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Proteins 'out of context'. A Type IV secretion system at the beach. PDBs: 7O3T, 7O3V, 7O41. Created in Blender3D. Image courtesy of Sarah Piper, Monash Institute of Pharmaceutical Sciences, Monash University, and the ARC Centre for Cryo-electron Microscopy of Membrane Proteins.

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Join us at Biomolecular Horizons 2024 to be held in Melbourne from 22-26 September 2024.

This important forum will bring together three prestigious congresses, each with a strong history of attracting the Bioscience and Biotechnology communities to discuss and examine the latest developments and research:

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- 17th Congress of the Federation of Asian & Oceanian Biochemists & Molecular Biologists (FAOBMB)
- 22nd ComBio Conference (ComBio)

Over the five days, the Congress will offer a series of plenary sessions, keynotes, symposia, and poster presentations. There will also be a dedicated Young Scientists Program, Outreach Events, Career Development Events, Education Events, Publication Workshops, Technical Workshops, Art Meets Science and Networking Events and a Government Industry Forum.

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The Congress is one of the biggest international research events in basic biomolecular science and will showcase developments in research and education to members of the academic, research and industry communities.

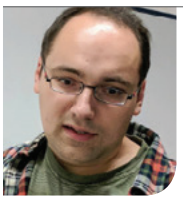
Join colleagues from across the world to exchange ideas and research and build valuable professional networks that will extend beyond the Congress itself. To complement the scientific program, you will also be able to experience a showcase of the latest products and services in the exhibition, an integral element of the Congress.

Mark the dates in your diary and plan to join us for what promises to be an outstanding Congress experience.

PLENARY SPEAKERS

PROFESSOR BRIAN KOBILKA
Stanford University
USA
Nobel Prize in Chemistry 2012
Grimwade Award Lecturer

PROFESSOR PAMELA SILVER
Harvard University
USA
IUBMB Jubilee Award Lecturer



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PROF. WEI XIE
Tsinghua University
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Editorial

It is a great pleasure to take over from our current *Australian Biochemist* Editor, Tatiana Soares da Costa, as she enjoys a few months maternity leave.

It is with sadness that this issue contains two In Memoriam pieces paying tribute to two stalwarts of the Australian biochemistry community who passed away in recent months. Leann Tilley chronicles the life of her former mentor and past ASBMB President, Bill Sawyer, while Danny Hatters and Barbara Howlett pay tribute to Geoff Howlett. As you will read, Bill and Geoff had wide-ranging careers and specialised in biophysical techniques, their knowledge and expertise of which have been passed down to many Australian researchers. Interestingly, Bill and Geoff's careers overlapped, with Bill acting as Geoff's PhD supervisor. Danny Hatters has been particularly busy this issue, contributing a second article on his experience in science as a member of the LGBTQIA+ community. We thank Danny for this enlightening piece, which was originally published in the American Society for Biochemistry and Molecular Biology magazine, *ASBMB Today*.

My involvement with the *Australian Biochemist* goes back several years, when I took over handling the Publications with Impact feaure. This is usually the largest section in the *Australian Biochemist* and is a great way to disseminate some of the fantastic work being published by our members. For each issue, we select papers of interest from the previous four to six months and endeavor to be as representative of the membership as possible in terms of states, institutions, genders and topics. This issue has some terrific articles ranging across immune responses in fungal infections, COVID immune structural biology, drug discovery and mitochondrial and lysosomal biology. While some selections are obvious due to their having a high profile

in the media (such as Stephanie Gras' article in this issue on her recent *Nature* paper, which garnered significant attention), we generate our initial shortlist for consideration using the Publications with Impact app and website I created (www.pubswithimpact.com) to assist with these selections. This site, which is freely available, provides real-time listings of all Australian (and any other country's) papers published in any of about 100 highly regarded journals I have curated, based not only on impact factor, but also their standing in the field. Further filtering is subsequently applied to identify papers with ASBMB members as first or corresponding authors. Give it a try and let me know your feedback for potential improvements.

Finally, I would like to thank Liana Friedman, our ASBMB Editorial Officer, for doing most of the heavy lifting in the production of this issue!

Doug Fairlie
Acting Editor, *Australian Biochemist*
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Publications with Impact

Publications with Impact profiles recent, high impact publications by ASBMB members. These short summaries showcase some of the latest research by presenting the work in a brief but accessible manner. If your work has recently been published in a high profile journal, please email doug.fairlie@onjcri.org.au.

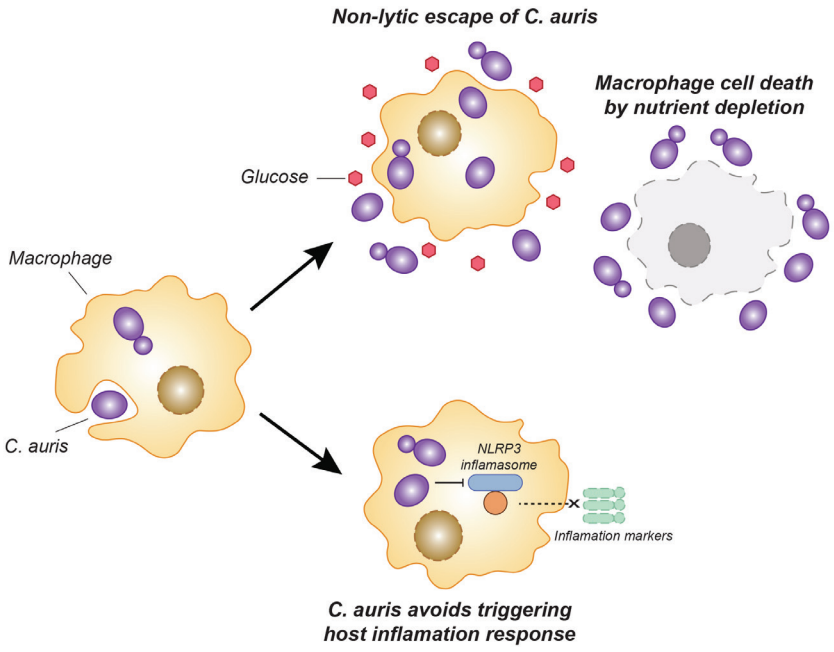
Metabolically Killing Me Softly: Insights Into the Roles of Metabolism in Immune Interactions of Drug-resistant *Candida auris*

Weerasinghe H, Simm C, Djajawi TM, Tedja I, Lo TL, Simpson DS, Shasha D, Mizrahi N, Olivier FAB, Speir M, Lawlor KE, Ben-Ami R, Traven A*. *Candida auris* uses metabolic strategies to escape and kill macrophages while avoiding robust activation of the NLRP3 inflammasome response. *Cell Rep* 2023;42(5):112522.
***Corresponding author: ana.traven@monash.edu**

Fungal pathogens cause life-threatening infections in immunocompromised patients in hospitals. Yet, we are dangerously underprepared to combat these infections. As is the case with other classes of pathogens, changing host and environmental conditions are leading to new fungal threats, for example the arrival of drug-resistant *Candida auris* in human settings in 2009. *C. auris* is considered a global public health threat carrying a 30–60% mortality rate according to some studies. *C. auris* causes outbreaks and persists on hospital surfaces, earning it an urgent threat classification by the Centers for Disease Control and Prevention's Antibiotic Resistance Threats in the United States 2019 report. *C. auris* infections spotlight the chronically unsuccessful nature of anti-fungal drug discovery, as most isolates are either single-, multi- or pan-drug resistant.

Immune system macrophages defend from infection, but they can also be reservoirs for fungal pathogens to proliferate. Fungal infection causes metabolic shifts in macrophages that assist with antifungal defences. These findings offer insights into how metabolic approaches can target fungal pathogen and host immune system interactions, with the hope of improving infection outcomes.

Our study aimed to understand the contributions of metabolism to *C. auris*–macrophage interactions. We identified that following proliferation within macrophages, *C. auris* escapes into the extracellular environment without significant killing of the immune cells, i.e. the escape appears to be non-lytic. Non-lytic escape is uncommon amongst fungal pathogens as most cause damage by growing morphological structures such as hyphae, or through increased fungal burden that bursts macrophages. We also observed that after egress, *C. auris* continues to replicate extracellularly, eventually inundating the infection and



C. auris *replicates within macrophages and then escapes. Fungal proliferation continues outside macrophages, which leads to* C. auris *depleting nutrients from the extracellular environment. This causes rapid macrophage cell death (upper pathway).* C. auris *also suppresses the hosts' antimicrobial immune responses by not triggering macrophage inflammation pathways (lower pathway). The mechanism by which* C. auris *'hides' from the NLRP3 inflammasome remains to be determined. Figure adapted from* Cell Reports *2023;42(5):112522 with permission from Elsevier.*

killing macrophages. *C. auris* isolates segregate into at least four clades and this replication, escape and killing mechanism is recapitulated in all four clades, indicating that it is a generally conserved feature of the infection process. We were able to rescue macrophages by supplementing glucose into the infection condition, delaying macrophage cell death. This suggests that *C. auris* causes macrophages to die by blocking their ability to use glycolysis and highlights metabolic interactions as a crucial aspect of immune cell survival following *C. auris* infection. Indeed, we observed that both macrophages and *C. auris* upregulate their respective glycolytic machinery during infection, and Δ*cdc19* pyruvate kinase mutants of *C. auris* (no glycolysis), do not escape nor kill macrophages.

As previously shown for another fungal pathogen and some bacterial infections, disruption of glycolysis in macrophages acts as a warning to alert the immune system of potential threats, causing activation of the NLRP3 inflammasome. However, our clinical isolate of *C. auris* behaved differently. *C. auris* infection caused little activation of key NLRP3 machinery such as proinflammatory cytokine interleukin (IL)-1β, caspase-1 and the pore-forming protein gasdermin D, which normally serve to elicit a strong immunological response from the host. We did not find evidence that inhibiting the cell death pathways of pyroptosis, necroptosis and extrinsic apoptosis can rescue the viability of *C. auris*-infected macrophages, suggesting that these pathways are not involved. Collectively, these results indicate that *C. auris* can optimise its infection potential by successfully hiding from the hosts' immune system.

Ana Traven (left) and Harshini Weerasinghe.

It is possible that metabolic interventions could aid in the recovery of infected patients. Our findings indicate that new therapeutic approaches to combat *C. auris* could emerge through having a better understanding of how host metabolic homeostasis improves disease outcomes.

Harshini Weerasinghe and Ana Traven
Department of Biochemistry and Molecular Biology, Biomedicine Discovery Institute, Monash University
Centre to Impact AMR, Monash University

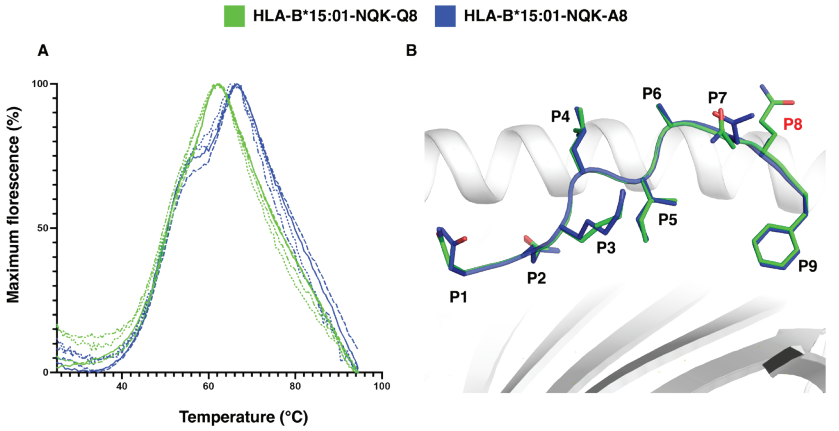
How Did Some of Us Dodge COVID?

