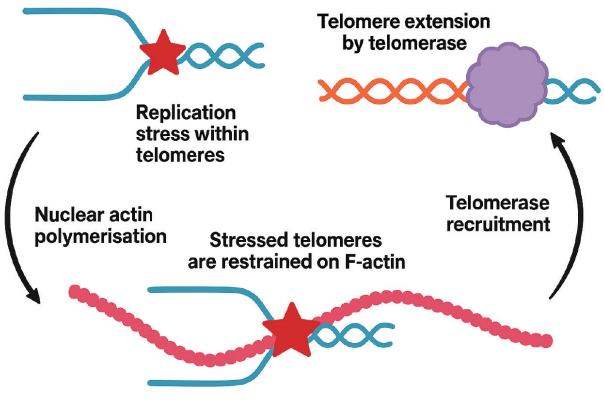
Given the convergence of these phenomena, we asked ourselves a logical question: does F-actin participate in telomerase recruitment following replication stress? We first inhibited F-actin polymerisation, which resulted in reduced telomerase presence at telomeres; this was assessed using a modified FISH protocol sensitive enough to detect the low abundance RNA component of telomerase at telomeres. This reduced recruitment also impacts telomere extension; using an *in situ* method to detect telomerase activity in cells, we again saw that inhibiting F-actin resulted in fewer extension events.

Given that F-actin forms a network of fibres in the nucleus following replication stress, we hypothesised this could act like train tracks which allow the two to find each other. Indeed, imaging of nuclear F-actin (stained using a fluorescently labelled chromobody) showed that telomerase molecules at telomeres frequently colocalised with actin fibres. This was also confirmed by live cell imaging using CRISPR-modified cells to track telomeres, telomerase and nuclear actin in real time, showing that recruitment events occurred in close proximity to F-actin.

However, we unexpectedly observed that the mobility of telomeres was significantly slower when on an F-actin fibre, suggesting that telomeres are restrained on F-actin instead of freely moving around the nucleus. This suggested that F-actin might instead act like a spiderweb; telomeres that undergo replication stress are tethered to F-actin like a fly caught in the web, which allows for scanning molecules of telomerase to find them and ultimately extend those telomeres.

Our work has highlighted the delicate tightrope that cancer cells walk to maintain their telomeres. The





Left: *Nuclear filamentous actin (F-actin; green) visualised in HeLa cells with telomere (pink) and telomerase (yellow) staining by FISH.*
Right: *Model for replication stress-mediated telomere tethering and subsequent telomerase recruitment.*

typical replication stress that cancer cells experience can result in the loss of cellular viability, but conversely, this very stress can promote their survival by driving telomerase recruitment to maintain telomere length.

Ashley Harman and Tracy Bryan
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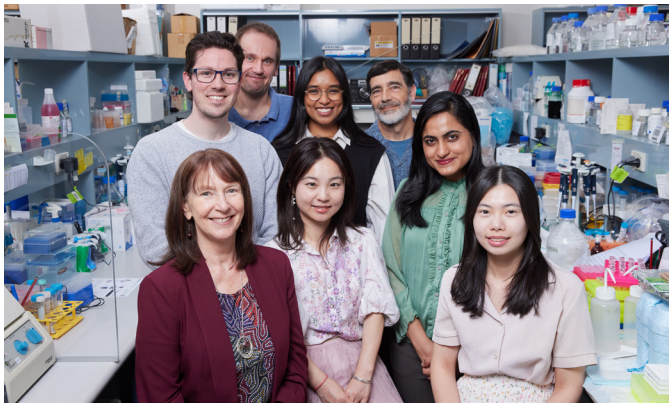

The Cell Biology Unit, headed by Tracy Bryan (front left), with authors Ashley Harman (back left), Shabita Rahman (middle middle) and Scott Cohen (back right).

Discovering the Cells That Present Bacterial Metabolites to T Cells

Deng J#, Yan Y#, Zhang X, Walsh CJ, Montassier E, Sinha D, Wang H, Mousavizadeh A, Ashayeripanah M, Mak JYW, Koay HF, Poch T, Alexandre YO, Mueller SN, Vasanthakumar A, Stinear TP, Jameson VJ, Perez-Gonzalez A, Kingham J, Phan TG, Potemkin N, Dryburgh L, Schroeder J, Fairlie DP, Mackay LK, Chen Z, Cook L, Hachani A, Corbett AJ, Roquilly A, Villadangos JA*, McWilliam HEG*. Macrophage MR1 antigen presentation promotes MAIT cell immunity and lung microbiota modulation. *Science* 2026;391(6782):eadr6322.
#Contributed equally
***Corresponding authors: j.villadangos@unimelb.edu.au; hamish.mcwilliam@unimelb.edu.au**

T cells are critical immune cells that enact immunity by detecting and responding to disease-causing pathogens. However, they do not recognise pathogens directly; they detect intact or processed components of pathogen molecules (antigens), bound to major histocompatibility complex (MHC) molecules. These MHC-antigen complexes are displayed to T cells on the surface of other cells, termed 'antigen presenting cells'. There are different types of T cells, each specialised at recognising a particular family of MHC-antigen complexes. For instance, the best-studied T cells recognise protein fragments (peptides), presented by MHC class I or class II molecules, that are derived from proteins degraded in cytosolic or endosomal cellular compartments, respectively. A parallel system exists for the detection of microbial metabolism. A highly abundant T cell subset, called mucosal-associated invariant T (MAIT) cells, recognise metabolite antigens. These metabolites are common to a wide range of bacteria and yeast, and they are presented by a dedicated MHC protein called MR1. MAIT cells are remarkably abundant in humans, where they continuously monitor microbial and metabolic disturbances. Their functions extend beyond antimicrobial defence to include wound repair, tumour surveillance and regulation of the microbiota.

Macrophages (purple) encounter pathogenic or commensal bacteria (blue) in barrier tissues such as the lungs, and express the MR1 protein (green). MR1 binds and then presents metabolite antigens on the cell surface to stimulate MAIT cells (orange) which triggers their activation. MAIT cells then help to control infections, or modulate the microbiota, to maintain homeostasis.

MAIT cell activation is inherently dependent on the detection of bacterial metabolites presented by MR1 on the surface of antigen presenting cells. But a fundamental mystery remained unresolved: **which cells actually present MR1 ligands to MAIT cells *in vivo*?** This question persisted not due to lack of interest, but because MR1 expression is notoriously low, making its cellular source exceptionally difficult to detect. To overcome this limitation, we engineered an MR1-reporter mouse line by replacing the MR1 coding sequence with a gene encoding the fluorescent protein, tdTomato. The amount of tdTomato made by the cells of these mice is a surrogate for the level of MR1 expression and as the fluorescent signal emitted by tdTomato is readily detectable by flow cytometry, this

strategy enabled us to construct the first high-resolution atlas of MR1 expression in individual mouse cells of different tissues.

The results revealed a surprising candidate for the title of MR1 presentation specialist: macrophages of various tissues, most notably the lungs and peritoneal cavity, showed the highest MR1 transcriptional activity. Expression, however, does not guarantee function. To test ligand capture and presentation capacity, we used a fluorescent MR1-antigen analogue developed by co-authors Jeffrey Mak and David Fairlie. This enabled real-time tracking of metabolite antigen uptake. Across all immune populations examined, macrophages proved the most efficient at ligand capture. Comparison of multiple cell types for their ability to actually display MR1-antigen complexes and stimulate MAIT cells confirmed macrophages were the most potent.

To establish the importance of macrophages in MR1 antigen presentation, we generated a conditional mouse model where MR1 was ablated primarily from macrophages. This alteration reshaped the lung microbiota of the mutant mice, revealing that macrophage-MR1 signalling is a homeostatic architect of microbial airway ecosystems. Furthermore, during bacterial infection, these mutant mice failed to recruit protective MAIT cells and were less able to clear the pathogen, demonstrating the importance of macrophages in recruitment of the anti-bacterial function of MAIT cells.

Taken together, these findings close a long-standing knowledge gap. Macrophages are the dominant MR1 antigen-presenting cells *in vivo*, directing microbial metabolite sensing, orchestrating MAIT expansion, maintaining microbiota balance, and enabling effective bacterial control. This positions macrophages as a compelling and clinically actionable target for therapeutic strategies seeking to modulate or engineer MAIT cell-mediated immunity.

These findings have opened up new questions. We are now uncovering how macrophage–MR1 signalling coordinates important MAIT cell functions, protecting us from bacterial infection, enacting tissue repair and participating in tumour immunity. Although macrophages stand as dominant MR1 antigen-presenting cells, immunity rarely relies on a single player. Other APCs may contribute, a question we are currently addressing with ongoing experiments. This expanding landscape brings us closer to precise, intentional manipulation of MR1-guided T cell immunity for future translational impact.

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Jose Villadangos.

Hamish McWilliam.

First Instrument-free Assay for Protein–DNA Interaction Studies: A Lab on a Strip

Toft CJ, Radford HM, Sorenson AE, Schaeffer PM*. A rapid test for protein–DNA interactions. *Nucleic Acids Research* 2026; 54(4):gkag142.
***Corresponding author: patrick.schaeffer@jcu.edu.au**

Protein–DNA interactions underpin essential biological processes such as gene regulation, DNA repair and RNA processing, yet existing analytical methods often require expensive instrumentation, specialised expertise and highly controlled experimental conditions. After decades of studying protein–DNA complexes, one question kept resurfacing: what if that entire tedious methodological workflow requiring a multitude of steps, hours of work and specialised equipment could be streamlined into a simple instrument-free 'mix-and-run' system that delivers high sensitivity and robustness at a minimal cost? The answer became apparent during the COVID-19 pandemic while we were examining the analytical sensitivity of commercial rapid antigen tests with a green fluorescent protein (GFP)-tagged SARS-CoV-2 nucleocapsid protein.

This work led to the design of the rapid protein–DNA interaction test (R-PNAI-T), which harnesses the principles of lateral flow assays. The system strategically exploits the ubiquitous GFP tag, widely used in cell and molecular biology laboratories to track transcription factors and other DNA-binding proteins. By combining a commercial dipstick with a FITC-labelled anti-GFP antibody, a GFP-tagged protein and a biotinylated

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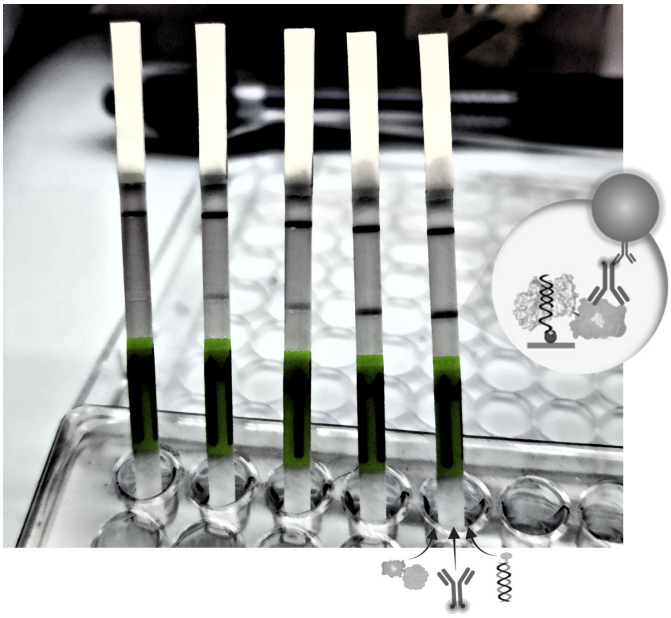

'Mix-and-run' workflow. *A GFP-tagged DNA-binding protein (Tus-GFP) is mixed with a FITC-labelled anti-GFP antibody and a biotinylated target DNA. A HybriDetect dipstick is inserted in the mixture and a band appears at the test line when the complex forms. In this example, increasing concentrations of Tus-GFP (left to right) were used to bind to biotinylated Ter DNA.*

DNA target, the R-PNAI-T enables rapid detection of protein–DNA interactions in a simple mix-and-run format. Two bacterial replication terminator proteins (Tus) from *Dickeya paradisiaca* and *Escherichia coli*, and a bifunctional group II biotin protein ligase (BirA), which also acts as a transcriptional repressor of the biosynthesis pathway in *E. coli*, were used for validation of the rapid test and to explore its limits. The R-PNAI-T was then adapted to investigate the binding of the putative initiator protein DnaA to specific PCR-amplified target sequences within the predicted origin of replication in chromosome I of *Burkholderia pseudomallei*, a bacterium responsible for melioidosis in North Queensland and other tropical regions.