Augusto DG[#], Murdolo LD[#], Chatzileontiadou DSM[#], Sabatino JJ Jr, Yusufali T, Peyser ND, Butcher X, Kizer K, Guthrie K, Murray VW, Pae V, Sarvadhavabhatla S, Beltran F, Gill GS, Lynch KL, Yun C, Maguire CT, Peluso MJ, Hoh R, Henrich TJ, Deeks SG, Davidson M, Lu S, Goldberg SA, Kelly JD, Martin JN, Vierra-Green CA, Spellman SR, Langton DJ, Dewar-Oldis MJ, Smith C, Barnard PJ, Lee S, Marcus GM, Olgin JE, Pletcher MJ, Maiers M, Gras S*, Hollenbach JA*. A common allele of HLA is associated with asymptomatic SARS-CoV-2 infection. *Nature* 2023;7972:128–136.
[#]Contributed equally to this work
***Co-senior authors s.gras@latrobe.edu.au, jill.hollenbach@ucsf.edu**

The rapid emergence of SARS-CoV-2 and the resulting pandemic led researchers to focus on severe illness after SARS-CoV-2 infection to provide relief and treatment against COVID. However, relatively little research has been conducted to understand why around 20% of individuals remain asymptomatic despite the infection. Therefore, our work aimed to provide the basis of the natural ability of asymptomatic individuals to 'dodge' COVID symptoms.

To better understand disease outcomes, we set up a collaboration with a specialist of population genetics, Professor Jill Hollenbach (USA). In 2021, participants in the USA that were already part of the bone marrow registry were asked to report and self describe their symptoms during the two weeks following SARS-CoV-2 infection using a smart phone app. While we currently don't regularly test for COVID, back in 2021, it was necessary in many cases, including to go to work or as close contacts. The advantage of enrolling participants from the bone marrow registry is that their genetic make up for their human leukocyte antigens (HLA molecules) is known. Based on this, a link was identified between the lack of symptoms upon SARS-CoV-2 infection and the expression of HLA-B*15:01 molecule.

Publications with Impact



*NQK-Q8 (green) and NQK-A8 (blue) presented by HLA-B*15:01.*
*(**A**) The thermal stability profile of both complexes, measured by 50% maximum fluorescence when the protein unfolded, was almost identical, with NQK-Q8 at 51.6°C and NQK-A8 at 51.0°C.*
*(**B**) The overlay crystal structure showed an almost identical presentation with both peptides anchored inside the cleft via residue P2-Glu and P9-Phe. While almost all residues had identical conformation, the single different residue P8-Gln>Ala (red) was solvent-exposed.*

This was the first discovery of a genetic association with an asymptomatic COVID profile. We wanted to understand how the HLA-B*15:01 molecule could provide a protective immune response to SARS-CoV-2 infection. $CD8^+$ T cells are key players of the immune system and they become activated through the recognition of peptides derived from pathogens (epitopes) that are presented on the cell surface by HLA molecules. This recognition is mediated by the T cell receptor (TCR) on the surface of the T cell, resulting in its activation.

We tested four already described SARS-CoV-2 derived epitopes able to be presented by HLA-B*15:01 in samples collected back in the 1990s. This means that the individuals that provided those samples were not in contact with SARS-CoV-2 (unexposed), were not vaccinated or even in contact with SARS-CoV-1. We found that one epitope, derived from the spike protein (NQKLIANQF, hereafter called NQK-Q8), elicits a strong T cell response in the unexposed individuals. Strikingly, most of the NQK-Q8-specific T cells were memory T cells, indicating previous activation due to prior infection. We then confirmed that the homologous peptide NQKLIANAF (NQK-A8), from the human seasonal coronaviruses HKU1-CoV and OC43-CoV, was recognised by the same T cells.

To determine if the single mutation between the two epitopes could change the stability of the peptide-HLA-B*15:01 complex, we used differential scanning fluorimetry to measure the melting temperature (Tm) (**Fig. A**). The Tm values remained identical, indicating both complexes were stable. Using X-ray crystallography, we showed that the only amino acid difference between the epitopes at position 8 (P8) was solvent exposed, thus a possible contact for circulating T cells (**Fig. B**). We therefore wanted to determine if this could impact on the affinity of TCRs. We found identical TCRs from COVID recovered, vaccinated and unexposed HLA-B*15:01$^+$ individuals and selected three representative TCRs. All three TCRs exhibited high and similar affinity for both peptides. Therefore, the TCRs might dock similarly resulting in both epitopes quickly activating T cells and providing efficient viral recognition and protection in HLA-B*15:01$^+$ individuals.

It remains unclear how effective current vaccines are at providing long-lasting immunity and their ability to protect against new variants of the virus. Our findings highlight the crucial role played by the activation of $CD8^+$ T cells through a specific HLA molecule in mounting an effective early-stage defence against the virus. This discovery not only enhances our understanding of the immunological factors facilitating rapid viral clearance but also establishes a solid foundation for the development of therapeutics capable of eliciting such a response, including T cell-based vaccines.

Lawton Murdolo, Demetra Chatzileontiadou and Stephanie Gras
La Trobe Institute for Molecular Science
La Trobe University

From left: Lawton Murdolo, Stephanie Gras and Demetra Chatzileontiadou.

Publications with Impact

Systems Genetics for Drug Discovery

Masson SWC, Madsen S, Cooke KC, Potter M, Vegas AD, Carroll L, Thillainadesan S, Cutler HB, Walder KR, Cooney GJ, Morahan G, Stöckli J, James DE*. Leveraging genetic diversity to identify small molecules that reverse mouse skeletal muscle insulin resistance. *Elife* 2023;12:RP86961.
***Corresponding author: david.james@sydney.edu.au**

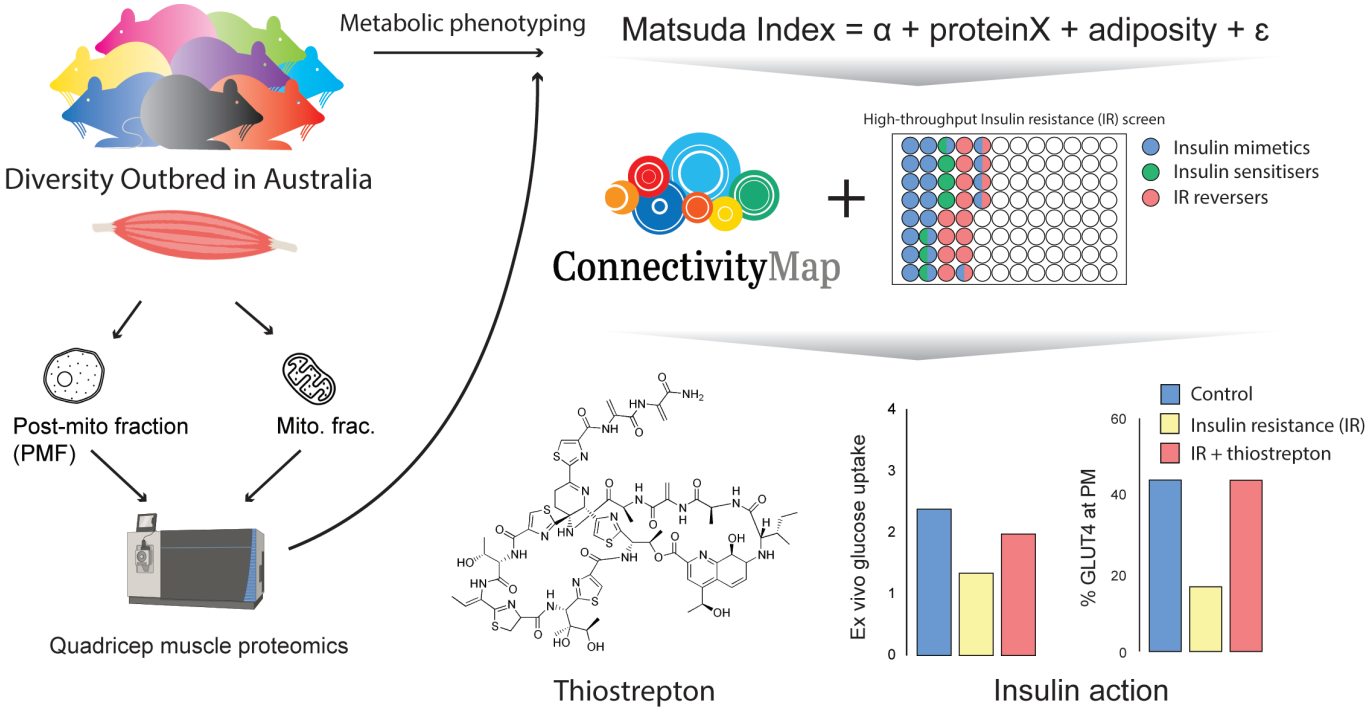
Biology is complex and, for a long time, we have avoided this complexity in favour of reductionist approaches. These have served us well, and current knowledge is largely founded on these efforts. Advances in computational and unbiased omics-based techniques have provided the impetus to harness biological complexity to discover key causal drivers of important physiological traits. This has given rise to the emergent field of systems genetics which attempts to decipher the connection between genetic and phenotypic variation via intermediate molecular phenotypes.

Our group is interested in understanding metabolic diseases like Type 2 diabetes and cardiovascular disease. One of the earliest defects associated with these diseases is insulin resistance. Despite the importance of insulin resistance, our molecular understanding of this condition remains relatively poor, partly because it is driven by environmental and genetic factors, the former being difficult to control and measure in humans. Thus, many groups have turned their attention to genetically diverse animal models where environmental control is much more feasible.

We have established a population of diversity outbred mice at the University of Sydney. This population, originally constructed by Grant Morahan in Perth, arose through crossbreeding five common laboratory strains and three wild-derived strains. Subsequent progenies were outbred to ensure genetic and phenotypic diversity on par with human populations. We are utilising this resource to study metabolic disease and long-term health.

In our *eLife* paper, we initially measured a suite of key metabolic phenotypes in several hundred mice and observed profound variation in all metabolic parameters, despite animals being fed normal, healthy food. Next, we undertook deep proteomic analysis of skeletal muscle from each mouse – muscle is one of the major contributors to whole body insulin sensitivity in mammals and protein expression defects have been found here in humans.

Using linear modelling of the muscle proteome, we identified proteins associated with whole body insulin sensitivity. One challenge with proteome-to-phenotype associations is distinguishing between cause and effect.



The genetic diversity of Diversity Outbred mice was harnessed by performing metabolic phenotyping and skeletal proteomics. These data were integrated to produce a molecular fingerprint of insulin resistance which was queried in the Broad Institute's Connectivity Map and cross-referenced against a small molecular screen of GLUT4 translocation. From this analysis, the thiopeptide antibiotic thiostrepton was identified as an insulin-sensitising agent. Figure adapted from eLife *2023;12:RP86961 (CC-BY license).*

To overcome this, we examined the genetic architecture of the muscle proteomes of these mice and attributed the variance in protein abundance to genetic differences. We reasoned if protein abundance was determined by genetics, the relationship between protein and insulin sensitivity was more likely to be causal. Using this approach, we developed a fingerprint of insulin resistance using proteins which negatively associate with insulin sensitivity and were genetically regulated (determined by cis-quantitative trait loci presence)

Next, we reasoned that we could use this insulin resistance protein signature to screen for insulin sensitising drugs as a proof of principle. To achieve this, we queried the Broad Institute Connectivity Map (CMAP) with our insulin resistance signature. CMAP is an elegant database containing over 1.5 million gene expression profiles from 5,000 small molecule compounds that have been screened in different cell types. This led to the generation of a list of candidate compounds that could modify our signature. To filter this list, we performed a drug screen in muscle cells using 1,200 compounds to identify insulin sensitisers. By combining hits from this screen with our CMAP screen, we generated a high confidence list of small molecules that potentially modulate insulin sensitivity. The top hit was the antibiotic thiostrepton. To validate these results, we undertook targeted analysis in *ex vivo* muscle preparations from insulin resistant mice and strikingly showed that thiostrepton is an insulin sensitising agent.