The R-PNAI-T yielded reproducible and comparable data across a panel of diverse DNA-binding proteins, while transforming a traditionally complex procedure into a fast, accessible and highly robust system. Detection of protein–DNA interactions was achieved in under 30 minutes with picomolar-sensitivity, without powered equipment or complex sample preparation. The simplicity of the R-PNAI-T will make the study of protein–DNA interactions accessible to laboratories with limited resources, helping to democratise a field traditionally restricted to well-equipped facilities. Its tolerance to matrix effects and common contaminants makes the assay well suited for real-world biological samples, opening new opportunities in drug discovery, biotechnology, and translational research.

Looking ahead, the incorporation of alternative affinity tags or protein-specific antibodies could extend the utility of the R-PNAI-T to a wide range of targets, enabling studies of diverse DNA-binding proteins as well as the evaluation of aptamer-based therapeutics and inhibitors of disease-relevant transcription factors. As a simple and accessible system, the R-PNAI-T is well positioned to complement established technologies, serving as a rapid screening or validation platform alongside approaches such as SPR and ChIP-seq. Its accessibility may help lower technical and financial barriers that have historically limited exploration of protein-DNA interactions in many laboratories. Finally, beyond research, the platform also holds promise as an educational tool, enabling hands-on investigation of protein–DNA interactions in university teaching laboratories and even advanced secondary-school classrooms.

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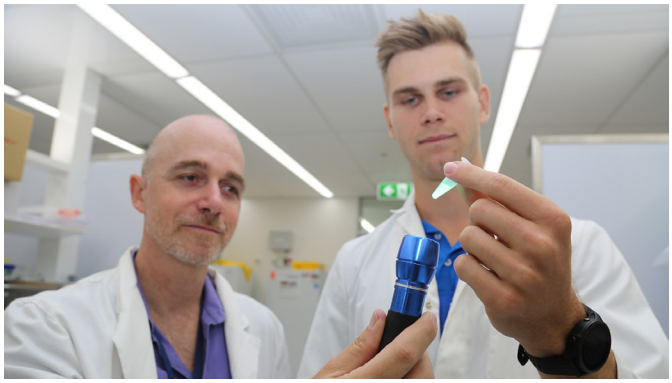
College of Medicine and Dentistry
James Cook University



Patrick Schaeffer (left) and Casey Toft illuminating a GFP-tagged DNA-binding protein sample. Image credit: James Cook University.

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The ASBMB Education Feature is coordinated by Amber Willems-Jones (amber.willems@unimelb.edu.au) and Matthew Clemson (matthew.clemson@sydney.edu.au). This issue was supported by Tracey Kuit (UNSW Sydney) and James Tsatsaronis (University of Sydney).

Lessons Learnt From Interactive Oral Assessments at Scale in a First-year Molecular Biology Unit

Masha Smallhorn and Narelle Hunter

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Context

The advances in generative AI technologies have made it difficult to rely on written tasks to evaluate understanding, as students increasingly turn to generative AI to create submissions. Molecular Basis of Life is a first-year molecular biology unit with over 600 students at Flinders University. Students are enrolled in a broad range of degrees, including the Bachelor of Science, Bachelor of Medical Science and Bachelor of Heath Sciences. Students attend a two-hour weekly inquiry-based practical in classes of 100 and record results in a laboratory book. Students have previously written a report based on one practical. To address the use of generative AI, in 2025 the report was replaced with an interactive oral assessment (IOA). Described as a two-way interactive, genuine and unscripted conversation between assessor and student, IOAs allow students to demonstrate learning through agile and critical analysis in a conversational manner (1).

IOA logistics

Practicals ran over 13 weeks, with all students timetabled into a two-hour IOA in week 13 (**Fig. 1**). Students were provided with two timetabled opportunities to practise the IOA with peers and a Cogniti chatbot, which allowed students to practise

Fig. 1. Timeline of IOA. *Students had weekly practical sessions and recorded experiments in a laboratory book. One practical was randomly selected from the semester and assessed through an IOA in week 13.*

asynchronously. During the IOA, students had a one-on-one conversation with an assessor, with a 15-minute allocation per student, focussing on one practical carried out during the semester. Assessors initiated a conversation about the experiment where students discussed their results in the context of their experimental design and explained the theoretical underpinnings, referring to their laboratory book. The practical selected for the assessment was chosen at the beginning of the IOA using a random generator. All IOAs were audio recorded on Microsoft Teams for moderation purposes. There were 10 to 12 assessors per session, facilitating assessment of up to 12 students at one time in an open plan classroom.

Impact and lessons learned

The impact of the IOA on learning outcomes was investigated using a pre-and-post survey and through the analysis of grades. Results revealed a statistically significant increase in grades in the IOA compared to the report ($p<.001$, Mann-Whitney U Test), suggesting meaningful learning. A thematic analysis was carried out using Copilot and prompts described by Turobov and colleagues (2) The results identified four emerging themes from the open-ended survey question, including content mastery, assessment anxiety, communication skills and active engagement. Students frequently described IOAs as a mechanism for deepening their understanding of content: *"I had to not only study for one practical but all of them which then allowed for me to essentially learn about all of the relevant key molecular aspects."* However, despite providing opportunities for preparation, students experienced anxiety: *"Despite preparing and understanding I was too nervous to get my thoughts out on the day."* Assessors reported on the ease of the assessment process and a reduction in marking time. These initial results suggest that IOAs promote deep learning and reinforce conceptual understanding, thus are an authentic, academically rigorous assessment task. However, the results also highlight that students need more opportunities to practise IOAs to reduce assessment anxiety, which will be built into future iterations of the assessment.

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Science Fiction Prototyping: Making the Impossible, Possible

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There is an undeniable link between science and science fiction. Writers of speculative fiction are often inspired by real-world science and technology and in turn scientists, although constrained by physical laws, often derive inspiration from fiction. There is a similarity to how both work in conducting *gedanken* (thought) experiments to test the logic and consequences of a hypothetical scenario (1). Science fiction prototyping is a methodology introduced to help formalise the link between speculative fiction and science and promote innovation by extrapolating trends from research. Science fiction narratives can further stimulate the moral imagination such that the social and ethical implications of novel technologies on individuals and society can be evaluated.

As part of our major in biochemistry at La Trobe University, we use science fiction prototyping to engage students, guide their exploration of cutting-edge research, provoke greater consideration for the societal and ethical consequences of research and foster creative thinking. Students begin by identifying a biotechnology or biological phenomenon in a work

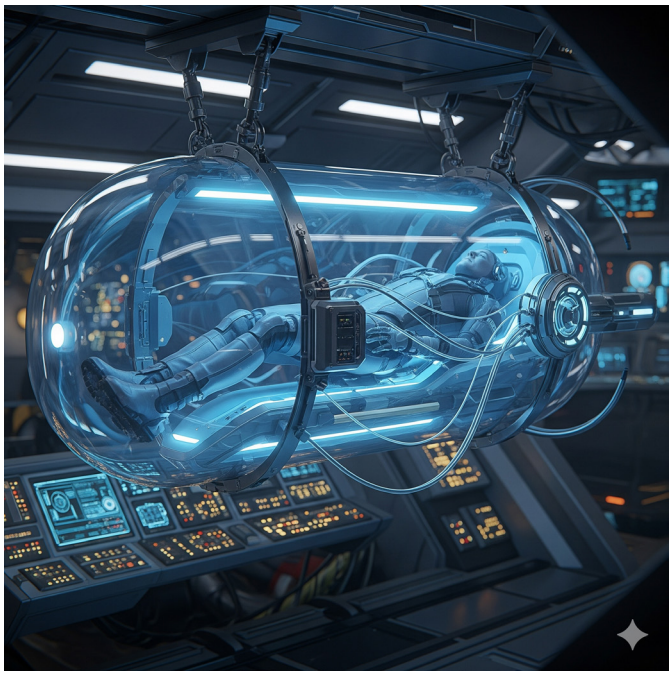

Fig. 1. *Putting humans in suspended animation to survive for extended periods of time on long space voyages is a common trope in science fiction. Although metabolic depression occurs naturally in diverse phyla, it represents a challenge to replicate it in humans. Image generated by Google Gemini, 2025.*

of science or speculative fiction (book, story, film or computer game). The one major caveat is that the idea must relate to biochemistry, molecular and/or cellular biology. So, although students start with a fictional prompt, they must extensively use the primary literature to investigate the scientific background and feasibility of the idea.

Depending on the inspiring fiction, we encourage students to ask:

- Is this an active area of research?
- Are there any real-world precedents for this innovation?
- If a biological system requires modification (e.g. through gene editing) for this innovation to be realised, describe how the base system works.
- What would we need to solve or discover first to make this innovation possible?

For example, the common science fiction trope of suspended animation to survive long space voyages has a real-world precedent in metabolic depression commonly seen in nature. Many organisms survive for extended periods by entering a state of estivation, hibernation or anhydrobiosis. In fact, and although we might be far from suspended animation for long space voyages, understanding metabolic depression in comparative systems has practical applications in trauma medicine and organ transplants (2) (**Fig. 1**).

In our experience, most ideas similarly provide agency to students to explore different aspects and implications. Even with seemingly far-fetched premises, it is possible to make links to real science (see **Table 1**).

For our unit, students present their science fiction prototype as a 15-minute seminar to examiners and their peers, pitched at the level of the informed, non-specialist. They are instructed to use the fictional prompt sparingly to engage audience attention before going into the scientific content, which should form the bulk of their presentation. They are then expected to conclude with speculation of the ethical and/or societal impact of their prototype. In assessing the task, we emphasise the clarity of presentation, engagement with the primary literature, demonstration of understanding and depth of reading in answering questions and if their thought experiment has yielded logical consequential conclusions.

The level of student agency with this assignment necessitates guidance. To this end, students pitch their ideas in the form of a 1000/24/7 lecture (a seven-word title, a 24 second pitch, accompanied by one image) (3). This early intervention pedagogical strategy allows ideas to be vetted for suitability to the task, helping students identify relevant primary sources and importantly a mechanism for students with similar topics to share. We also incorporate a formal drafting and peer review session before their final presentation. Students also benefit from guest seminars on novel research and ethics. This year, we have had guest lectures from researchers working in deep learning and AI, space biology and speculative bioethics. We have also previously attempted this assessment as a group project, however, the choice of inspiring fiction seems to be highly personal. Based on our experience, we would advise that groups are given a topic or are grouped only following an individual pitch.

Although students find this assignment difficult, feedback suggests that they also find it engaging and that it inspires curiosity:

"This assignment not only reinforced what I've learned but also inspired a curiosity to understand how these concepts can drive future advancements. Exploring potential emerging technologies through our current understanding of biochemistry was truly motivating."

"I was the kid who spent a lot of time reading comics while fantasising about being a superhero. And although that is possibly still centuries away, I have learned how gene editing technologies may truly achieve that."

"I found it enjoyable to research through the prism of science fiction and relate it to current scientific understandings. Overall, it was a great assignment."

This assessment replaced a previous task where students investigated an emerging biotechnology, with most choosing recent iterations on established technologies, such as gene editing. Since most undergraduate work is confirmatory, we prefer this assessment which forces students to think critically and consider the hypothetical. In this way, we increase

Table 1. Previous science fiction prototyping student projects.