This highlights the power of systems genetics and provides a novel approach for discovery of novel compounds with efficacy in a range of diseases. We are now studying the molecular mechanism of thiostrepton in the context of insulin action as well as more focused approaches to identify its molecular target. There are also additional compounds identified using this approach that we are yet to follow up on. Finally, this study provides a framework for validation of systems genetics results without relying on traditional 'gene-by-gene' reductionist approaches.

David James and Stewart Masson
Charles Perkins Centre
University of Sydney

From left: Kristen Cooke, Søren Madsen, Stewart Masson, David James, Meg Potter (front) and Jacky Stöckli (back).

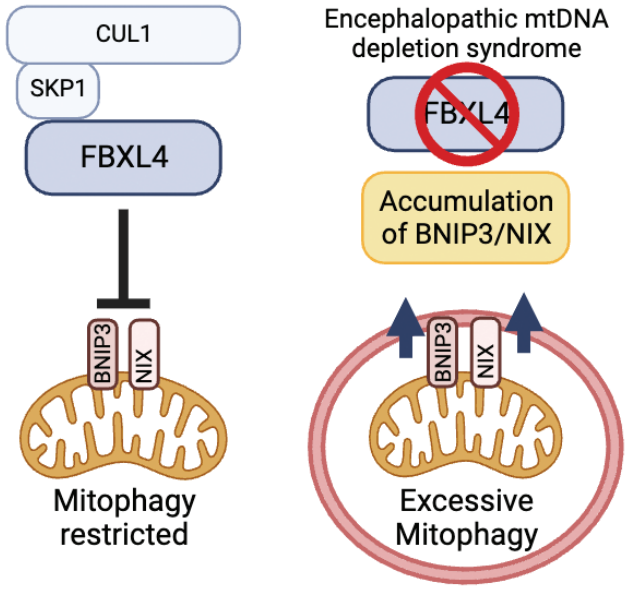
Turning Mitophagy Off to Prevent Mitochondrial Disease

Nguyen-Dien GT#, Kozul KL#, Cui Y#, Townsend B, Kulkarni PG, Ooi SS, Marzio A, Carrodus N, Zuryn S, Pagano M, Parton RG, Lazarou M, Millard SS, Taylor RW, Collins BM, Jones MJ, Pagan JK. FBXL4 suppresses mitophagy by restricting the accumulation of NIX and BNIP3 mitophagy receptors. *EMBO J* 2023;42(13):e112767.
#Contributed equally to this work
***Corresponding author: j.pagan@uq.edu.au**

Mitophagy serves as an important quality control mechanism to remove any dysfunctional or excessive mitochondria via the autophagy–lysosome pathway. It is a finely tuned process to ensure that cells neither experience an insufficiency of mitophagy, which can result in the buildup of damaged mitochondria and subsequent cellular degeneration, nor an excess, which can lead to the depletion of mitochondria. We recently uncovered that the Skp1-CUL1-F-box (SCF)-FBXL4 E3 ubiquitin ligase serves as a negative regulator of mitophagy. It accomplishes this by localising to the mitochondrial outer membrane where it mediates the constant turnover of NIX and BNIP3 mitophagy receptors. Our results suggest the molecular explanation for the aetiology of mitochondrial DNA depletion syndrome 13 (MTDPS13), a disease caused by mutations in the *FBXL4* gene characterised by elevated mitophagy in cells.

NIX and BNIP3 are mitophagy receptors that reside on the outer membrane of the mitochondria and serve as docking sites for the nascent autophagosome. Under normal conditions, these proteins are maintained at low levels on mitochondria. However, to promote mitophagy, they undergo transcriptional upregulation mediated by HIF1α. We postulated that they might

Publications with Impact



Model for the dysregulation of FBXL4-mediated turnover of BNIP3 and NIX in mitochondrial disease.

also be subject to post-translational regulation and our investigations indeed confirmed this hypothesis. Through a combination of approaches, we identified the Skp1-CUL1-F-box (SCF)-FBXL4 complex as the E3 ubiquitin ligase targeting NIX and BNIP for ubiquitin-mediated turnover.

We hypothesised that the upregulation of NIX and BNIP3 in FBXL4-deficient cells would result in an elevation of cellular mitophagy levels in the context of mitochondrial disease. As predicted, cells lacking FBXL4 indeed displayed high levels of mitophagy, which required BNIP3 and NIX. We also found that pathogenic FBXL4 variants responsible for MTDPS13 disrupt FBXL4's ability to control BNIP3 and NIX levels and suppress mitophagy. This suggests that the characteristic mitochondrial depletion seen in MTDPS13 arises from the accumulation of NIX and BNIP3. The elucidation of the mechanism by which FBXL4 prevents MDDS-mitochondrial disease suggests several potential therapeutic intervention strategies, such as the use of autophagy inhibitors to reduce mitophagy in these patients.

Our future studies will focus on understanding how FBXL4 is regulated. Post-translational modifications may play a role in either promoting or disrupting FBXL4's recognition of BNIP3 and NIX. Thus, the identification of upstream regulatory enzymes like kinases and phosphatases that modulate the stability of NIX and BNIP3 in basal conditions will shed light on the precise regulatory mechanisms involved. Likewise, the identification of metabolic conditions that modulate the recognition of NIX and BNIP3 by FBXL4, directly or indirectly, will be informative. Indeed, almost nothing is known about the regulation of FBXL4, including its function, abundance, and localisation, leaving numerous questions to explore.

Julia Pagan, Prajakta Kulkarni, Giang Nguyen-Dien, Keri-lyn Kozul, Brendan Townsend and Soo Siang Ooi
Institute for Molecular Bioscience
University of Queensland

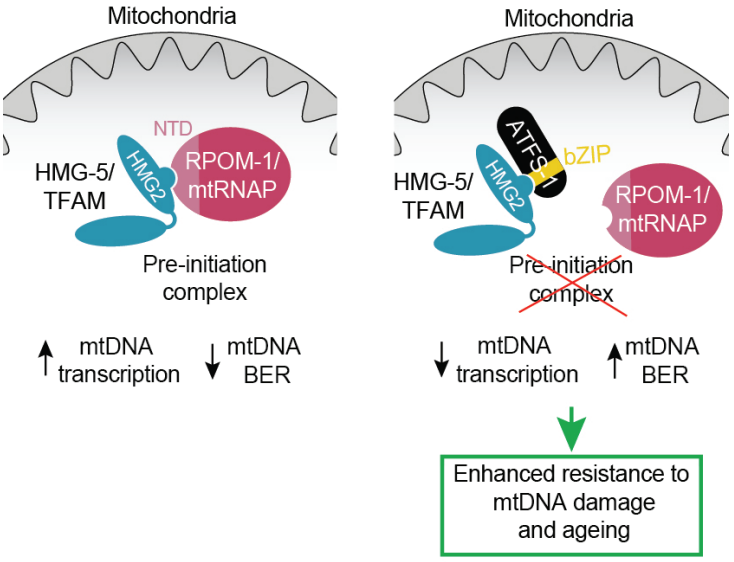
From left: Prajakta Kulkarni, Keri-lyn Kozul, Brendan Townsend, Giang Nguyen-Dien, Julia Pagan and Soo Siang Ooi.

A Mitochondrial Protein that Reduces the Signs of Ageing on the Mitochondrial Genome

Dai CY, Ng CC, Hung GCC, Kirmes I, Hughes LA, Du Y, Brosnan CA, Ahier A, Hahn A, Haynes CM, Rackham O, Filipovska A, Zuryn S*. ATFS-1 counteracts mitochondrial DNA damage by promoting repair over transcription. *Nat Cell Biol* 2023;25(8):1111–1120.
***Corresponding authors: s.zuryn@uq.edu.au**

Within each of our nucleated cells, hundreds to thousands of mitochondrial genomes (mtDNAs) produce essential proteins used for oxidative phosphorylation, as well as the non-coding RNA molecules required for their translation. Molecular damage to mtDNAs is inevitable and can result in transcription mistakes and promote mutagenesis events that likely contribute to tissue damage, age-related decline and disease. However, mitochondrial processes of DNA repair and transcription sterically conflict at the molecular level, suggesting that a lifelong trade-off between the maintenance and

Publications with Impact



Schematic model of ATFS-1 functions. Normally, HMG-5/TFAM interacts with RNA polymerase (RPOM-1/mtRNAP) via its HMG-2 domain to form the pre-initiation complex inside mitochondria, which mediates mtDNA transcription (left side). However, transcription interferes with mtDNA base excision repair (BER). Accumulation of ATFS-1 inside the mitochondria (right side) disrupts assembly of the preinitiation complex through competitive inhibition between ATFS-1 and RPOM-1/mtRNAP for HMG-5/TFAM interaction. Subsequently, mtDNA transcription is reduced but BER is promoted. As a result, the accumulation of damaged mtDNAs is reduced during ageing, enabling resistance to further mtDNA damage and age-associated decline in mitochondrial function.

expression of mtDNAs occurs. Such a trade-off may be critical in coordinating an organism's ability to fulfil both immediate energetic needs and ensure the long-term integrity of the mitochondrial genome.

To understand whether and how this trade-off is regulated, we sought to identify genes that could modulate mtDNA damage levels in the model organism, *Caenorhabditis elegans*. We genetically sensitised animals by firstly expressing *Pst*I, a mitochondrial-targeted endonuclease, that localised to body wall muscle mitochondria and cleaved mtDNAs. These transgenic animals presented with a paralysed phenotype, which we aimed to reverse by screening for genes that could help restore mobility. We found that a mutation in the bZIP transcription factor ATFS-1 (activating transcription factor associated with stress 1), which prevented its nuclear localisation but enabled mitochondrial localisation, suppressed paralysis. ATFS-1 has both a nuclear localisation signal and a mitochondrial targeting sequence. Interestingly, we found that nuclear ATFS-1, which has a role in activating a transcriptional program known as the mitochondrial unfolded protein response (UPR^{mt}), is detrimental during mtDNA damage, whereas this newly identified role inside the mitochondria was beneficial.

Remarkably, we found that mitochondrial ATFS-1 interacted with TFAM/HMG-5, a key component of the mitochondrial nucleoid that is essential for initiating mtDNA transcription. Importantly, the dual high-mobility group family of proteins such as TFAM reduce the rate of base excision repair (BER) *in vitro* by allosterically inhibiting DNA incision by DNA glycosylases. This led us to question whether mitochondrial ATFS-1 interferes with TFAM-mediated transcription initiation, thereby promoting reductions in mtDNA damage through BER. Indeed, by interacting with HMG-5 inside the mitochondria, we found that ATFS-1 prevented the assembly of the core mitochondrial transcription apparatus, which also contains the single-subunit mitochondrial RNA polymerase. In doing so, we observed a decrease in the overall transcription rate of mtDNAs and increased rates of mtDNA base excision repair. As such, we discovered a key molecular regulator of the balance of expression and maintenance of mtDNAs.

By artificially enhancing ATFS-1 mitochondrial levels, we reduced age-associated mtDNA damage levels in muscle cells, prolonging their function for much longer and enabling animals to be more mobile when they were older. Demonstrating that this function was conserved outside of *C. elegans*, we produced similar effects by expressing ATFS-1 in mammalian cells grown in culture. In the opposite experiment, introduction of Atf5, the mammalian orthologue of ATFS-1, into *C. elegans* recapitulated the activity of ATFS-1. Finally, we found that ATFS-1 naturally accumulated in mitochondria when mtDNA is damaged, as well as during ageing. Taken together, our work demonstrates that ATFS-1/Atf5 act as a molecular focal point that regulate the trade-off between the expression and maintenance of the mitochondrial genome in response to the physiological state of the cell.

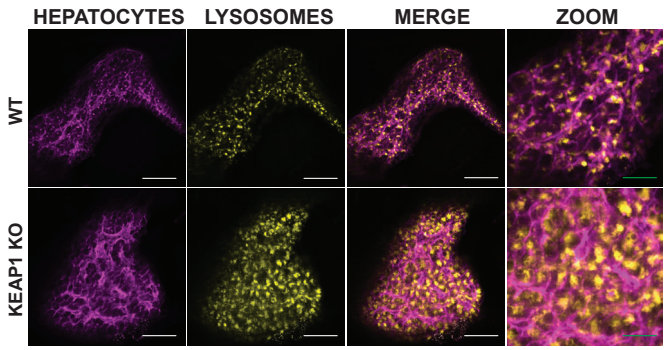
Steven Zuryn
Queensland Brain Institute
University of Queensland

Chuan-Yang (Michael) Dai (left) and Steven Zuryn.

Publications with Impact

Regulation of Lysosomal Biogenesis as a Novel Function of NRF2

Ong AJS, Bladen CE, Tigani TA, Karamalakis AP, Evason KJ, Brown KK*, Cox AG*.
The KEAP1-NRF2 pathway regulates TFEB/TFE3-dependent lysosomal biogenesis.
***Proc Natl Acad Sci USA* 2023;120(22):e2217425120.**
***Corresponding authors: kristin.brown@petermac.org, andrew.cox@petermac.org**



Representative multiphoton images of hepatocyte membrane (magenta) and lysosomes (yellow) in wildtype (WT) and KEAP1 knockout (KO) zebrafish at seven days post fertilisation.

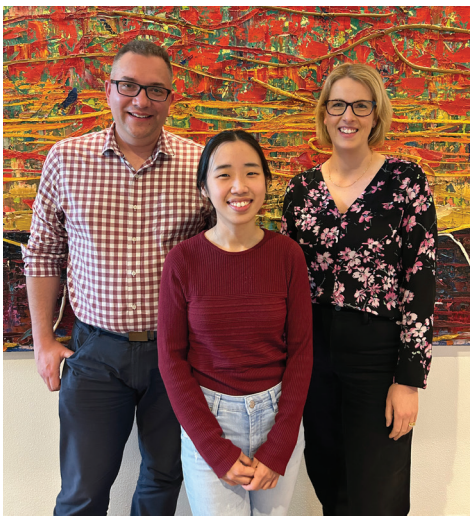
NRF2 is a transcription factor known for its role in the regulation of redox homeostasis and cellular metabolism. Although NRF2 has been extensively investigated in the context of a variety of disease states including cancer, there is a paucity of knowledge regarding the role of NRF2 during development. By exploring the consequences of NRF2 activation during embryogenesis, we have uncovered a novel role for this transcription factor in the regulation of lysosomal biogenesis.

In this study, we employed CRISPR/Cas9 gene editing to knockout the negative regulator of NRF2, KEAP1, in zebrafish larvae. Using this model, we demonstrated that KEAP1 deficiency results in a loss of viability that is preceded by severe liver abnormalities. Furthermore, through lysosomal staining and live-imaging of lysosomes in KEAP1 knockout zebrafish larvae, we have also shown that loss of KEAP1 induces an increase in lysosomal biogenesis in the liver.

We examined whether this process was evolutionarily conserved in mammalian systems by using CRISPR/Cas9 to knockout KEAP1 in a liver cell line. Consistent with our *in vivo* data, loss of KEAP1 in liver cells induced lysosomal biogenesis. Mechanistically, we have demonstrated that KEAP1-dependent regulation of lysosomal biogenesis is dependent on the master transcriptional regulators of lysosomal biogenesis, TFEB and TFE3.

Overall, our study has revealed that NRF2 can regulate TFEB/TFE3-dependent lysosomal biogenesis in a cell-autonomous and evolutionarily conserved manner. Lysosomes are catabolic organelles that regulate a range of cellular processes, including nutrient signalling and the degradation/recycling of macromolecules. Altered lysosomal abundance has been implicated in the initiation and progression of diseases, including cancer. Our studies highlight a previously unrecognised role for the maintenance of lysosomal homeostasis during embryonic development. Moreover, our findings suggest that aberrant lysosomal biogenesis may be a hallmark of NRF2-driven pathologies. Future studies will examine the metabolic vulnerabilities arising from increased lysosomal content with the potential to develop novel strategies to treat diseases characterised by NRF2 hyperactivation.

Athena Ong, Kristin Brown and Andrew Cox
Peter MacCallum Cancer Centre



From left: Andrew Cox, Athena Ong and Kristin Brown.

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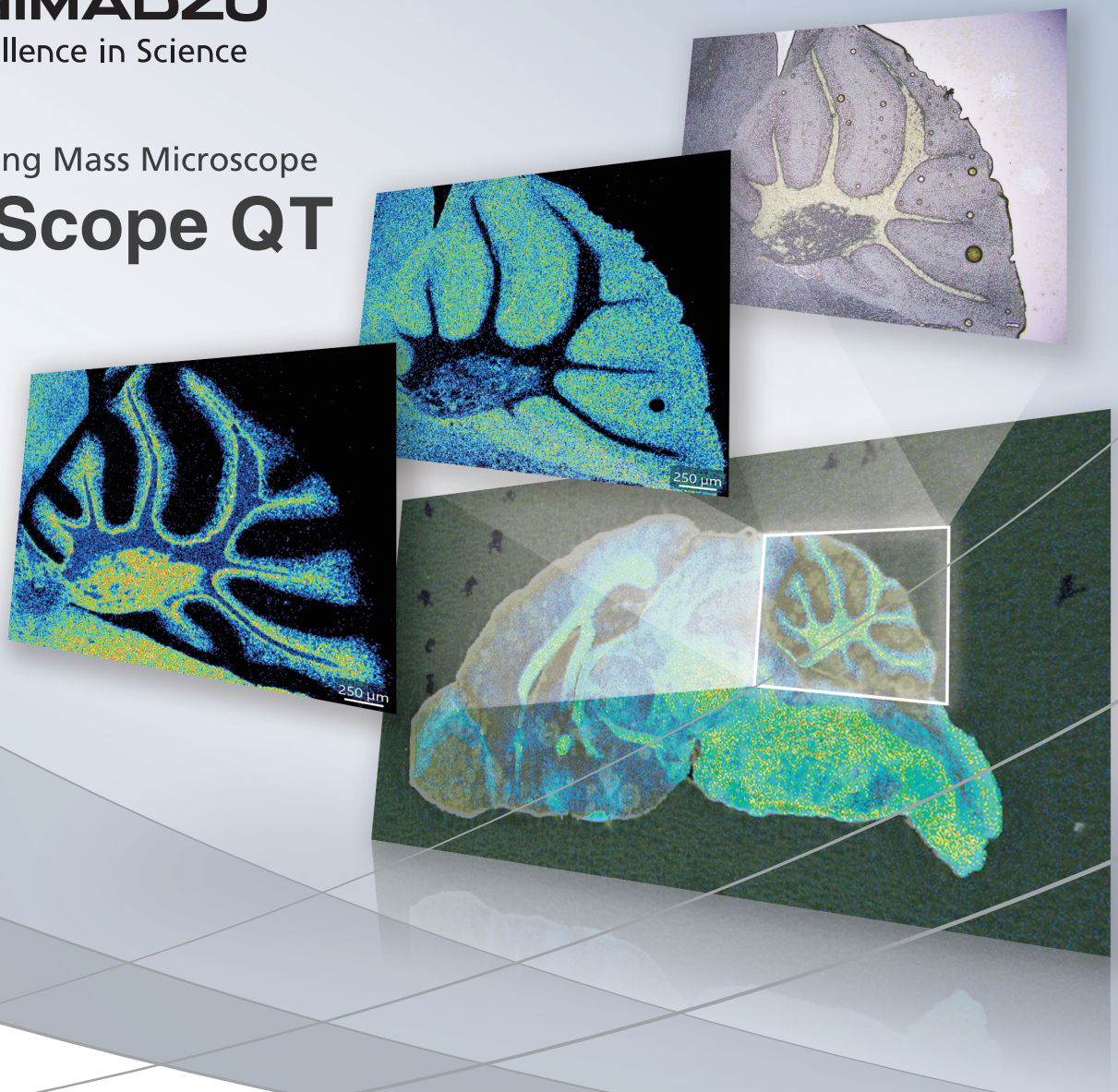

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ASBMB Medallists and Awardees at ASBMB2023

ASBMB President Ross Hannan with Lemberg medallist, Mike Ryan (left).

ASBMB President Ross Hannan with Shimadzu Research medallist, Stephanie Gras (left).

Simon Rushworth of SDR Scientific with SDR Scientific Education awardee, Maurizio Costabile (left).

Andreas Kick of Eppendorf South Pacific with Eppendorf Edman ECR awardee, Pirooz Zareie (right).

From left: ASBMB Secretary Dominic Ng and ASBMB Fellowship awardees, Adam Hagg and Chathura Suraweera.

ASBMB2023 Meeting Report

Colin Jackson and Christina Spry, Co-Chairs of ASBMB2023

The 67th annual meeting of the ASBMB, ASBMB2023, was held in the newly-built Kambri cultural precinct at the heart of the Australian National University, Canberra, from 15–17 November. The meeting, a fully in-person event attended by 213 delegates and run over 2.5 days, was officially opened by ASBMB President, Professor Ross Hannan (Australian National University), who welcomed the attendees to Ngunnawal and Ngambri country and to the conference. The scientific program kicked off with a plenary by Professor John Kuriyan of Vanderbilt University, Nashville, Tennessee. John talked about his career in structural biology, including some of his recent work on the role of sliding clamps and clamp-loader complexes in DNA replication. He discussed the structural principles underlying these complexes and their allosteric responses to ATP, DNA and each other. The second plenary presentation was delivered on day 2 of the conference by Dr Seemay Chou, co-founder and CEO of Acardia Science, Berkeley, California. Seemay shared her journey as a scientist and the challenges she faced in academia, including issues with rigour, specialisation and gatekeeping. She highlighted how these challenges led her to step back from traditional academia and pursue exploratory research (including on tick-borne diseases), and how this led to the establishment of her company Arcadia Science. Seemay described the non-traditional approach Arcadia Science takes regarding research and publication, and shared one of their tools, Protein Cartography, for the exploration and discovery of novel protein properties within protein families.

Plenary speakers, John Kuriyan (left) and Seemay Chou.

In addition to the inspiring plenary presentations, there was a total of 14 Symposia, run in two parallel sessions, on a broad spectrum of topics: Gene Regulation, Drug Discovery, RNA Biology, Computation, Pathogens, Protein and Peptide Engineering and Evolution, Membrane Transporter Biology, Immunology, Plant Biochemistry, Education, Structural Biology, Signalling and Cell Biology, Biotechnology, and Cancer. Each Symposium featured an invited keynote speaker, two additional invited speakers and two speakers selected from abstracts. At least one speaking slot per Symposium showcased an EMCR, including those chosen to represent ASBMB Special Interest Groups: Qian Guo (Queensland Protein Group),

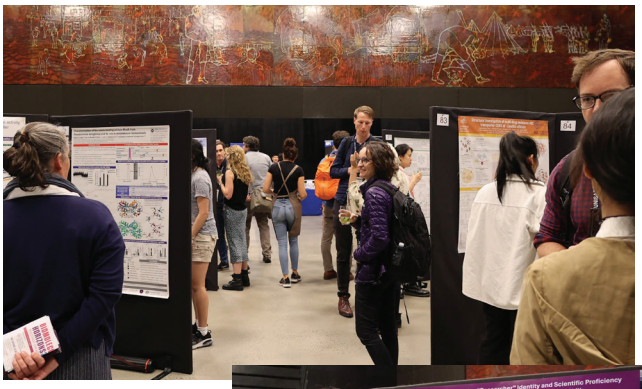
Kambri cultural precinct in the centre of the ANU.

Lani Davies (Canberra Protein Group), Dr Joshua Hardy (Melbourne Protein Group), Hannah Brown (Sydney Protein Group) and Dr Emma Watson (Melbourne Protein Group). In total, there were 14 keynote speakers, 28 additional invited speakers and 27 speakers selected from abstracts. This culminated in an exciting scientific program with something for everyone, and researchers of all career stages from overseas and across Australia represented. We thank Program Organiser, Dr Emily Furlong, for overseeing such a vibrant program. We also thank all Symposium Chairs for their great choice of invited speakers and careful selection of abstract speakers, as well as all the speakers for their engaging and high-quality presentations describing cutting-edge, often unpublished, research, which sparked many excellent questions and scientific discussions.