Inspiring Fiction	Technology	Real-world Science
Green Mars (1993) novel by Kim Stanley Robinson	Terra-forming Mars	Genetic engineering for enhanced biological nitrogen fixation in cereal crops
Star Wars Universe	Bacta-tank – accelerated healing	Promoting tissue regeneration by immune system modulation
Reanimator (1922) novella by HP Lovecraft	Reanimating the recently dead	Comparative approaches to understand the limited regenerative capacity of mature human neurons.
Epic of Gilgamesh (c2100–1200 BCE) poem from ancient Mesopotamia	Lifespan extension	Therapies for eliminating senescent cells
Altered Carbon (2002) novel by Richard Morgan	Mind uploading	Neural mapping and the human connectome
The Pod Generation (2023) film by Sophie Barthes	Artificial wombs – ectogenesis	Understanding the role of maternal–foetal interactions in foetal immune system development

engagement and importantly also reduce issues with academic integrity and the misuse of generative AI (4). This assessment also serves to provide a better understanding of how research functions in society where, like in science fiction, it works to make the impossible, possible!

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Hit Play Before You Pipette: Pre-laboratory Videos to Boost Biochemistry Practicals

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Foundations and Techniques in Biochemistry (BCM210) is a second-year subject that is offered at Charles Sturt University (CSU) in internal (face-to-face) and distance (online) modes over twelve teaching weeks. There are weekly practical sessions for internal students and a three-day intensive school for distance students. A recurring challenge observed in both cohorts is a lack of preparedness for practical sessions. The internal cohort predominantly comprises young school leavers who often struggle with sustained engagement and self-directed learning (1). In contrast, distance education students tend to be mature-aged and highly committed; however, their participation is frequently constrained by competing demands such as employment and family

responsibilities (2–4). Students in these practical classes work in small groups (two or three students per group), thereby allowing student–student interaction learning (5). To address the issue of inadequate preparation, interactive pre-laboratory videos (6,7) were introduced as a pedagogical strategy to enhance readiness and engagement prior to practical sessions.

BCM210 introduces key biological macromolecules and essential metabolic pathways, alongside hands-on experience with standard biochemical techniques. It serves as a foundation subject which scaffolds other advanced studies in life sciences and health disciplines. With approximately 200 students enrolled annually (about 135 internal and 65 distance), BCM210 draws students from a wide range of science and health degrees and is considered one of the most challenging subjects for students to master.

Students have very different experiences and preparation for learning biochemistry. While intensive schools offer some logistical benefits, being designed in blocks to facilitate managing other responsibilities (8), their condensed schedule is usually tiring for students, which makes it difficult to introduce new concepts. It became evident that fundamental laboratory techniques and biochemical principles needed to be presented to students before they attempted complex and nuanced experiments. Rayment and coauthors recommended pre-laboratory activities in chemistry and biosciences classes in the UK to reduce cognitive demand during laboratory classes (9).

In collaboration with a media technologist from the Division of Learning and Teaching at CSU, interactive pre-laboratory videos for the practical component were recorded while the lead demonstrator carried out the experiments in the laboratory, using equipment consistent with what students encounter during practical sessions, for students to watch before attending each practical session (10). On average, the videos were about 25 minutes to maintain attention. They started with a brief explanation of the scientific relevance of the experiment, followed by an overview of the key biochemical concepts related to the experiment. The experimental procedure then included a step-by-step walkthrough of the practical task, identifying equipment, reagents and techniques while highlighting safety considerations and common errors. The videos contained embedded questions that students needed to correctly answer to be able to continue watching (**Fig. 1**), otherwise they needed to watch that part again. Finally, the videos showed example data or outcomes with an explanation of how to analyse and interpret results. The videos were made easily accessible to both internal and distance students

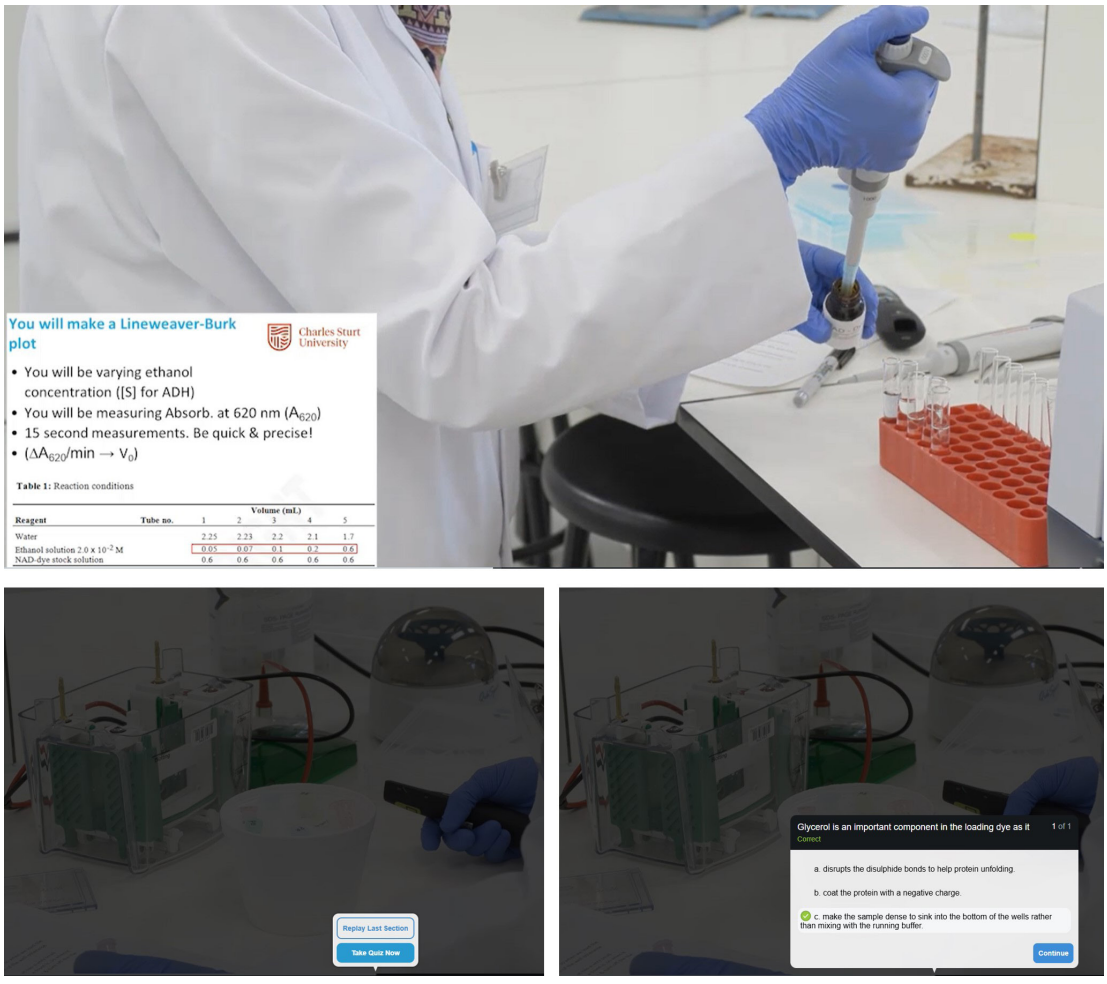

Fig. 1. *Screenshots from the pre-lab videos showing examples of instructions provided and embedded questions.*

weeks before the practical classes on the subject's Learning Management System. These videos prepared students for the practicals by familiarising them with the instruments and the techniques they were going to use, which made efficient use of their time and made the practical sessions much more organised, productive and enjoyable. Students were able to watch the videos in their own time, which provided flexible and adaptive learning to students to fit with other commitments (11). In addition, the embedded questions helped to reinforce students' understanding.

Numerous students liked the inclusion of the pre-laboratory videos, as evidenced by the following end-of-session survey responses:

"The pre-lab videos explaining the experiment were of significant help and majorly aided in my learning prior to and during the practical."

"I also appreciated the very clear instructions given about expectations for intensive school, and the opportunity to have a video presentation."

"The practical videos before going into the practical helped and made it quick and easy to complete."

This feedback suggests that student engagement and learning were enhanced as a consequence of the implemented pre-laboratory video strategy. The benefits of the videos did not directly translate into a higher average grade in the practical assessment; however, the end-of-session survey positive response rate increased from 44% and 57% for internal and distance modes, respectively, before implementing the pre-laboratory videos, to 64% and 93% for internal and distance modes, respectively, after introducing the pre-laboratory videos. This approach allowed students to apply their knowledge about what they learnt from BCM210 topics in a practical way (applying theory into practice), thus fostering their learning (12).

In summary, biochemistry practicals supported with pre-laboratory videos enabled students to acquire important laboratory technical skills (13,14), thereby preparing them for their chosen profession. The development of pre-laboratory videos has proven to be a valuable strategy in supporting student learning by reducing cognitive demand and increasing familiarity with equipment and procedures, which have helped students approach practical sessions with greater confidence and preparedness. Producing these videos using the same equipment students use was essential in minimising confusion and building familiarity. Looking forward, several enhancements could further improve their impact and accessibility features such as using captions and multilingual options. This approach not only supports academic success but also contributes to a more inclusive and confident learning environment.

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Sketching Science: Graphical Abstracts as an Authentic Assessment

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Mind maps, concept maps, schematics and other visual representations have long been used by educators to break down complex concepts and to enhance student learning and engagement (1). What's relatively new is the requirement by scientific journals for authors to include visual representations of their research upon publication (2,3). While these can encompass formats like short videos, they most frequently take the form of 2D schematics or graphical abstracts, which help readers quickly identify relevant articles and allow authors and publishers to drive traffic to their work (4,5). This publishing trend inspired us to design an authentic communication assessment for undergraduate science students that also fosters higher-order cognitive skills and creativity.

How it works

At La Trobe University, students in the second-year biochemistry subject BCH2MBC learn core concepts of metabolic biochemistry. For their graphical abstract assignment, students select from several provided research articles focused on central carbon metabolism. They read the article and create a visual representation of its findings (**Fig. 1a**–**b**). As part of our blended learning approach, we support students in completing this assessment through an online video explaining the task. This video helps students design their graphical abstract through annotating exemplars and introduces basic graphic design principles, including typography, colour and layout to enhance their communication skills. In-person workshops and ad hoc support sessions allow academics to assist students in interpreting scientific findings and provide informal design feedback.