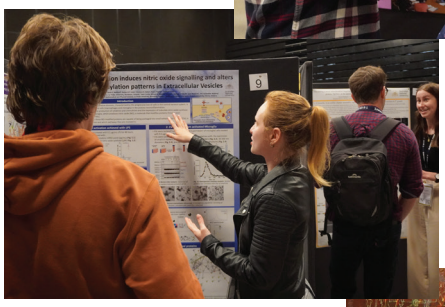
Between sessions, delegates congregated in the foyer and new purpose-built Manning Clark Hall where they enjoyed the delicious meals, snacks and drinks provided by Bella's Feast. On display were 13 trade exhibits that provided delegates the chance to interact with our trade partners and collect stamps to enter the Passport Prize draw. There were also 109 high-quality posters covering a breadth of topics. Day 1 of the conference concluded with a lively 2-hour poster session during which poster presenters shared their work with researchers of all career stages (including the anonymous poster judges) while enjoying mocktails and cocktails.

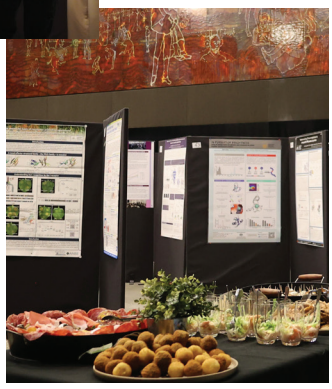
The ASBMB2023 Organising Committee was committed to providing EMCRs with opportunities to present their research, network and advance their career development. One of the EMCR career development initiatives was a lunch where EMCRs could have casual conversations about research careers with senior academics and invited speakers. Approximately 30 EMCRs and 12 senior academics attended this lunch. Positive feedback was obtained from EMCRs, one of whom highlighted that they appreciated the opportunity to receive career advice from senior researchers across diverse fields. Travel grants were also provided to ten EMCRs who presented

ASBMB2023 Meeting Report



Poster display at ASBMB2023.





Poster prize winners, from left: Rachel Leonard, Lawton Murdolo, Suyan Yee, Dalton Ngu, Colin Jackson (Chair), Erekle Kobakhidze, Zahra Falahati and Jeeeun Shin.

their work: Ranjith Meemanage Cebreco (University of Adelaide), Dr Aidan Grosas (University of Woollongong), Dr Dimitra Chatzileontiadou (La Trobe University), Natalia Pinello (University of Sydney), Jyoti Gurung (University of NSW), Ciara Wallis (Australian National University), Dr Joshua Hamey (University of NSW), Dr Hilary Hunt (Oxford University), Gurveer Kaur Gaddu (Deakin University) and Dr Ashleigh Paparella (University of Sydney).

A highlight of the program was the presentation of the 2023 ASBMB medals and awards, which occurred on days 2 and 3 of the conference. ASBMB President, Ross Hannan, introduced our medallists and awardees

ASBMB2023 Poster Prize Winners

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John Chen (Australian National University)
Exploring the uncharacterized sequence space of periplasmic binding protein transcription regulators

Zahra Falahati (University of Sydney)
The development of novel ecofriendly selective pesticides for the maintenance of managed honeybees

Seyed Mohammad Ghafoori (UNSW Sydney)
Deciphering neurocognitive landscapes: a comprehensive genomic exploration of copy number variants' role in neurodevelopmental disorders

Erekle Kobakhidze (University of Sydney)
Investigating the role of histone variant H2A.Z in gene regulation

Rachel Leonard (Australian National University)
Identification of a novel, highly potent inhibitor of the mitochondrial electron transport chain in the parasites that cause malaria and toxoplasmosis

Lawton Murdolo (La Trobe University)
How some of us remain asymptomatic after COVID-19

Jeeeun Shin (Australian National University)
Structurally investigating multi-drug resistance ABC transporter of Candida albicans

SPONSORED BY THE SOCIETY FOR REDOX RESEARCH AUSTRALASIA

Dalton Ngu (University of Queensland)
Characterisation of the solute-binding protein ModA from Pseudomonas aeruginosa *and its role in molybdenum homeostasis*

Suyan Yee (Australian National University)
Linking the biochemical specialisation of organelles to cell type-specific stress signalling in plants

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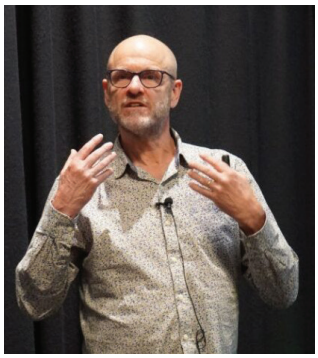
Li Jin Chan (Walter and Eliza Hall Institute)
Nanobodies to inhibit malaria parasite fertilization and development in mosquitoes

ASBMB2023 Meeting Report






Keynote speakers, clockwise from top left: Renae Ryan, Magdalena Plebanski, Adam Perriman and Barry Pogson.

before we had a chance to hear directly from them about their careers and research. The ASBMB Eppendorf Edman Award winner was Dr Pirooz Zareie from Monash University. Pirooz presented his recent research on covalent interactions between T-cell receptors (TCRs) and peptide epitopes. His work demonstrated that introducing disulfide bonds between these molecules can dramatically enhance TCR signalling with minimal structural consequences, offering new insights into T-cell activation for both basic immunology and clinical applications in improving adoptive T-cell therapies.

The ASBMB SDR Scientific Education Award winner was Associate Professor Maurizio Costabile from the University of South Australia. Maurizio shared his scientific approach to biochemistry education, emphasising problem identification, result assessment and the significance of disseminating education study outcomes. He also discussed his successful use of interactive simulations to boost student engagement and comprehension, and shared advice for EMCRs wanting to further the teaching aspects of their career.

The Shimadzu Research Medal recipient was Professor Stephanie Gras from La Trobe University. Stephanie gave an encouraging and honest account of some of the highs and lows of her career before sharing her work studying the interactions between SARS-CoV-2-derived peptides and human leukocyte antigen variants. The work has revealed key molecular insights into pre-existing immunity to the virus.

The ASBMB Lemberg Medal recipient was Professor Mike Ryan of Monash University who engaged us with an overview of his career studying mitochondrial biology and disease. He shared highlights of his research combining gene editing with proteomics to study assembly of mitochondrial complex I, which, among other things, has led to the identification of mutations that cause mitochondrial disease.

On the final day of the meeting, the presentations of the Shimadzu Research Medal and ASBMB Lemberg Medal were followed by the presentation of the ASBMB Fellowships. ASBMB Secretary, Associate Professor Dominic Ng, presented the awardees in attendance, Dr Adam Hagg and Dr Chathura Suraweera, with their certificates. Thereafter, the meeting concluded with a word of thanks from meeting Chair, Professor Colin Jackson, along with the Passport Prize Draw and presentation of the Poster Prizes.

We'd like to extend our thanks to the Local Organising Committee, Dr Emily Furlong (Program), Dr Simon Williams (Venue), Dr Rebecca Frkic (Social Media), Dr Kai Chan (EMCR and Posters), Associate Professor Tracey Kuit (Education), Associate Professor Kate Quinlan (Treasurer), Dr Joe Brock (Website and Registration), Dr Joe Kaczmarski (Trade), and, in particular, Jack Horton – our one-man professional conference organiser. We'd also like to thank the subcommittees, Symposium Chairs and poster judges. A special thanks also goes to the army of volunteers who manned the registration desk, provided directions, ran around the lecture halls with microphones during question time, and did various other tasks, as well as to Sharyn Wragg and Jack Dalton for capturing the special moments of the meeting. We also thank all the sponsors for supporting the meeting, and finally, thank all the presenters of talks and posters that contributed to the stimulating scientific program.

Colin Jackson and Christina Spry
Australian National University

ASBMB2023 Organising Committee members, from left: Kai Chan, Rebecca Frkic, Jack Horton, Joe Kaczmarski, Simon Williams, Joe Brock, Emily Furlong, Christina Spry, Tracey Kuit and Colin Jackson.

Education Day at ASBMB2023

Canberra turned on the sunshine for ASBMB2023. The Education Symposium started with the 2023 ASBMB SDR Scientific Education Award presentation by Associate Professor Maurizio Costabile (University of South Australia). Maurizio told us about his career pathway from biochemistry and immunology research to his current role in educational research and leadership. He provided tips for EMCRs and educators and took the audience on a reflective journey along the changing nature of higher education, while provoking thoughts about how we can adapt to current challenges. Maurizio shared his experiences with supporting students to master key concepts in biochemistry and molecular biology, all underpinned by the innovative use of technology and developing strategies to research the impacts. This presentation set the tone for a day that continued with sharing experiences and ideas, whilst creating a space for collaboration and ongoing discussions.

Left: 2023 ASBMB SDR Scientific Education Award recipient, Maurizio Costabile.

Right: Education Keynote speaker, Danny Liu.

As 2023 saw the emergence of generative artificial intelligence (GenAI), the Education keynote was given on this provocative topic. Who better to give this address than friend of ASBMB, Associate Professor Danny Liu (University of Sydney). For many of us who have attended webinars, read articles, reports or researched websites about GenAI this year, the name Danny Liu is prominent. Danny and his colleagues have provided practical insights that have helped us explore and navigate our way with this new technology. His keynote presentation, 'A Year On: Getting Real With Generative AI in Science Education', took us on a journey of the constantly emerging capabilities of GenAI. Danny's central message focused on the ethical use of such tools whilst embracing the educational affordances for our students by incorporating this technology into teaching, and to support academics and educators in the workplace. There was something in this keynote presentation for everyone, and Danny's passion and expertise, alongside his understanding of the discipline as a molecular biologist, kept the room abuzz with discussion.

Education Symposium presenters and chairs, from left: Amber Willems-Jones, Reece Sophocleous, Matthew Clemson, Tracey Kuit, Jacqui Matthews, Maurizio Costabile, Danny Liu and Alexander Maier.

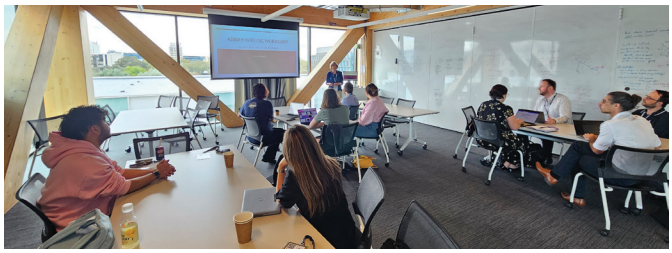
Through a series of presentations, the Education Symposium continued the focus on supporting our students' learning and skill development, whilst maintaining the quality of our programs through the incorporation of technology. Dr Amber Willems-Jones (University of Melbourne) discussed the results of a pilot study evaluating an online module that successfully supports student development of assessment literacy skills. By promoting students' abilities to review assessments, learning how to apply rubrics and provide feedback, students became more self-aware of their good practices and where there were opportunities for improvement. Dr Matthew Clemson and Professor Jacqui Matthews (University of Sydney) each shared their experiences incorporating an online experiment simulation tool that generates authentic data as students undertake laboratory experimentation. Matthew described the incorporation of the Data Generator tool in second year biochemistry classes to assist students to explore enzyme kinetics and extend their laboratory learning by applying new and extensive experimental parameters. Jacqui presented on how her team utilises the tool with senior undergraduate students through personalised student research projects. Use of such technology allows students to explore the experimental exercises, to change parameters and generate authentic results that would not be possible in class due to time, cost, facility, and other laboratory class constraints. To round out the Education Symposium, Dr Reece Sophocleous (University of Wollongong) shared his experiences in a partnership with students and colleagues across Australia and Canada to develop a computer game to teach first year molecular biology students about cellular activities during Type I diabetes states. Reece posed many points to consider when looking to embrace game-based technology in teaching, ultimately highlighting that students do not need to be regular gamers to see benefits in their learning following engagement with such tools.