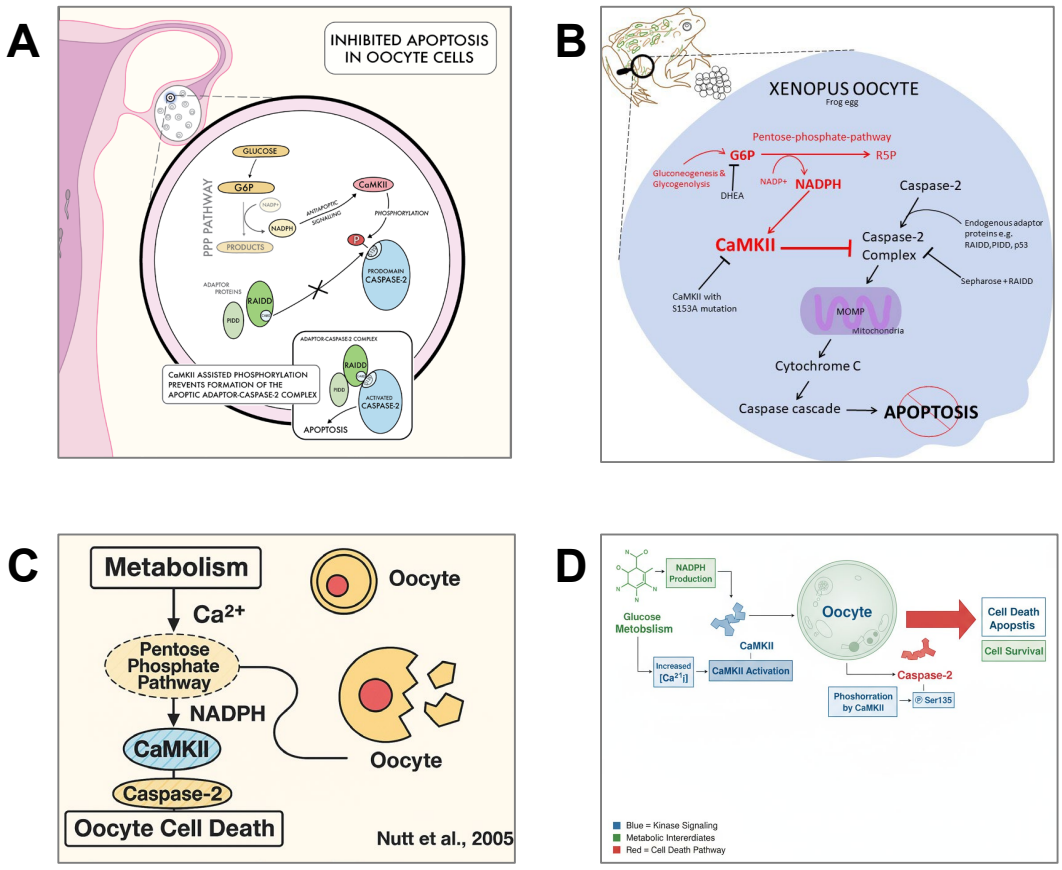

Fig. 1. Comparison of student-created and AI-generated graphical abstracts. *Examples of graphical abstracts submitted by BCH2MBC students for the article 'Metabolic regulation of oocyte cell death through the CaMKII-mediated phosphorylation of caspase 2' by Nutt* et al., *2005. Reproduced with permission from Tara Santamaria* ***(a)*** *and Sarah Hughes* ***(b)****. AI-generated graphical abstracts for the same article, created using Microsoft Copilot* ***(c)*** *and Lovart* ***(d)****.*

Impact and challenges

We used NVivo to analyse deidentified qualitative student feedback responses collected as part of routine subject evaluation. We found 64.5% of students who referenced the assignment expressed positive sentiments. Common words included “understand”, “different” and “creative”. For academics, while marking the assignment requires a deep understanding of the article, the process is efficient as it involves reviewing a single image. The main challenge lies in selecting suitable research articles – those without existing graphical abstracts, not heavily featured in review articles (which often contain visual representations), and of appropriate complexity and length for our second-year cohort. As a result, we primarily offer older research articles published before graphical abstracts became common and avoid those with complex ‘omics datasets.

Formative and/or summative

In BCH2MBC, this assignment is summative, but we also see its value as a formative tool. At Monash University, third-year immunology students in IMM3031 complete a written News & Views piece based on a provided research article. Since 2023, we have added a graphical abstract as a formative component (weighted as 5% to ensure completion) to this subject. Students submit their graphical abstract in weeks 4–5 and receive detailed feedback and marks. This approach helps us identify students who have misinterpreted or struggled with their article, allowing us to offer targeted support. Prior to implementation, the proportion of students receiving a HD/D (>70) or Pass/Fail (<59) for their News & Views assignment was 62% and 15.4%, respectively. Since inclusion of the graphical abstract, we observed a shift to 67.1% HD/D and 10.3% Pass/Fail, demonstrating the positive impact of this scaffolding.

Impact of generative AI to this assignment

The rise of generative AI has prompted many academics to reassess open-ended assignments. In our experience, current generative AI tools cannot effectively complete a graphical abstract task. Our testing, and the limited AI-generated student submissions we have seen, suggests these tools struggle with the higher-order skills needed to synthesise research findings and create accurate visual representations. Common issues include biologically inaccurate cell morphologies, spelling errors and incorrect placement or connection of molecules in pathways (**Fig. 1c–d**). While generative AI may eventually improve and prompt us to reassess this assignment, we currently see its value in helping students understand their chosen research article, which remains the most challenging part. This year, we encouraged students to use AI tools to break down experimental methods and interpret results, providing example prompts to support their learning.

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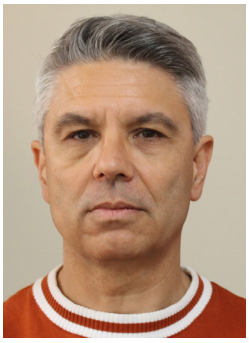

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SDS Page: Short Discussions for Students Page

Careers in Small Biotech – Where to Start?

Michal Pasternak

PhD students and postdoctoral researchers bring enormous value to early-stage biotech companies, yet many are unsure how to begin their transition outside academia. Here, refelect on my move from leading academic institutions to a biotech startup, along with some practical tips for those considering a similar path.

Michal Pasternak.

My journey

I completed my PhD at the University of Cambridge, where I studied molecular mechanisms governing early embryonic development. I loved the topic but have always struggled to focus on just one thing and wanted to gain experience in other areas. After my PhD, I received a Wellcome Trust fellowship to study malaria-causing parasites, a joint project between the Imperial College London and WEHI. The science was outstanding and I loved every bit of it, but again, I could not picture myself specialising in one research theme, which is important for building momentum in academia.

An internship at the WEHI's Business Development Office was pivotal and exposed me to translating scientific discoveries into actual products that can improve people's lives. I became involved in entrepreneurship programs and later commenced an MBA at the Melbourne Business School. Before completing my studies, I moved to Denteric, a company developing therapeutic vaccines against chronic inflammatory diseases such as periodontitis. Initially, I joined as a Research Project Manager. Today, as a Senior Drug Development Manager, I work across R&D, clinical development and commercial strategy. Wearing so many hats really suits me because every day brings new interesting challenges and learnings.

Tip 1: Understand the different functions within biotech companies

On the outside, it is often hard to understand the difference between different functional streams within biotech companies. Understanding their structure helps you identify where you best fit and where you can add value. Small biotech companies typically operate across several core functions:

- **R&D** – Preclinical research, lead optimisation, proof-of-concept experiments and understanding the mode of action. This is the most common entry point for PhD graduates.
- **Clinical** – Trial design and execution. High demand but require good knowledge on clinical trials and the regulatory environment. Many researchers first gain experience at a CRO (contract research organisation) in trial monitoring or in regulatory position before moving to a leadership role in a biotech company.
- **CMC/Manufacturing** – Process development, manufacturing and product characterisation. Heavily regulated but experience in chemistry or protein biochemistry is highly valued.
- **Operations and Program Management** – Coordinating budgets, timelines, contracts and delivery of cross-functional milestones. You can leverage your project management experience, exposure to steering committees and managing grant budgets.
- **Business Development** – Partnerships, licensing and fundraising. Often absent or minimal in early-stage biotech. Volunteer at your institute's business development office if this is the path for you.

Understanding these streams will allow you to apply for roles that match your long-term aspirations and skills.

Tip 2: Focus on skills

In biotech, hiring managers rarely look at your publication record. They prioritise skills and experiences that suggest industry readiness. Project management, external collaborations, working towards tight deadlines and problem-solving skills are critical. Ask yourself what experience will help you to make the transition and differentiate you from the crowd. For me, it was managing two grants and having experience at the business development office. The MBA helped me to stand out but didn't really make much difference until later on. For you, it may be industry collaborations, clinical exposure or committee work.

SDS Page: Short Discussions for Students Page

Tip 3: Network like your job depends on it

Australia's biotech ecosystem is highly interconnected. While most hiring managers prefer candidates with previous industry experience, strategic networking can compensate for lack thereof. Networking alone won't get you the job, but it will get you at least an informal interview and may help being remembered when opportunities arise. How to start? Go to networking events, talk to recruiters or connect to people on LinkedIn (always leave a note!). And an important lesson my boss once taught me: you only have one first impression.

Final thoughts

Moving from academia to small biotech can be a very rewarding process. You trade the depth of expertise for exposure to various aspects of drug development lifecycle. It may feel uncertain at times but this makes it even more exciting if you are willing to embrace the journey.

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Election of Council 2027

Nominations are called for the following positions on the Council of the Australian Society for Biochemistry and Molecular Biology Inc for 2027: 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 2026 to 31 December 2026 is composed of the following members:	President	M Maher
	President Elect	K Quinlan
	Secretary	V Anggono #
	Treasurer	A Achuthan #
	Editor	T Soares da Costa #
	Education Representative	A Willems-Jones #
	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	K Fairfax #
	VIC	N Kershaw #
	WA	J Haywood #

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 2026
(PRIOR TO THE ANNUAL GENERAL MEETING TO BE HELD ON 30 SEPTEMBER 2026).

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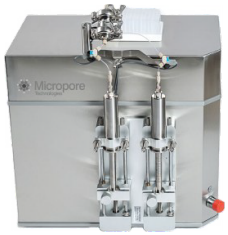

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Off the Beaten Track

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.

Who Says Academia was the Beaten Track?

Samuel Nonis
Associate Dean of Student Engagement and Academics, St Catherine's College, Curtin University

The night I received the final call after a three-stage interview for my first postdoc position in Wales, I hung up and heaved a huge sigh of relief – I had been rejected. The reaction, though it was mine, caught me by surprise.

At that time, if I wasn't writing my thesis, I was desperately searching for my first postdoc position while working at the university café to avoid depleting my savings. Before that phone call, it didn't occur to me that I hadn't given myself the mental space to reconsider my next step. So, rather than knocking on another research group's door, I stepped back from my job hunt to understand my reaction. This was the fringe benefit I had been looking forward to for so long: the opportunity to immerse myself in another culture while plying my trade.

There was no denying the value of what I had learnt; if I could go back in time, I'd do a PhD all over again. This time, however, having seen the vast majority of my PhD mates pursue careers outside the research lab, I do so with the awareness that staying in academia is the option that *takes you off the beaten track.*

Still working at the café at that time, I contemplated placing Dr on my name tag as a cheeky invitation to undergrads curious enough to ask why a doctor was making their coffee. I would explain that I had already given up a chunk of my youth for this noble but lower-than-minimum-wage endeavour. And that, as much as I enjoyed being a researcher, I didn't want to spend the next decade being rewarded for good work with a higher-than-50% chance of losing my job every three years.

I am now in my fifth year as Associate Dean of Student Engagement and Academics at St Catherine's College, Curtin University. The implicit understanding that I can keep my job as long as I am reliable has worked wonders for my long-term wellbeing.

My day-to-day responsibilities range from managing the college's tutoring program and having one-on-one meetings with students seeking academic or life advice, to organising faculty and industry dinners where academics and industry professionals share controversial opinions and career-changing insights with students. Great days are when a student tells me that a guest speaker I invited changed their perspective, or when a student leader shares how they've grown through working in my team. Some days are emotionally draining, particularly when I am supporting students affected by gender-based violence.

Samuel Nonis.

The steepest learning curve was transitioning from managing a team of one in the lab to managing a team of more than twenty student leaders organising more than a hundred activities and events each month. I do miss the days when the outcome of an experiment often directly affected only me, and when it was acceptable to fail often. In this role, every action I take feels heavier as it could have a lasting impact on any of the 400 students in the accommodation. What brings me the most satisfaction is seeing students step out of their comfort zone each year and make decisions they might never have made otherwise.

How did I end up with a job like this? Without realising it at that time, I had spent the first two years of my PhD interviewing for my current job. As a postgraduate, I lived in St Catherine's College at the University of Western Australia, where I worked as a Residential Advisor providing pastoral support to undergraduate students. I left a positive impression on the college staff that I worked closely with at the time. So when they began operations on a new campus and needed someone they could rely on to carry the college culture across, they reached out to me.

Off the Beaten Track

Despite being headhunted soon after graduating, the transition out of academia wasn't a walk in the park. Leaving academia was a practical matter; breaking my identity as a scientist was the existential and, arguably, more challenging one. I took pride in having an intuitive sense for how amino acid residues influence protein function, in being able to inspire students to pursue academic research, in being one of a handful of experts in my field of study, and so much more. Furthermore, being a scientist came easily to me; it suited my temperament. But I didn't know how to lay down the hard-earned knowledge and skills I had acquired to answer questions that scientists have been circling for decades… and simply move on. When my former labmate secured his first postdoc in Europe, I was happy for him, partly because that had been my dream too, and at least one of us had made it a reality.

Half a decade on, I can now appreciate that a career is sustainable only if it fits into a fulfilling life. Staying in academia required that I sacrifice other things that I valued. My former lab mate is now looking for jobs outside of research to accommodate the next stage of his life with his partner. As before, I am happy for him because he is making a decision that will allow him to lead a fulfilling life.

I've come to realise that the reluctance to lose my identity as a scientist was, in fact, my inability to see what I could become. That realisation shapes the advice I would offer. If you're thinking about career options, be mindful that the advice you get is shaped by the path the advisor took. Your research supervisor can give great advice, but you'll want to find mentors outside of academia, individuals who are living, breathing representations of who you could become: people who can help you focus on the possibilities rather than what you might be leaving behind.

Without a clear example of what life outside academia could look like, I had to walk the path before I recognised that the things that mattered to me hadn't changed. I am still comfortable trying new things and failing. I still read scientific papers late into the night to feed my interest in biotech. I now also read research articles on leadership and management to review the way I work with my team. And I still enjoy learning every day. In many ways, I never left the track.

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Maximising Figure Value in Patent Applications

Dr Julie Murison (Associate) from FPA Patent Attorneys discusses how to maximise the value of figures in patent applications.

Julie Murison.

Figures can be the most important part of a scientific publication. Authors put a lot of effort into preparing beautiful and eye-catching figures, and figures can really increase the impact of a publication. However, the same figures often don't translate into high-value figures in patent applications. Patents are legal documents, which describe an invention, and the boundaries of the invention in *words*. A picture may be worth a thousand words, but a thousand words may be more valuable in a patent.

Some scientific concepts or results or invention features are difficult to capture by words alone. And when prepared and described properly, figures can boost the clarity and strength of a patent application.

This article discusses how to maximise the value of figures in patent applications. This advice is based on typical inventions in the life science space and so does not discuss mechanical drawings.

Black and white figures

Where possible, black and white figures are best for patent applications. Black and white figures are not a requirement when filing a provisional application but are a requirement at the PCT (international) stage.

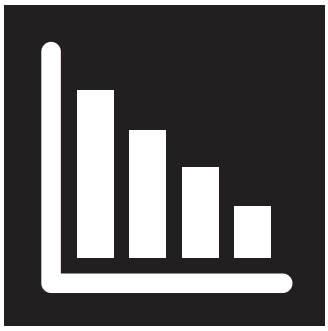
When a PCT application is filed, a lower resolution form of the specification is uploaded to the World Intellectual Property Organisation (WIPO). Unfortunately, this can sometimes result in figures becoming blurred and hard to read, and chemical structures may become fuzzy. The figure(s) may then need correcting, potentially incurring additional cost. Even if the figures are not required to be corrected, if important details become obscured, it may be harder to rely on them at a later date.

The best way to avoid this is to prepare black and white figures with thick line size and at least 10-point font size for any embedded text. If you can prepare them as a vector graphic – even better! While a greyscale figure may give you some idea how a coloured figure will be rendered, a black and white figure, which can be prepared using image software, for example ImageJ, and converting the figure to black and white, or 8-bit, typically renders better. Using different symbols or hatching rather than shading is also helpful.

Bigger is better, but can be more expensive

Bigger figures, typically one per page, with more detail, and larger text size, render better in patent applications. However, there are costs associated for PCT applications with more than 30 pages. And figure pages count towards this limit. Page numbers also impact filing costs at the national phase (i.e. when you file a patent application in individual countries).

While it is common to prepare composite or panel figures for journal publications to save space, in patent applications, a better strategy may be to separate individual figures onto separate pages. Data might be better presented in a table in the description, rather than in a graph. When deciding which figures to prepare, favour figures that match the level of detail in the examples and either provide evidence for key features of the invention or help explain how it works.



Photographs and detailed images

Preparing a black and white image is suitable for graphs, however, will not always be possible for other types of data, for example microscopy images. You can maximise the value of this type of data by describing, in words, the important features in the image, and how these features relate to the invention. If there is important colour detail in the image, describing this feature in a way that it can still be recognised from a black and white image can be helpful. For example, instead of describing a feature as "shown in red in figure 1", try describing it as "the large circular feature in the top right hand corner of figure 1 (in red)." Highlighting portions of interest, using a solid black arrow, and describing what the arrow indicates can be a valuable addition to a figure and figure description. Additionally, providing your patent attorney with a description of the figures at the drafting stage is very helpful. The more detail you can include on which features of the figures are important, and what you want the reader of the patent application to understand when they look at the figure, the better. Including text describing these features increases the chance of being able to rely on a feature of a figure if needed later when the patent application is being prosecuted.

Maximising Figure Value in Patent Applications

Chemical schemes and structures

Chemical schemes and structures which are included in the specification as images, rather than vector graphics or embedded objects, may become fuzzy when the specification is uploaded to WIPO. Embedding the schemes and structures as, for example, a Chemdraw object, is typically better, but not essential. If preparing structures and schemes as image files for adding to the specification, increasing the line thickness and text size will improve the clarity of the structures post-PCT rendering.

Fuzzy figures and the defects notice

Sometimes, despite everyone's best intentions, it is not possible to prepare the ideal figures or schemes for a patent application by the deadline. This might be because the filing is urgent, or because a key person is unavailable. Patent attorneys are familiar with this situation. And they will file the application with the figures on hand to meet the deadline.

If the rendered figures are low resolution, and the receiving office (the office that checks the PCT filing and issues the search report and written opinion) considers the figures unclear, a defects notice will be issued. You will have an opportunity re-file figures that are objected to, with bigger text size and thicker lines. You cannot, however, add any information not included in the filed specification.

Sometimes, it may still not be possible to file replacement figures in response to the defects notice. It is possible to respond by saying that the filed figures are the best figures available. It is best to discuss this option with a patent attorney, as filing replacement figures during the national phase can be more expensive because this has to be done individually at each patent office.

Technicoloured patents

Can you file colour figures? You can – sort of. Several patent offices do allow you to file coloured figures, including the US patent office. But your patent attorney will need to request this, along with a justification (and a fee) for why the figures need to be in colour. A fluorescence microscopy image showing the results of a colocalisation study might be an example of an image that needs to be in colour.

From 1 October 2025, the European Patent Office (EPO) is now accepting colour figures for European patent office filings. However, the PCT rules haven't changed. And so, while it is potentially possible to file coloured figures during the national phase, it is still necessary to file black and white figures for the PCT application (and navigate a potential defects notice). So, when considering whether to include coloured figures, the additional costs need to be balanced with the potential benefit.

Figuring it out

To get your 1,000 words worth out of your figures, consider which figures best support the invention, prepare patent-specific figures, and describe the figures and all their important features in words. This is an important part of the drafting process and your patent attorney will work with you to achieve the best outcome.

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Adelaide Protein Group: an ASBMB Special Interest Group

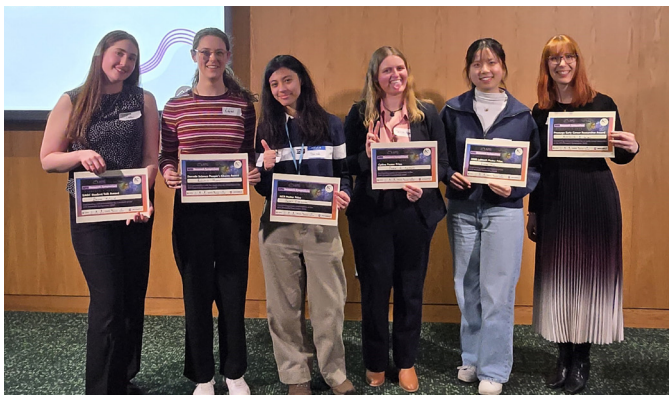
The Adelaide Protein Group (APG) was founded in 2008 to bring together South Australian researchers who share similar interests in protein and molecular biology science. Our goal is to encourage SA researchers to participate in academic collaboration, to share and discuss cutting-edge research among peers, and to promote established and emerging researchers in Adelaide. A secondary goal of the APG is to help students to engage directly with scientists from Adelaide's numerous academic and research institutions. The members of the APG committee represent the Adelaide University (AU), Flinders University, South Australian Health and Medical Research Institute (SAHMRI), South Australian immunoGENomics Cancer Institute (SAiGENCI). We continue to find new ways to bring together Adelaide's brightest minds in protein science and to showcase the excellent research being performed by postgraduate students and early-career researchers (ECRs).

To serve this goal, the APG has recently increased our networking efforts, kicking off our annual activities with events that bring together our existing community and welcome new scientists to Adelaide's thriving molecular biology scene. In 2024, we hosted the Protein Pathways Networking Night which featured a range of experts who took their protein knowledge into different scientific careers including research and industry roles. Our guest speakers shared their unique career insights and experiences in navigating their scientific roles following their studies. In 2025, the theme was 'Pep(Tide) Talk: Science Stories, Services and Solutions' with invited guest speaker Professor Stephanie Gras (La Trobe University). This event also offered the opportunity to hear from and network with several of South Australia's leading service providers in the biological sciences field.

The APG Research Symposium (formerly Awards Fest) is the premier event we host annually. Over the past three years, we have been honoured to host many leading Australian scientists, with Dr Adrienne Sullivan (SAiGENCI) and Associate Professor Michael Lazarou (Walter and Eliza Hall Institute of Medical Research) as our keynote speakers in 2023, Professor Brett Collins (University of Queensland) and Dr Luke Isbel (SAiGENCI) in 2024, and Professor Renae Ryan (University of Sydney) and Dr Michael Roy (SAiGENCI) in 2025. These invited speakers gave exciting and engaging talks about their research, from their postgraduate studies to lab head positions.

This event provides the opportunity to hear about the cutting-edge research performed by postgraduate students and ECRs from across Adelaide and recognise great contributions to the field of protein science. Each year, four PhD students and four ECRs are selected to present talks, and thirty researchers are selected to present at our poster session. Thanks to our generous sponsors, we offer over $2,000 in prizes annually to our presenters. Last year's symposium was a great success, with over 130 researchers in attendance, and we look forward to many more joining us for the APG Research Symposium in 2026!

Keynote speaker Renae Ryan presenting at the 2025 APG Research Symposium.



2025 APG Research Symposium award winners, from left: Dayna Holroyd (AU), Rebekah Munro (AU), Sarah Eismann (AU), Jesse Kennedy (SAHMRI), Emma Mao (AU) and Ashleigh Geiger (SAiGENCI).

The APG and Perth Protein Group (PPG) launched an exciting new initiative in 2025, providing the opportunity for Dr Danielle Rudler (University of Western Australia), who won the ECR Talk Award at the PPG Symposium in 2024, to travel to the 2025 APG Research Symposium as an invited speaker. In return, the APG had the opportunity to provide a travel bursary to our Student Talk Award winner, Dayna Holroyd (AU) to present at the 2025 PPG Symposium. We look forward to continuing

Adelaide Protein Group: an ASBMB Special Interest Group

Close competition in the tip box packing table game at the 2025 APG Quiz Night.

this collaboration with the PPG, to further increase our reach and offer unique opportunities for our students and ECRs to network outside of SA.

We're not just serious scientists here at the APG, we also know how to have fun! The APG hosts an annual quiz night full of protein-flavoured questions, table games, prizes, drinks and plenty of pizza. With over 100 attendees each year, the quiz night provides a fun opportunity to test your general and protein knowledge while networking with fellow researchers. In recent years, the winners have been awarded the highly coveted APG protein meme mug, a prize that's both functional and hilarious.

We love to round out the year with our annual Proteins in the Pub event. This provides a wonderful opportunity for our protein researchers and sponsors to come together for an informal end of year networking event and dinner. In addition to this, in 2025, eight students and ECRs presented lightning talks on their exciting research.