Following on from a successful webinar in July with the Editor-in-Chief of the *international Biochemistry and Molecular Biology Education (BAMBEd)* journal, Professor Susan Howitt (Australian National University and *BAMBEd* Editor) facilitated a writing workshop,

Education Day at ASBMB2023

sharing tips for writing for education journals. Participants included academics with a spectrum of experiences and graduate students. After exploring the scholarship of teaching and learning, types of educational research and journals, the group explored models of writing and approaches to educational research and gathering meaningful data to answer educational research questions. Susan also asked participants to explore the important ways our science background and skills can support our educational research, and to reflect upon the barriers to their writing and the importance of prioritising this work. Following a successful workshop, many participants gathered again during the last session of the day to explore research ideas and collaborations, and the creation of a cross-institutional writing group.

ASBMB2023 provided an important space for education enthusiasts within the Society, across all career stages, to gather, share ideas and explore future opportunities in a relaxed atmosphere, supported by great food and drink and a fantastic venue. We thank the ASBMB for ongoing support of the Education SIG, and the conference Organising Committee for supporting our activities throughout the day. Additional thanks go to the Education Symposium co-chair, Professor Alexander Maier (Australian National University), as well as the presenters, facilitators and participants. We look forward to coming together again in Melbourne in September 2024 for BioMolecular Horizons.



Above: Education writing workshop. Below: Workshop participants, with facilitator, Susan Howitt (second from left).

Tracey Kuit (University of Wollongong) and
Amber Willems-Jones (University of Melbourne)
Chair and Deputy Chair
ASBMB Education Special Interest Group

ASBMB Education Feature

The ASBMB Education Feature is coordinated by Tracey Kuit (tracey_kuit@uow.edu.au) and Amber Willems-Jones (amber.willems@unimelb.edu.au).

Empowering Students Through Curriculum Choices and Assessment Design: A Students as Partners Approach That Enhances Engagement and Assessment Literacy

Chris Love, Griffith University

I have been teaching biochemistry and molecular biology for more than 18 years and, in more recent times, have observed an unwillingness of students to participate in classroom based problem-solving in biochemistry. Students have anecdotally mentioned that they "feel embarrassed" or "fear being ridiculed" if they answer questions incorrectly which had led to their silence. While I was trying to grapple with this student engagement issue, I attended a workshop at Griffith University on Students as Partners (SaP) facilitated by Mick Healey, a higher education consultant. Prior to this workshop, I had not heard of the concept of Students as Partners, which is based on the principle of engaging students as active collaborators and co-creators in the teaching and learning process (1,2). I became fascinated with how this teaching approach empowered students and at some point, in this workshop, I stopped participating in the activities and in my scribblings, had created a plan to transform my second year Protein Science course (Advanced Biochemistry, approximately 120 students), providing students with curriculum choices and co-creation of assessment. This is where my foray into Students as Partners began.

Chris and student partner, Natalyha Phister, at the RAISE Conference.

Students as Partners strategy and considerations

The implementation of my SaP teaching approach aimed to foster a genuine partnership that was inclusive, empowering and transformative. The process was guided by the five principles for genuine partnerships (3) to ensure that partnership activities were active-learning tasks and nurtured power-sharing relationships through dialogue and reflection. The main goal was getting buy-in from students and therefore, increased engagement. I hoped that empowering students to collaborate in partnership activities would lead to increasing participation and engagement in the course. The strategy to partner with students in the curricula was threefold:

1. Allow students to select a topic from a list to learn for part of the course (proteomics, protein therapies, protein–DNA interactions and protein engineering).
2. Create an opportunity for students to design multiple choice questions, with scaffolding, and negotiate the number of student-generated questions that would appear in the assessment.
3. Provide a 'safe' environment (PebblePad, Personal Learning Environment) for students to complete the partnership activities and reflect on their experiences.

Partnership outcomes

I was surprised at the level of engagement by students in the partnership and, in particular, the positive reflections provided. Of the students who participated, 80.5% indicated that they were engaged (32%) or more engaged (48.5%) because of being involved in the course design and assessment co-creation. Student reflections provided direct insight into students' perceptions of the partnership. Most of the reflections on topic selection related to their future courses or degree programs or topics that they thought would be interesting, for example, "I believe these topics could be of use in my future as a researcher," and "I chose protein therapeutics because I find it fascinating how proteins can be used to treat medical conditions." Another student stated, "I liked that I got to study a topic I chose for once." With respect to

designing multiple choice questions for assessment, the emerging themes included: the difficulty of the task, particularly designing feasible incorrect answers; the need to have a good understanding of the topic; and that understanding how questions are designed could improve their ability to correctly answer questions. Student comments such as "Activities like these make me feel more involved in the course and increases my interest" suggested the partnership was genuine and inclusive (3). Other reflections supported Deeley and Bovill's (4) notion that developing assessment improves assessment literacy, "I think this process will help us in choosing the correct answer when doing other multiple choice questions". This student comment sums up the success of this student–staff partnership, "Choosing a topic meant an increase in engagement and interest, and choosing questions for assessment meant I had to filter through what I know, didn't know and what gaps I had in my knowledge."

I collaborated with undergraduate student partners in research projects on my SaP approach and supported them to secure funding to attend and copresent our findings at an international conference, Researching, Advancing & Inspiring Student Engagement (RAISE) 2019, held in Newcastle, UK. During the COVID pandemic, this teaching approach helped me maintain a connection with students and I continue to be amazed by their engagement in the partnership.

References

1. Healey M, Flint A, Harrington K. Engagement Through Partnership: Students as Partners in Learning and Teaching in Higher Education. 2014, Advance HE.
2. Cook-Sather A, Bovill C, Felten P. *Engaging Students as Partners in Learning and Teaching: a Guide for Faculty.* 2014, Josey-Bass.
3. Matthews KE. *Int J Students Partners*, 2017;(2):1–9.
4. Deeley S, Bovill C. *Assess Eval High Educ* 2015; 42(3):463–477.

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Getting the 'VIBE' in Biochemistry Education (Virtual Reality In Biochemistry Education)

Anna Lohning[a], Susan Hall[b], Oladayo Folasire[a], Ryan Wirth[a] and Shai Anoopkumar-Dukie[b]

[a]Bond University and [b]Griffith University, Queensland

Adapting to the recent changes in the educational landscape has provided unique opportunities for educators to explore emerging technologies and modalities, with the aim of improving engagement and understanding. In this article, we share our experience of incorporating 3D technologies, including virtual reality (VR), into a second year undergraduate biochemistry course. Our research, conducted over four years, between 2020–2023, focused on a key learning objective – the interrelationship between biomolecular structure and function.

In our experience, the gap in abilities within each student cohort is widening, especially in terms of prior learning in chemistry, mathematics and visual literacy, yet little time is available for knowledge catch up. Visual representations of molecules must be manipulated mentally to form an accurate 3D conceptual understanding of molecular structure and characteristics. This is a fundamental skill in biochemistry, yet can pose significant hurdles for some students (1,2,3). Such abilities can enhance understanding the biomolecular structure–function relationship (4). The challenge for educators in this space is finding engaging ways which efficiently showcase these concepts. We sought to promote student engagement and learning by incorporating a series of guided workshops harnessing a range of 3D technologies.

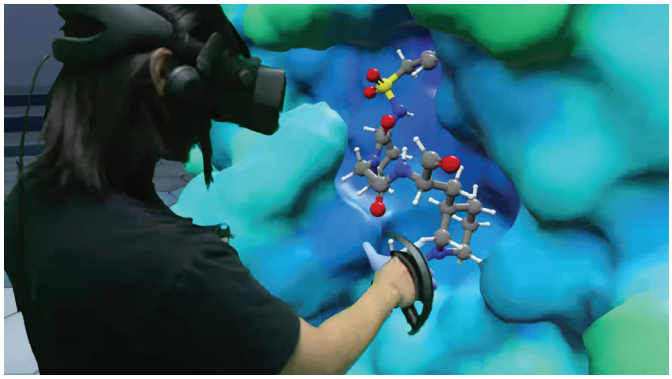

Fig. 1. *Student probing the drug–protein interaction using Nanome (5) and Oculus headset.*

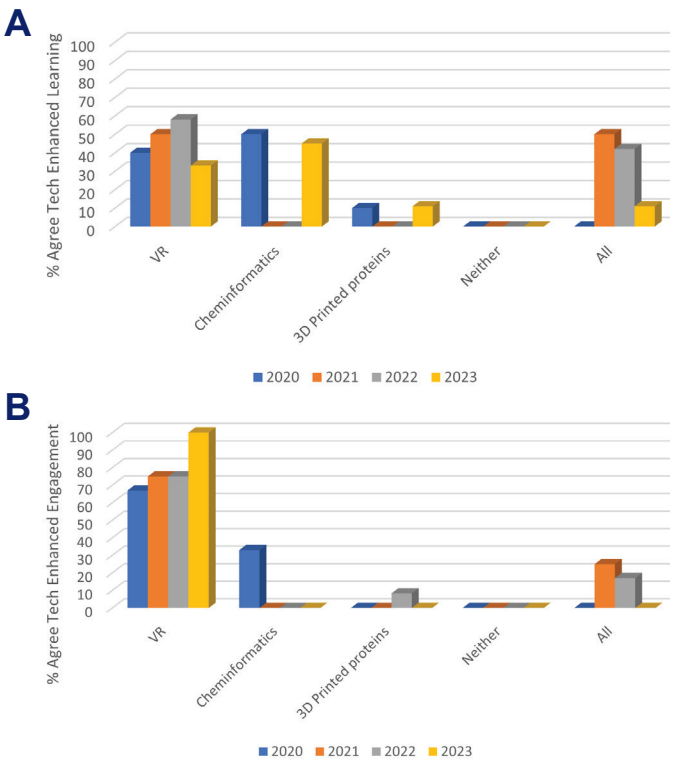

Fig. 2. *Student responses to level of agreement with the statement 'This activity helped the most to* ***A. learn*** *or* ***B. engage with*** *protein–ligand interactions'.*

Our ethically-approved research involved inviting students to participate in a one-hour workshop – the content of which was relevant to a summative subject assessment on protein structure. Despite this, participation was low (7 in 2020 (9%), 4 in 2021 (7%), 12 in 2022 (16%), 9 in 2023 (10%)). The activity was based on investigating a therapeutically interesting protein–drug model (human sialidase, 4ncs.pdb, bound to 2,3-difluorosialic acid), adapted for either 3D printing, virtual modelling or VR. Our VIBE (**V**irtual Reality **I**n **B**iochemistry **E**ducation) sessions involved allowing students to either physically hold the model (3D printed proteins), manipulate it in real time on-screen (FirstGlance in JMol) or 'step inside' a protein using Oculus headsets (VR, Nanome software). Firstglance in JMol is a free online tool providing guided macromolecular visualisation, though somewhat limited in functionality. Although relatively easy to use, we provided students with step-by-step instructions to expedite progress. For the VR activity, we purchased educational licenses for Nanome (5) and Oculus Quest or Quest2 headsets (**Fig 1**). Nanome is an advanced VR software package used in pharmaceutical research. Both virtual modelling and VR enable students to interact with the protein/drug system, using different renders and colouring to highlight specific structural characteristics.

During the sessions, students completed a workbook designed to probe their understanding of key non-covalent interactions underpinning binding affinity. Afterwards, students were invited to participate in a Qualtrics feedback survey on their experience, perceived learning and engagement. The survey consisted of three main 5-point Likert scale questions as well as a provision for an open-ended response. Qualitative data was analysed thematically while quantitative data comparing students' preferences and perceptions was represented graphically as percentage of participant pool (**Fig 2 and 3**).

Notwithstanding the challenges imposed by COVID-19 over the past four years, we've managed to maintain deployment of the VIBE workshop, and found consistently that the student data supports continual incorporation of these technologies into the curriculum. Results showed that for each iteration of the activity, 80 to 100% of participants (n=31) agreed that both VR and 3D modelling improved understanding of protein – ligand interactions. One reason for this is that, compared to 3D printed proteins, both VR and 3D modelling enable students to probe different features of molecular structure in a manner that was meaningful to them. Thematic analysis open-ended feedback also demonstrated increased engagement using both VR and virtual 3D modelling platforms. 3D printed proteins were less useful due to print quality limitations. Improving the quality of 3D printing, for example by adding colour or texture in chemically meaningful ways, as can be done with the other technologies, would level the playing field considerably since some students enjoy the tactile approach or, importantly, may offer a unique experience for visually challenged students (6). Additional challenges identified for deployment of these workshops included cost, preparation time, timetabling, university Wi-Fi security and other technical aspects. Thus, these workshops are best limited to small groups. Deployment of this type of hands-on workshop requires sufficient staffing to ensure students are safe and comfortable with the equipment. Despite this, our results have provided valuable feedback which will help guide future deployment of 3D technology supported activities. Our group would be pleased to hear from anyone interested in collaborating on future projects in this space and to share our experiences.

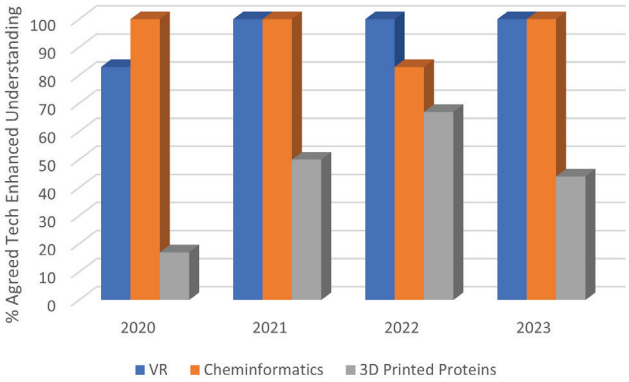

Fig. 3. *Student responses when asked the degree to which they agreed that this technology helped them understand how ligands interact with proteins.*

References

1. Linenberger KJ, Bretz SL. *Biochem Mol Biol Educ* 2015;43(4):213–222.
2. Hall S, Grant G, Arora D, Karaksha A, McFarland A, Lohning A, Anoopkumar-Dukie S. *Curr Pharm Teach Learn* 2017;9(4):723–728.
3. Lohning AE, Hall S, Dukie S. *J Chem Educ* 2019; 96(11):2497-2502.
4. Ainsworth S, Prain V, Tytler R. *Science* 2011;333(6046):1096–1097.
5. Bennie S, Maritan M, Gast J, Loschen M, Gruffat D, Bartolotta R, Hessenauer S, Leija E, McCloskey S. A Virtual and Mixed Reality Platform for Molecular Design & Drug Discovery – Nanome Version 1.24. 5th Workshop on Molecular Graphics and Visual Analysis of Molecular Data, 2023, The Eurographics Association.
6. Oakley A. *Australian Biochemist* 2023;54(2):19.

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Assessment Workload – It's Not About the Number

Fiona Carroll, La Trobe University

Mapping assessment numbers across the Bachelor degrees in Agriculture and Biomedicine at La Trobe University showed that full-time students at first year level complete on average 55 assessments per semester; this is reduced to 30 in later years. It should be noted that from the data it is unclear how many of these tasks are completed as learning tasks during classes. However, assessment concerns are universal, and when presenting this data, educators frequently start justifying these decisions, whereas management suggest we're over-assessing.

There is no clear definition of what over-assessment is, or indeed discussion of its impact in the education literature. Indeed, it seems that over-assessment is a somewhat nebulous term mostly used in relation to workload.

As assessment in higher education has shifted from large summative exams to ongoing assessment, pedagogical advantages have been indicated for frequent low stakes assessment tasks, particularly in online and blended learning environments (1,2). However, it becomes easy to see that in our 12-week semester, weekly low stakes assessment across four subjects plus additional summative tasks, results in high assessment numbers. I have not yet explored any correlation between task number and workload, and this will likely be highly

variable. However, I strongly feel that we should shift the discussion to focus on the quality of assessments rather than the quantity.

It is well-established that assessment drives student behaviour (3,4) and an increasing tendency to incentivise task completion to drive student behaviour leads to an assessment-driven curriculum. As such, the quality of assessment design and the need for learning to occur during task completion becomes paramount as students prioritise tests and assessments over general weekly study (5).

Despite a nominal grade being assigned, low-stakes assessments are frequently intended to be formative. Formative assessment essentially supports learning as opposed to summative assessment that measures learning that has occurred (6). Formative tasks provide feedback that informs and potentially improves teaching and curriculum design and aids the learner to identify strengths and weaknesses while providing feedback for improvement (6).

If regular low-stakes tasks are embedded in learning materials it is important to define their purpose. What is the desired learning outcome? If tasks are meant to be formative, then are they promoting learning? Considerations should include: Are outcomes used to modify teaching or learning activities? Do tasks provide feed-forward feedback students can use to improve? Do students engage with feedback and use it to improve their learning? Are they given an opportunity to do so? Are the stakes so low or the workload so high that students are not engaging with the task and simply guessing? Overall, are assessment tasks promoting and achieving learning at the desired level?

Another consideration is the complexity of low-stakes formative tasks. Consider, for example a pre-laboratory class quiz. If used as laboratory preparation, it is likely we want poorly performing students to engage with the feedback and achieve a threshold mark before they complete the laboratory class. Similarly, tasks completed in class where help is readily available typically result in high scores. However, this doesn't mean that all low-stakes assessment tasks should generate high scores. Indeed, one could argue that they are low-stakes so students can afford to try and fail, as this promotes learning. If students easily achieve high marks in a task does this give them a false impression of their ability and more importantly, expectations for subsequent summative tasks?

There is no one-size-fits-all approach to assessment. Different people and different disciplines use different tasks to achieve different outcomes. However, the need to have quality assessment tasks designed for, and achieving defined learning outcomes, is something we should all strive for.

Finally, is 55 tasks in a semester over-assessing? It is impossible to put an optimal number on assessment tasks. Indeed, if we focus on quality design and analysis of outcomes, we may find we can achieve similar outcomes with fewer, better designed tasks. However, quality assessment design, validation and review require a lot more peer collaboration and staff time than are typically allocated for these tasks. Addressing this is a more worthy workload conversation than reduction in assessment number due to over-assessing.

References

1. Holmes N *Assess Eval High Educ* 2015;40(1):1–14.
2. Morris R, Perry T, Wardle L. *Rev Educ* 2021;9(3): e3292.
3. Biggs J, Tang C. *Teaching for Quality Learning at University.* 3rd edition, 2007, McGraw-Hill Education.
4. Ramsden P, Ramsden P. *Learning to Teach in Higher Education*. 2003, Taylor & Francis Group.
5. Hattingh T, Dison L, Woollacott L. *Australas J Eng Educ* 2019;24(1):14–24.
6. Bennett RE. *Assess Educ Principles Policy Pract* 2011;18(1):5-25.

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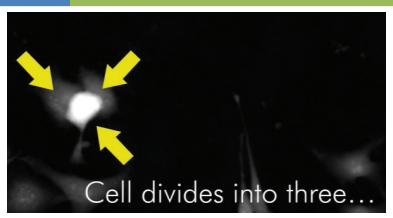

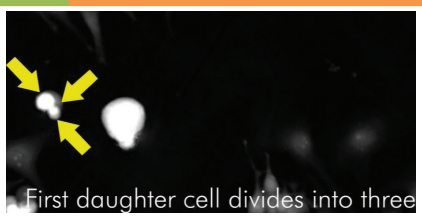

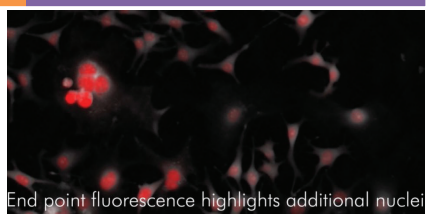

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SDS Page: Short Discussions for Students Page

What Does a Protein Look Like?

Sarah Piper

Monash University

Close your eyes and imagine your favourite protein. You might 'see'' a polypeptide chain, a more complex ribbon or beta-sheet style, a sphere inside a cell, or just light yellow powder (if you're a gym junkie). Chances are low that two people have the same image in their head when they think about proteins. Proteins are diverse in their shapes, forms and functions. The various ways of visualising them results in even higher diversity.

I've been passionate about science visualisation for a few years now, primarily using the software ChimeraX (**Figure 1**) and Blender3D. My images and animations are available online, through my social media accounts (@PiperProteins on Twitter and PiperProteinProductions on YouTube). I also produce engaging illustrations of membrane proteins to feature research from the ARC Centre for Cryo-electron Microscopy of Membrane Proteins (CCeMMP). My illustrations can be used to communicate scientific data or simply be viewed as artistic pieces. For example, see what happens if we 'scale up' proteins and bring them into our day-to-day 'dimensional reality' (**Figure 2**), perhaps, a day at the beach? Or we can turn our protein chains into atomic jewellery!

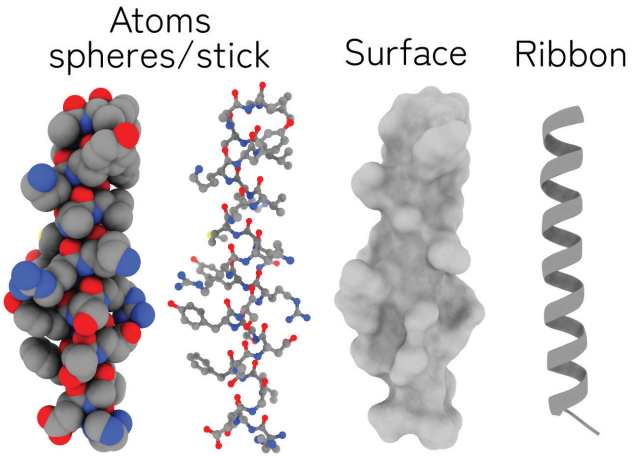

Figure 1. *A simple alpha helix can be displayed in a variety of ways. PDB: 8E3X (chain P). Created in ChimeraX.*

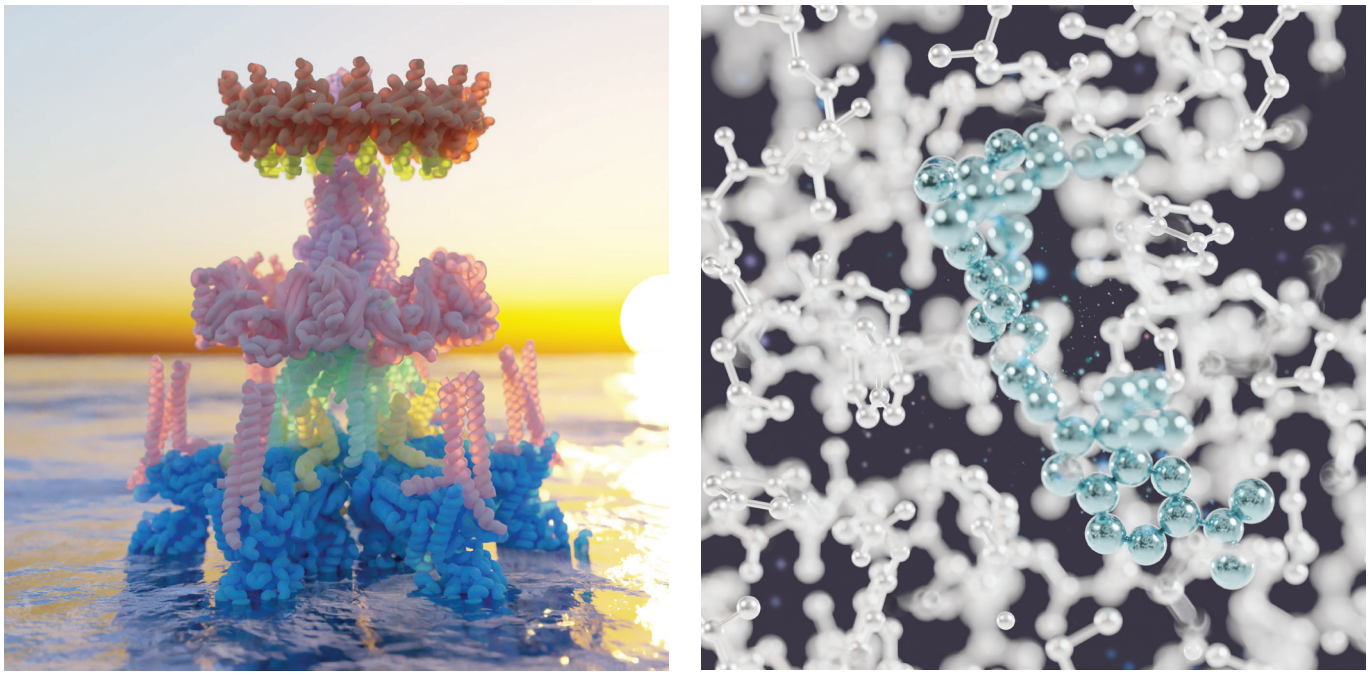

Figure 2. *Proteins 'out of context'. Created in Blender3D.*
Left: a Type IV secretion system at the beach. PDBs: 7O3T, 7O3V, 7O41.
Right: an obesity and diabetes target as 'atomic jewellery'. PDB: 7LCI. Runner-up for the 2023 NHMRC biennial Science to Art Award.