A highlight of 2025 was remodelling our social media pages and launching our new website. In addition, we published the first issue of our new biannual APG newsletter which aims to highlight APG events and celebrate outstanding research performed by our SA protein scientists.

A major aim of the APG is to keep our events cheap or free for our members, especially our students, to encourage engagement and equality of access. Of course, this would not be possible without the support from the ASBMB and our incredible sponsors. We would like to extend our gratitude to the ASBMB and our sponsors over the last three years: Cytiva, Decode Science, NEB, Promega, University of Adelaide, University of South Australia, SAGC, BMG Labtech, ATA Scientific and Metagene.

In 2026, we look forward to starting the year with another networking event in April ahead of our 2026 APG Research Symposium in July. We look forward to hearing about the new research emerging from Adelaide this year!

APG Committee

President: Dr Ashleigh Geiger (SAiGENCI)
Secretary: Emma Mao (AU)
Treasurer and Scholarship Officer: Dayna Holroyd (AU)
ASBMB Liaison Officer: Samuel Wallis (AU)
Webmaster: Jack Scanlon (AU)
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Events Coordinators: Lachlan Staker (SAHMRI), Shruti Deshpande (AU), Saba Ataei Kachooei (AU) and Dr Marion Turpin (SAiGENCI)
General Committee Members: Alison Roennfeldt (AU), Dr Alix Harlington (AU) and Renee Green (Flinders)

Samuel Wallis
ASBMB Liaison Officer
Adelaide Protein Group
Email apg.asbmb@gmail.com
Web https://apg.asn.au
X @AdelaideProtein

Winner of the Proteins in the Pub lightning talk award, Shamit Singla (AU) (left) for his thrilling lightning talk titled 'Malaria, Proteins and Diapers' with APG Past President, Alison Roennfeldt (AU).

In Memoriam

Gerhard Hans Schreiber 1932–2026

Gerhard Hans Schreiber was a creative and distinguished scientist whose career as a biochemist and molecular biologist spanned nearly fifty years. During his initial research career, he made seminal discoveries on the synthesis and processing of proteins, focussing on the hepatically synthesised plasma proteins. In later work, he studied thyroid hormone transport proteins in more detail, particularly transthyretin, where he made seminal discoveries that were recognised worldwide. Gerhard also made important contributions to the teaching of medical students at the University of Melbourne, and in his laboratory through the mentoring and training of the next generation of researcher scientists who today continue his passion of biomedical scientific research.

Symposium celebrating Gerhard's 70th birthday, University of Melbourne, in 2002.

Gerhard was born in Berlin, Germany, where he met his future wife, Margot, at high school. He then undertook university studies in Mainz (Physics and Medicine) and later, together with Margot, in Freiburg (Medicine). He then worked as a medical doctor at the University Hospital in Kiel in northern Germany but soon found he could not resist the call to research and more postdoctoral work. With a NATO Research Fellowship from the Deutsche Akademische Austauschdienst (DAAD) Germany, Gerhard spent two years in the USA, first in 1965 at the McArdle Lab for Cancer Research in Madison, Wisconsin, and then in 1966 with Professor Phillip Feigelson at Columbia University in New York studying the immunological-based purification of proteins (1). This overseas work led him into the world of scientific biomedical research where he thrived and found a lifelong passion. In 1967, after returning from the USA, Gerhard moved to Freiburg to take up a lab head position at the Biochemical Institute led by Helmut Holzer at the University of Freiburg im Breisgau where he established his own research laboratory and undertook 'habilitation' training to qualify as a university lecturer. Here, together with Kurt Weigand and others, he commenced research on the production and processing of the key blood transport protein albumin (2). Gerhard studied the synthesis and processed forms of albumin (and other proteins) using cell-free systems and hepatic cell suspensions, leading to high profile publications in the *Journal of Biological Chemistry, Cancer Research*, *Journal of Cell Biology* and *European Journal of Biochemistry*, among others, that led to a strong international reputation in the field of protein synthesis and biochemistry (3,4).

In 1973, Gerhard, Margot and their growing young family of three children, made the bold move from Germany to Melbourne, Australia, where Gerhard took up the key position of Professor of Biochemistry (Medical) at the Russell Grimwade School of Biochemistry at the University of Melbourne. These were the days of more relaxed travel regulations and six of Gerhard's special Buffalo rat strain also travelled on the same plane (in the hold) to Melbourne. This was a big step and a significant change from bustling cosmopolitan Europe, but they settled into life in Melbourne and Gerhard began teaching medical students, established his research program and began to make lifelong connections to the local research community. He expanded his research on albumin to study the expression, synthesis and processing of further members of the secreted hepatic plasma proteins using the rat as a model. Dr Joerg Urban, a member of his research group in Freiburg, also made the journey to Melbourne and, together with a second Department-funded position (filled by Heide Dryburgh), this helped to quickly establish a productive and vibrant research laboratory. Gerhard was a firm believer in using the best approaches and techniques to understand and discover new biological knowledge and discover new biological mechanisms. This included sophisticated protein purification approaches, making in-house polyclonal antibodies and using cell-free protein synthesis systems. In the early 1980s, together

Schreiber lab in 1976, from left: Kaylene Edwards (his first Australian PhD student), Gerhard Schreiber, Anne Millership (MSc student) and Dr Joerg Urban.

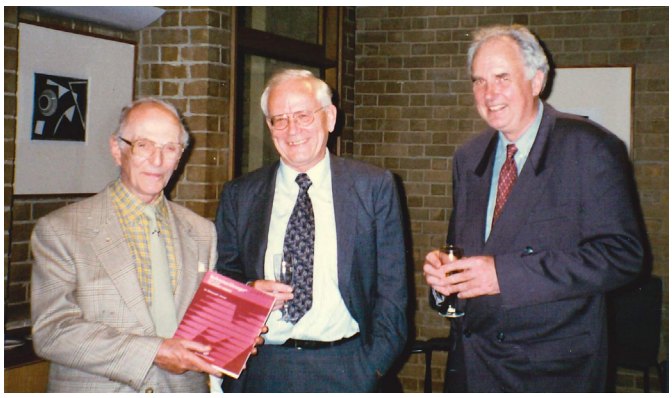
In Memoriam

Gerhard addresses the 14th Meeting of the International Society for Neurochemistry in Montpellier, France, in 1993.

with close collaborator Geoff Howlett in the Department, he was a very early adopter of the techniques of molecular biology, gene cloning and genome analysis. The Molecular Cloning manual by Tom Maniatis (Cold Spring Harbour, USA) became the 'bible' of the lab. In 1982 there were only six available restriction enzymes and two basic cloning plasmids (pBR322/M13). Geoff had recently returned from a sabbatical at Stanford with George Stark, and brought back with him key bacteriophage rat cDNA libraries. Gerhard's lab proceeded to clone and 'M13-Sanger' sequence a dozen or more cDNAs encoding rat hepatic plasma proteins. This led to many high-profile publications and the cloning of their genome-encoded genes and their full sequencing and characterisation, particularly in the context of transcriptional regulation (5). Gerhard's work could now be classified under Biochemistry and Molecular Biology, a name the Department would also soon adopt. Gerhard sought collaborations with researchers across Melbourne [Monash University, the Walter and Eliza Hall Institute, CSIRO Parkville, Victorian College of Pharmacy (now Monash Institute of Pharmacological Sciences)] and Australia (University of Adelaide, University of Western Australia, University of Sydney, University of Tasmania) to further the impact of his research.

In later years, Gerhard focussed on one specific plasma protein, transthyretin (TTR). He had made the seminal observation that TTR was also synthesised at high levels in the choroid plexus of the brain, a remarkable discovery that explained its key role in transport of thyroid hormones from the blood via the choroid plexus (the blood–cerebrospinal fluid barrier) into the brain (6). Gerhard was interested in the 'big picture' of TTR and its role in transport of thyroid hormone from the blood to the brain in terms of evolution, well before evolutionary/comparative biochemistry became popular. This was yet another example of his creative thinking. He proposed that TTR was first synthesised by the choroid plexus of stem reptiles and that they were the first vertebrates to develop a neocortex of the brain, thus requiring an enhanced thyroid hormone distribution system in the brain (7). He then identified the evolutionary differences (and potential selection pressures) for differential TTR synthesis in the liver compared to the choroid plexus and relevant selection pressures including endothermy. Investigation of Australian marsupials proved to be critical in these analyses! Concurrently at the molecular level, Gerhard noticed that whilst the binding sites of all TTRs were identical, some preferentially bound the active thyroid hormone (T3) whilst others preferentially bound the precursor thyroid hormone T4. He identified a series of point mutations that enabled the evolution of TTR from distributing the active form of thyroid hormone to distributing the 'biologically safer' precursor form of thyroid hormone (8). This was the first demonstration of a region of a protein other than the binding site (i.e. the N-terminal region), determining its ligand preference.

Gerhard strongly believed in participating in the local and national research community to support biochemical research, allow communication of research outcomes, and in particular train/mentor the next generation of biochemists and molecular biologists. Gerhard therefore quickly joined the Australian Biochemical Society (ABS, now ASBMB) in 1974, and was the ABS State Representative for Victoria from 1982–1985. He recalled some very lively National ASBMB Council meetings that involved some strong personalities, such as Tony Linnane and John Ballard. In 1983, Gerhard was awarded the ASBMB LKB Medal. This was very timely for Gerhard as the medal stipend supported a lecture tour to many different universities across Australia, allowing him to talk about his research and make many new connections and collaborations that endured through his career. Gerhard also made use of invitations to international research meetings to speak about his work and made many connections and collaborations overseas. In the mid-1970s, Gerhard also participated in the formation of the first Lorne Protein Meetings, that grew from a weekly Tuesday Protein Discussion Group in the Department, organised by Syd Leach. It was Bruce Grant who suggested Erskine House in Lorne as a possible location for a longer more formal Protein meeting and in 1976, the Lorne Meetings were born.



From left: Syd Leach, Gerhard Schreiber and Dick Wettenhall at Gerhard's retirement in 1997.

In Memoriam

Former Schreiber Lab members at Gerhard's retirement in 1997. From left: Porntip Prapunpoj, Sam Richardson, Marc Achen, Gerhard, Angela Aldred, Tim Cole, Phil Dickson, Linus Chang and Wei Duan.

Gerhard also understood that he had an important role with the mentoring and skills development of his laboratory research students and staff. This included technical training, writing skills, critical thinking about data and presentation skills. Gerhard also adopted new technologies at the first opportunity to make his lab more efficient. In 1983, the lab took possession of one of the first Apple Mac-E computers in the Department, which allowed the typing and printing of manuscripts and documents. He also believed that the lab that played together stayed together. When weather allowed there were weekly tennis matches that were keenly contested. For many years, there was a yearly lab trip to the snow where many of us were taught both downhill and cross-country (langlaufen) skiing. There were also lab outings to the beach and also to Gerhard and Margot's house in Rosanna to celebrate Christmas in June with a particularly potent Glühwein (mulled wine) that Gerhard prepared himself. Gerhard trained, mentored and inspired many bright graduate students in his laboratory who then ventured overseas to postdoc positions in high profile Biochemistry and Molecular Biology labs around the world. Many of his former PhD students have gone on to their own distinguished academic, pharma and research careers, including Kaylene Edwards, Anne Millership, Mariko Nagashima, Wei-Ping Fung, Felice DeJong, Phil Dickson, Tim Cole, Tim Thomas, Wei Duan, Anna Tsykin, Marc Achen, Samantha Richardson, Paul Harms, Bridgett Southwell, Linus Chang, and Porntip Prapunpoj. Gerhard retired in 1997 after 34 years at the university but remained connected to the university as Professor Emeritus. Gerhard published over 150 refereed journal publications with Scopus metrics of over 6,000 citations and a H-index of 44. He continued collaborating and writing scientific articles with a final publication in 2007. Gerhard's wife of 68 years, Margot, passed away in 2025. Gerhard is survived by his three children, Andreas, Sabine and Susanne, four grandchildren and four great-grandchildren.

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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
David James

Professor David E. James is an internationally recognised leader in metabolic biology whose work has transformed understanding of insulin action, nutrient sensing and the molecular basis of metabolic disease. He is an ARC Laureate Fellow and Professor at the Charles Perkins Centre at the University of Sydney, where he leads major multidisciplinary programs investigating the systems biology of cardiometabolic disease.

Professor James' career has focused on uncovering how cells regulate glucose and lipid metabolism and how these processes fail in insulin resistance and type 2 diabetes. As a postdoctoral researcher, he discovered the insulin-responsive glucose transporter GLUT4, a landmark advance that provided the molecular explanation for insulin-stimulated glucose uptake and fundamentally reshaped research in diabetes and endocrinology. His laboratory subsequently identified key components of the GLUT4 trafficking machinery and defined how insulin signalling through Akt coordinates vesicle trafficking and glucose transport.

Over the past two decades, Professor James has pioneered the application of proteomics, phosphoproteomics, and systems genetics to metabolic disease. His group was among the first to map insulin-regulated phosphorylation networks at scale, revealing how signalling pathways integrate nutrient status with cellular metabolism. More recently, his work has expanded to genetically diverse mouse populations and multi-omic approaches to identify causal genes and pathways underlying insulin resistance, fatty liver disease, and healthy ageing. These studies aim to move beyond descriptive association toward mechanistic understanding and therapeutic target discovery.

Professor James has published extensively in leading journals and is one of Australia's most highly cited biomedical scientists. His contributions have been recognised through election as Fellow of the Australian Academy of Science, many international keynote invitations and major national research fellowships. Beyond his research achievements, he has spearheaded the development of Cell Biology as a major research discipline in Australia as well as playing a central leadership role in building large-scale collaborative infrastructure for metabolic research, including multi-omics platforms, genetically diverse model resources, and translational partnerships spanning academia and industry.

Through a career spanning fundamental discovery to systems-level biology, Professor James' work has provided foundational insights into how metabolism is regulated in health and disease and continues to shape strategies for preventing and treating cardiometabolic disorders.

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
Morten Thaysen-Andersen

Professor Morten Andersen's research aims to unravel the glycobiology of the immune system and immune-related diseases including microbial infections, inflammation and cancer. He integrates glycoproteomics technologies into multi-omics workflows and employs methods in immunology, structural biology and molecular/cell biology to elucidate glycobiological processes of the immune system. While fundamental at its core, his research is increasingly pushing towards applications and translation by revealing new therapeutic targets and diagnostic markers as shown through growing collaborations with industry.

He obtained a PhD degree in protein chemistry in 2009 from the University of Southern Denmark under the guidance of Professor Peter Højrup. He thereafter relocated to Australia to complete two fellowships awarded by the Danish Research Agency and the Australian Research Council under the mentorship of Distinguished Professor Nicki Packer (2010–2014). Enabled by a Cancer Institute NSW ECR Fellowship (2014–2017), he then established the Analytical Glycoimmunology group at Macquarie University. He is currently an ARC Future Fellow (2022–2026) and was recently recruited as Visiting Professor (20% load, 2022–2027) to the Institute for Glyco-core Research at Nagoya University, Japan, to set up a clinical glycoproteomics lab as part of a large Japanese glycoscience program (2023–2033).

He is highly active in research as documented by his 120 peer-reviewed papers published in leading journals including *Nature Methods*, *Nature Communications*, *Proceedings of the National Academy of Sciences*, *Cell Reports*, *Cell*, *Molecular & Cellular Proteomics*, *Analytical Chemistry*, *Journal of Biological Chemistry* and *Glycobiology* (H-index 50, 7,000 citations, Google Scholar). He has been invited to speak at 70 international conferences and has received 18 awards for scientific achievements including the 2013 Ken Mitchelhill Young Investigator Award (Australian Proteomics Society), the 2024 Career Development Award (Australian Proteomics Society) and the 2026 Shimadzu Mid-Career Award (Australian Glycoscience Society).

He has trained 18 HDR students (10 PhD and 8 Master of Research students) as a principal supervisor and mentored 13 postdocs and ECRs, many of which attracted their own competitive fellowships. Several have started independent academic careers.

Andersen has contributed to the scientific community as Chair of the Human Glycoproteomics Initiative (HGI) under HUPO since 2020 and through conference organisation such as AusOmics 2025 and World Congress HUPO 2019. He is currently serving on the ARC Medical Research Advisory Group and is an ARC College of Expert (2025–2027). He is also the Australian representative to the International Glycoconjugate Organization and Associate Editor of the *Glycoconjugate Journal* (Springer). He is also a lead co-founder of the Australian Glycoscience Society (AGS/Glyco@Oz) inaugurated in 2022 with approximately 130 members and is the inaugural President of the AGS (2022–2027).

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
Matthew Clemson

My biochemistry journey began at UNSW, Sydney, where I completed a Bachelor of Science (Honours, Class 1) in 2002, investigating a novel application of the enzyme gamma-glutamyl transferase to synthesise the glutathione precursor gamma-glutamyl-cysteine – work that was later patented and commercialised. Intrigued by projects that could positively impact human health, I pursued a PhD and postdoctoral research exploring the genetic and epigenetic determinants of human diseases. However, even within the research environment, I found myself consistently gravitating toward teaching – helping students design experiments, interpret data, and develop their scientific instincts. Whenever teaching or outreach opportunities arose, I was eager to be involved.

When I joined the University of Sydney in 2020 as Coordinator of Biochemistry and Molecular Biology, I found the role that allowed me to pursue that calling fully. My teaching philosophy centres on creating a welcoming, inspiring environment where biochemistry becomes accessible and relevant to every student. I have redesigned large-cohort lectures to incorporate active learning, peer interaction, and scaffolded support. These approaches, grounded in cognitive science, have resulted in sustained improvements in student experience and learning. This commitment extends beyond the lecture theatre to mentoring a large, diverse team of casual academics, knowing that every student's experience depends on the people working closely with them.

Metabolism is considered one of the most daunting areas of biochemistry and tackling that perception has become a personal mission. The development of *Dr MattTabolism* (a custom AI Socratic tutor trained on biochemistry content and evidence-informed pedagogy) has enabled tens of thousands of personalised student-AI conversations, fostering deeper engagement with complex concepts. Alongside this, I have co-developed online laboratory simulators that replicate authentic experimental variability, published in *Biochemistry and Molecular Biology Education*, giving students meaningful opportunities to engage with practical skills beyond the timetabled lab.

My leadership in the ethical and effective use of generative AI in teaching and assessment has grown to national and international significance. I lead conversations on adapting teaching practice to the challenges and opportunities of generative AI, sharing this work at FAOBMB in Korea, the FEBS Education Training Conference in Turkey, universities across Australia, and through the ASBMB Education SIG Committee.

Receiving the 2026 ASBMB SDR Scientific Education Award is a tremendous honour, and I am sincerely grateful to SDR Scientific for their generous support of biochemistry education in Australia. This recognition belongs equally to the incredible students, colleagues, and collaborators within the ASBMB Education SIG who have shaped and inspired this work. I look forward to sharing my journey at ComBio 2026 and believe the approaches being pioneered here position Australia as a world leader in biochemistry and molecular biology education – and I welcome this award as an opportunity to share our innovations more broadly.

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
Pamali Fonseka

Pamali Fonseka completed her PhD in Biochemistry at La Trobe University in 2018 and has since established herself as an emerging leader in extracellular vesicle (EV) biology and translational cancer research. Following her PhD, she undertook postdoctoral training under the mentorship of Professor Suresh Mathivanan, progressing rapidly to Group Leader (2024) while developing an independent research program focused on EV-mediated communication and therapeutic innovation.

With less than six years of post-PhD experience (accounting for 13.5 months of career disruptions), Pamali has built a strong and competitive research profile. She has secured more than $875,000 in competitive funding as sole Chief Investigator, including NHMRC Investigator Grant (EL1-2023), Jack Brockhoff Foundation Early Career Grant (2021) and CASS Foundation Medicine/Science Grant (2019), reflecting both her scientific vision and her capacity to lead high-impact research. Her work has resulted in 33 publications (H-index 21, >6,650 citations, Google Scholar) in leading journals such as *Nature Communications*, *Journal of Extracellular Vesicles*, *Nucleic Acids Research* and *Nature Immunology*. Notably, half of her publications rank among the top 10% most cited globally, and her co-first and co-corresponding author papers in *Nucleic Acids Research* have been recognised as ESI Highly Cited. She has been awarded many competitive research awards, including the Theo Murphy Initiative Participation Support Grant (2026), FAOBMB YSP Fellowship (2025), ISEV2024 Conference Award (2024), The CASS Foundation Travel Award (2023), La Trobe Vice-Chancellor's Award for Excellence in Research (2022), ANZSEV Young Investigator Award (2021) and the ASBMB Fred Collins Fellowship (2021).

Pamali currently serves as Deputy Director of the Research Centre for Extracellular Vesicles, where she leads multidisciplinary collaborations spanning cancer cell biology, immunology and molecular biology. Her research aims to harness the unique properties of EVs to develop alternative therapeutic strategies for aggressive and treatment-resistant cancers. EVs, secreted by nearly all cell types, carry diverse bioactive cargo protected by a lipid bilayer, enabling the horizontal transfer of molecular information that shapes cellular behaviour and disease progression. Leveraging this biology, Pamali's recent work demonstrates that systemically delivered EVs can protect and transport tumour suppressor genes to metastatic sites *in vivo*, significantly reducing tumour burden and lung metastasis while improving survival without detectable toxicity.

Beyond her research achievements, Pamali is strongly committed to training and mentorship. She is the primary supervisor of two PhD students and has co-supervised five PhD and three Masters students to completion. As an early-career researcher, she continues to drive innovative translational science aimed at improving therapeutic outcomes for patients with metastatic cancer.

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.

Noah Graves – recipient of the Fred Collins Award for the most outstanding ASBMB Fellowship applicant

Noah J. Graves is a PhD candidate in Physiology and Pharmacology at UNSW Sydney under the supervision of Associate Professor Emma Sierecki. He completed his Bachelor of Science in Biology and International Development Studies from Dalhousie University (Halifax, Canada) in 2021. During his undergraduate studies, Noah spent a semester at Sorbonne Université in Paris, further developing his interest in molecular biology and neurodegenerative disease research.

His doctoral research focuses on the biochemical and biophysical properties of distinct α-synuclein fibril strains and their role in neurodegenerative diseases such as Parkinson's disease and other related synucleinopathies. Using advanced single-molecule fluorescence techniques and structural biology approaches, he aims to better understand how different protein conformations influence disease pathology.

Noah's research has been published in peer-reviewed journals including *ACS Chemical Neuroscience*. He has also presented his research at several international conferences including the International Society for Molecular Neurodegeneration meeting in Seoul, South Korea, the Protein Society 38 in Vancouver, Canada, and the International Symposium on Frontiers in Molecular Science in Kyoto, Japan. He has received several awards, including the Regeneron Scholarship Award, the Protein Society Diversity and Inclusion Award, the BrightFocus Travel Grant and the Best Resolved Structure award at the 2025 Cold Spring Harbor Laboratory cryo-EM course.

Through the ASBMB Fellowship, Noah will present his work at the European Academy of Neurology Congress in Geneva, Switzerland, and continue building collaborations within the global neurodegeneration research community.

Huw Morgan

Huw Morgan completed a Bachelor of Science (Honours) at the University of Melbourne in 2019, where his research focussed on the molecular mechanisms regulating immune cell function and tumour immunotherapy in the laboratory of Professor Justine Mintern. He subsequently worked as a research assistant before returning to the laboratory of Professor Mintern to commence his PhD in mid-2022. Currently, he is in the final year of his PhD under the supervision of Professor Mintern and Associate Professor Laura Edgington-Mitchell at the Bio21 Institute, University of Melbourne. His research investigates the molecular regulation of antigen-presenting cells such as dendritic cells and thymic epithelial cells, with a focus of identifying new roles for ubiquitination and deubiquitination enzymes in regulating dendritic cell function using CRISPR/Cas9 screening, activity-based protein profiling and *in vivo* knockout models.

Huw has published a first-author paper covering one aim of his PhD in the *European Journal of Immunology*, and is also co-author in journals such as *Blood* and *Blood Neoplasia*. He has presented his work at the Australian and New Zealand Society of Immunology (ASI) annual meetings and Biomolecular Horizons 2024, as well as numerous other local meetings. He was awarded an ASI Student Travel Bursary in 2025 and won a poster prize at the 2024 ASI Annual Meeting. This ASBMB Fellowship will allow Huw to travel to Lisbon, Portugal, to attend the 4th Ubiquitin Function in Health & Disease Conference, and a laboratory visit in London, UK.

ASBMB Fellowship Profiles

You Min Ahn

You Min Ahn completed her Bachelor of Science in Biochemistry and Genetics in 2021 at Monash University. She undertook a Work Integrated Learning Internship in Distinguished Professor Stephanie Gras' lab at La Trobe University in 2021 and completed Bachelor of Biomedicine Honours year (First class) in the same laboratory. Her honours research project focused on understanding the impact of SARS-CoV-2 mutations on antigen presentation by Human Leukocyte Antigen (HLA) molecules. Currently, she is in her final year of her PhD under the supervision of Distinguished Professor Gras, Dr Dimitra Chatzileontiadou and Dr Janesha Maddumage at La Trobe University. Her current research explores the specific molecular mechanism of $CD8^+$ T cell-mediated responses against SARS-CoV-2.

Her research has been published in *Nature Communications* and *Current Research in Structural Biology*. She took part in writing two book chapters published in *Reference Module in Life Sciences* and *Methods in Molecular Biology*.

You Min has presented her work at Biomolecular Horizons 2024, EMCRs of the La Trobe Institute for Molecular Science Symposium 2025 and the Federation of Asian and Oceanian Biochemists and Molecular Biologists 2025 in Busan, South Korea. She was awarded the LIMS HDR Travel Award in 2024 and the AINSE Postgraduate Research Award top-up scholarship.

This ASBMB Fellowship will support You Min to attend the 2026 19th International HLA & Immunogenetics Workshop followed by the Asia–Pacific Hitocompatibility and Immunogenetics Association Conference in Numazu, Japan, and a visit to the laboratory of collaborator, Associate Professor Chihiro Motozono, in Kumamoto, Japan.

Michael O'Dea

Michael O'Dea completed both a Bachelor of Advanced Science (First Class Honours) and a Bachelor of Computer Science at UNSW Sydney in 2022. His Honours research lay at the intersection of these interests, training AI models on multi-omics data to better understand the problem of endocrine resistance in breast cancer. In his PhD, Michael has shifted from focusing on the whole genome to just one gene – fetal hemoglobin. Currently in his final year and jointly supervised by Professor Merlin Crossley and Professor Kate Quinlan, his project has developed software which harnesses recent advances in epigenetic sequencing to map nucleosome positions and reveal the role the chromatin landscape plays in repression of this key erythroid gene. He has also separately used CRISPR base-editing to dissect the mechanism by which ZBTB7A, a transcriptional repressor, mediates this repression.

His research has recently been published in *Nature Communications* and he has received several awards, including an ASMR Best Lightning Talk Prize, ASBMB Poster Prize, two Best 1-Minute Thesis Prizes, an ATA Scientific Young Scientist Grant and two ASBMB travel grants.

Michael is deeply passionate about the impact that scientists can have on the broader scientific community. He has played a key role in advancing sustainability across UNSW through the internationally accredited LEAF program, developed outreach programs for National Science Week and recently received an award for his teaching.

This ASBMB Fellowship will enable Michael to present his PhD research at the 17th EMBL Transcription and Chromatin Conference in Heidelberg, Germany, in August 2026.

Boomerang Award Report

Coming a Full Circle – My Boomerang Tour

During a visit to Australia back in 2024, I was fortunate to catch up with Professor Kate Quinlan and Professor Merlin Crossley, my former PhD mentors at the University of New South Wales. As well as enjoying the opportunity to reconnect, I was also introduced to the ASBMB's Boomerang Award. After growing up then completing my PhD training in Australia, I set my sights on the US for a postdoc position in 2019. I was fortunate to receive the Boomerang Award in 2025, affording me a phenomenal opportunity to return to Australia and present my work at venues around the country. The award came at the perfect time, as I was finishing up my postdoctoral training and about to launch my independent lab in the US.

In Spring 2025, I journeyed back down under to embark on my Boomerang tour. The prospect of sharing my work, reconnecting with old colleagues and making new connections was very exciting. My first stop was in Brisbane at the Translational Research Institute, where I was hosted by renowned bone immunologist, Dr Allison Pettit. Here, I was fortunate to share my research findings on cellular crosstalk in arthritis to a room full of trainees, investigators and clinicians. My sisters Emily and Grace were also in the audience! I then had the opportunity to connect over lunch with a clinical physiotherapist, which was invaluable for gaining insights into the first-hand experience of patients suffering from joint stiffness (arthrofibrosis), and how it's such an unmet clinical need.

Alexander joined by his sisters, Emily and Grace, at the Translational Research Institute seminar.

From there, I ventured across town to the University of Queensland for the ASBMB meeting. I was blown away by how beautiful the UQ campus was – a perfect location for the meeting. My highlight was receiving the award from Kate Quinlan after delivering the Boomerang Plenary Lecture. A refreshing aspect of the ASBMB meeting was listening to talks and connecting with researchers focused on basic science questions, especially given my current clinically-oriented research environment.

The next stop of my tour took me to my hometown of Sydney, the best city in the world. Kate had invited me to give a research seminar back at my alma mater, UNSW. I was amazed at the progress being made on campus, scientifically, and in terms of infrastructure. At the same time, seeing familiar faces and walking those corridors was very nostalgic. A highlight of this visit was delivering a workshop on Growing Fruitful Collaborations in Science to the Early Career Researchers at UNSW. Interacting with passionate researchers and seeing their ambitions to be the next generation of scientific investigators was very rewarding. It was simply wonderful to visit Sydney and take a trip down memory lane. The harbour is as beautiful as ever and the weather did not disappoint!

Alexander receives the ASBMB Boomerang Award, presented by his former PhD mentor, Kate Quinlan.

Alexander returns to his old stomping ground, UNSW Sydney.

The final leg of my Boomerang tour took me to Adelaide, where the International Combined Orthopaedic Research Societies were meeting. I presented my work on how stem cells in arthritis cause fibrosis (stiffening) to an international audience of basic, translational and clinical researchers. Interacting with so many former and current US colleagues in Australia was enjoyable, as was showing them the charm of Adelaide – somewhere I spent a decent amount of time as a child. The most impactful thing to come out of the ICORS meeting was connecting with Australian musculoskeletal and orthopaedic researchers. Having pivoted to this field during my postdoc in the US, I hadn't had the opportunity to properly interact with Australian colleagues. Growing my Australian network has been a long-term goal of mine, and now there are opportunities to attend Australian conferences plus ripe areas for collaboration.

Returning home to the US was bittersweet. While I was excited to see my wife and two boys (plus one more arriving shortly), I relished my time in Australia connecting with old and new colleagues. The Boomerang tour was a tremendous opportunity to share my research, broaden my network and (re)experience Australia.

Alexander Knights, PhD, is an Assistant Professor studying arthritis at Washington University in St Louis, USA.

Alexander reunites with his postdoc mentor, Kurt Hankenson, and former labmate, Lindsey Lammlin, at the ICORS meeting.

Eppendorf Edman ECR Award Report

Immune Molecules Explore Taipei

I appreciate the support provided by the ASBMB Eppendorf Edman Award which enabled me to attend the 9th Federation of Immunological Societies of Asia–Oceania Congress (FIMSA) held in Taipei, Taiwan, from 23–27 October 2024. The FIMSA Congress, held every three years, provides opportunities for scientists and researchers around the world to meet and discuss cutting-edge research in the fields of immunology, molecular biology and cell biology. The conference, attended by over 670 delegates from 26 countries, featured a series of engaging sessions covering topics such as cancer immunity, autoimmunity, mucosa–immunity interaction, host–pathogen interactions, immune regulation and inflammation. This five-day meeting showcased presentations by senior scientists, students and postdoctoral researchers, fostering an international exchange of knowledge and ideas in immunology.

I had the opportunity to deliver an oral presentation on my research titled 'Insights into Mucosal Immunity: Natural Killer T-cell Receptor Recognition of *Bacteroides fragilis* Glycosphingolipids' in the Mucosal Immunity session. This provided a valuable platform to share my findings with leading experts in the field, receive constructive feedback and engage in discussions for future research. Additionally, it offered opportunities for networking and increasing the visibility of my work within the scientific community.

With the emergence of mRNA technology, the second day of the conference had a lunch symposium which included two presentations: 'mRNA Technology: Fundamentals, Advantages and its Future in Transforming Medicine' and 'The Immunological Landscape of mRNA Vaccines: Mechanisms, Cellular Responses and Innovations'. These talks provided an overview of the cutting-edge developments in mRNA research and highlighted its transformative potential in medicine.

On the third day of the conference, another lunch symposium featured two insightful presentations: 'Advancing Flow Cytometry: From Single-colour to Multi-omics Profiling' and 'Immunoprofiling of Human and Mouse Samples'. These sessions illustrated the recent advances in key immunological technologies, highlighting the transition from conventional single-parameter analyses to high-dimensional, multi-omics approaches needed for detailed characterisation of immune responses.

Following the conference, I had the opportunity to visit Academia Sinica, Taiwan's premier research institution, renowned for its interdisciplinary research excellence across the sciences and humanities. Extending this experience beyond academia, I visited the National Palace Museum, which showcased an extraordinary collection of Chinese imperial art and artefacts spanning thousands of years. The museum offered profound insight into the cultural and artistic legacy of Chinese civilisation. I also explored two of Taipei's renowned night markets, including Shilin Night Market, which vividly reflect the city's vibrant culture. The bustling atmosphere, diverse street food and large crowds captured the dynamic spirit of Taiwanese urban life.

FIMSA Congress.

Mucosa Immunity session.

Praveena presents her research.

Attending FIMSA 2024 was an invaluable experience as it provided insights into recent advances across multidisciplinary research areas and offered the unique opportunity to network and exchange ideas with like-minded scientists in the field.

Dr Praveena Thirunavukkarasu is an Australian Research Council Discovery Early Career Researcher Fellow in the Biomedicine Discovery Institute at Monash University.

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More information about the Research 3 neo:
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Azure Biosystems SAPPHIRE FL+ Large Format Biomolecular Imager

From large-format phosphor screens to high-throughput imaging workflows, the Sapphire FL+ by Azure Biosystems, offers a 46 cm x 25 cm scanning bed – a scan area spacious enough to accommodate even oversized samples. From Western blots, 2D gels to microscope slides, model organism imaging, multi-well plates, tissue arrays and protein arrays ensures unparalleled flexibility and precise quantitation of molecular assays.

The Sapphire FL+ is one of only two biomolecular imagers in its class that supports phosphor imaging – a highly sensitive assay that utilises radioactivity. It can scan storage phosphor screens up to 20 x 40 cm, delivering outstanding 24-bit dynamic range and image quality through its use of laser excitation and photon multiplier tube (PMT) detection.

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PUBLICATION SCHEDULE FOR *AUSTRALIAN BIOCHEMIST*, volume 57, 2026

Issue	ASBMB Content	Copy Deadline	Issue Date
April 2026 57(1)	Profiles of medal, award and fellowship winners Nominations for Executive/Council	Monday 2 February	Monday 30 March
August 2026 57(2)	Nominations for medals, awards and fellowships Notice of AGM/proposed constitutional changes	Monday 1 June	Monday 3 August
December 2026 57(3)	Annual reports ASBMB meeting report	Monday 5 October	Monday 30 November

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