SDS Page: Short Discussions for Students Page

How can we tell visual stories of proteins?

Popular software to analyse and display protein structures are Pymol, ChimeraX and VMD. Taking this a step further, free computer graphics software, such as Blender3D, has been made more accessible to scientists to create amazing images and animations of biological processes. Tools such as the Molecular Nodes addon for Blender3D (**Figure 3**), developed by Brady Johnston, make it very easy to import structural biology data and make it look beautiful in a few clicks. I've come up with a few tips on how to learn about and create scientific illustrations and animations.

Tips for creating beautiful protein illustrations for publications or outreach

1. **Think about your message and audience.** Before you start a project, think about one to two key points that you want to convey, and who is viewing your figures or animations. If you want to address a broader audience, include simple shapes, such as surface representations of your proteins (see tip 4).

2. **Create a draft: showing figure ideas separated by scenes or panels on paper.** Especially for longer animations or complex figure panels. Use good old paper and pen to create a storyboard, and use placeholders if you don't have any images yet. Check whether your story 'flows'.

3. **Practice, practice, practice!** And get feedback from others, especially from those outside your field. I've learned to use Blender3D through YouTube tutorials, mostly from outside the science field. You can learn new techniques and apply them to your own molecules. Follow online tutorials for ChimeraX and Blender3D/MolecularNodes for scientific figures and movies.

4. **Less is more.** Think about (a few) colours to focus on your main object. Use complementing and colourblind-friendly palettes (e.g. from Coolors). Camera settings can help the viewer focus on particular parts of the image, e.g. using depth of field, zoom or cutaway views. Use light to your advantage (e.g. to highlight an important interaction), but be wary of shadows (in scientific figures, they are mostly distracting).

5. **Be creative and have fun!** At first, making protein artwork and animations might seem elaborate and time consuming, but it will be worth it. Get inspiration from the real world for displaying your images. Especially if you want to design a (journal) cover or any artistic piece.

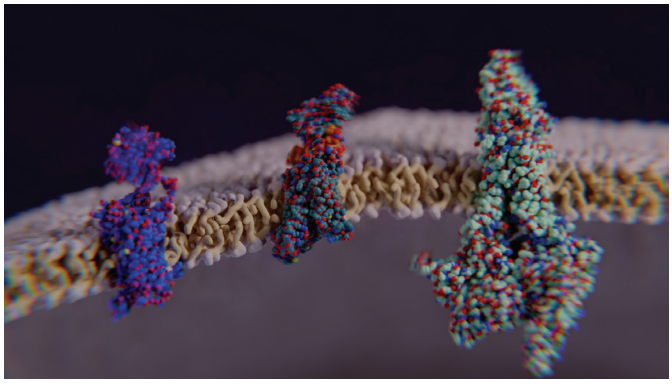

Figure 3. *Highlighting membrane proteins. Created in Blender3D. Frame of an animation, using the MolecularNodes addon. Animation available on YouTube.*

Thanks for reading this article. Feel free to reach out if you have any questions or are looking for some feedback.

Dr Sarah Piper is a postdoctoral researcher in the Drug Discovery Biology Theme at the Monash Institute of Pharmaceutical Sciences, Monash University, and the ARC Centre for Cryo-electron Microscopy of Membrane Proteins.
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Sydney Protein Group: an ASBMB Special Interest Group

sydney protein group

Sydney Protein Group: fostering excellence in protein science research

In the realm of scientific communities, the Sydney Protein Group (SPG) stands as a stalwart, bringing together a diverse assembly of scientists and students from academia, research institutions, hospitals and industry. Their shared passion for protein science research has been the driving force behind SPG's endeavours since its establishment in the 1980s. With an unwavering commitment to promoting protein science and fostering inclusivity, SPG provides a vital platform for budding protein researchers and scientists at various stages of their careers.

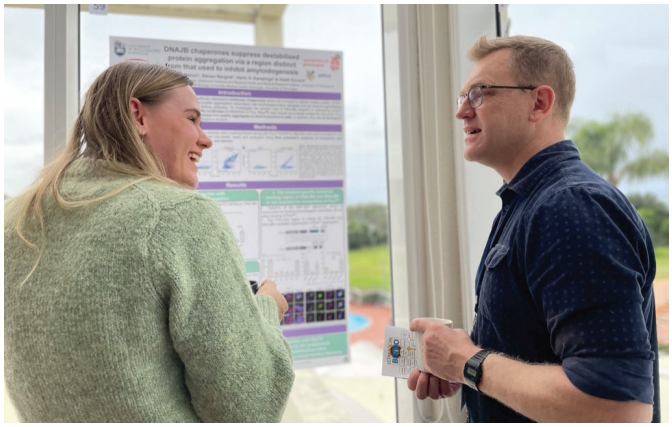
One of SPG's primary objectives is nurturing the growth of students and early- to mid-career researchers (EMCRs) in the field of protein science. SPG firmly believes in the power of knowledge sharing and interaction. As such, the group orchestrates several events throughout the year, providing opportunities for individuals to connect, discuss and present their research.

EVENTS THAT SHAPED THE PROTEIN SCIENCE LANDSCAPE 2022–2023

East Coast Protein Meeting

In light of the global pandemic, the majority of SPG events had been shifted online. Despite the successful transition, there was a growing demand for in-person meetings, culminating in the eagerly awaited East Coast Protein meeting in July 2022, the first since 2020.

The East Coast Protein Meeting, held in picturesque Coffs Harbour, is alternately organised by the Sydney and Queensland Protein Groups every two years. It was the SPG's turn to organise the July 2022 meeting.



Poster session at the 2022 East Coast Protein Meeting.

Prize-winners at the 2022 East Coast Protein Meeting, from left: Nikhil Varghese, Emily Furlong, Dylan Harney, Yan Li, Michael Healy, Yanni Chin and Derrick Lau.

After a rocky start with cyclone-like conditions sending several planes back to Sydney and disrupting a number of allocated talks, the meeting attendees settled into an amazing showcase of science. The meeting attracted over 110 enthusiastic registrants who experienced two compelling plenaries, an insightful industry talk, 34 EMCR presentations and more than 40 poster presentations. A huge thanks goes to SPG past President, Tara Christie, who did a large share of the organisation of this meeting.

Prizes were awarded for the best student talk (Dylan Harney) and runner-up (Carl McCombe), best postdoc talk (Emily Furlong), best student posters (Yan Li and Nikhil Varghese), best open category poster (Yanni Chin), the SPG ComBio Award (Derrick Lau), the QPG ComBio Award (Michael Healy) and Social Bingo prize (Forhad Saikot).

Thompson Prize

A prestigious honour in the field of protein science in NSW is the award of the SPG Thompson Prize. This award is named after Professor Ted Thompson – a pioneer of molecular biology who worked with Fred Sanger on the sequencing of insulin and was a professor at UNSW for many years. Ted was a strong supporter of young researchers and of the Sydney Protein Group. In 2022, the SPG Thompson Prize event was hosted in-person at Western Sydney University's Parramatta South Campus in November, organised by Liza Cubeddu and Roland Gamsjaeger.

The Thompson Prize is awarded to the best scientific presentation by an Early Career Scientist. Five speakers, Hudson Coates (UNSW), Jason Johansen-Leete (University of Sydney), Serene El-Kamand (Western Sydney University), Julian van Gerwen (University of Sydney) and Kelsey Whinn (University of Wollongong), were selected from submitted abstracts and presented their work in a short talk format. Hudson Coates was the

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successful awardee who delivered a beautiful story of a truncated form of squalene monooxygenase and its role in cholesterol synthesis. His talk encompassed suspense, the motivation and explanation of the methods he used, followed by results that made his findings very easy to follow and their overall significance obvious. All finalists were applauded for their exceptional presentations.

Thompson Prize winner Hudson Coates (left) with Liza Cubeddu.

Awards for supporting early career scientists to attend conferences were bestowed upon Gayatri Mani and Mohammad Pourhassan Moghaddam (Lorne Travel Awards), and Madeline McRae (Greg Ralston Award).

SPG Annual General Meeting

The AGM, held concurrently with the Thompson Prize event, witnessed pivotal developments within SPG's leadership. The meeting resulted in changes to the SPG Constitution, renaming the role of Webmaster to Communications Officer. Three of our long-service officers, Jason Low (Secretary), Ben Crossett (Treasurer) and Alastair Stewart (Webmaster) stepped down, making way for fresh faces. Derrick Lau assumed the role of Secretary, Mark Larance as Treasurer and Taylor Szyszka as Communications Officer.

SPG Postdoc Symposium

Held at UNSW in May 2023, the SPG Postdoc Symposium brought together early-career scientists to listen to science from their peers and network afterwards. Five speakers were selected from submitted abstracts – Conall McGuiness (University of Wollongong), Stefan Mueller (University of Wollongong), Yan Jiang (University of Sydney), Dylan Harney (University of Sydney) and Tahnee McEwan (University of Wollongong).

Each person delivered a 15-minute scientific presentation. Connall McGuiness (first prize) and Stefan Mueller (highly commended) were recognised for their outstanding contributions with cash prizes however, the judges noted that all presenters were of outstanding quality.

ASBMB Speaker Prize Competition

The ASBMB speaker prize is aimed at ECRs to support their attendance, and present their work at the ASBMB conference. The prize consists of the registration for the ASBMB meeting and a speaking slot in the program. In August 2023, Hannah Brown, a PhD student from University of Technology Sydney, earned the opportunity to showcase her scientific communication skills at the 2023 meeting of the ASBMB in Canberra.

Looking forward

The SPG's commitment to advancing protein science remains unwavering. With a calendar of seminars, travel awards and networking opportunities, SPG is dedicated to nurturing the next generation of protein scientists and furthering the field. For those interested in learning more about SPG, its initiatives, and upcoming events, please visit our website or reach out for further information.

Kate Michie, President, Sydney Protein Group
www.asbmb.org.au/sydney-protein-group
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2023 SPG Postdoc Symposium speakers, from left: Tahnee McEwan, Conall McGuiness, Stefan Mueller, Yan Jiang and Dylan Harney.

2023 SPG Postdoc Symposium prize-winners Conall McGuiness (left) and Stefan Mueller with Kate Michie.

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.

Swapping Research for Regulations

Amanda Highet, Senior Research Compliance Officer, University of Adelaide

I graduated from the University of South Australia in 2006 with First Class Honours in Laboratory Medicine, followed by a PhD at the University of Adelaide in 2009, and an NHMRC Early Career Fellowship from 2011–2016 at the Robinson Research Institute. While I managed to get through my postgraduate study and early career with some success, competition for mid-career fellowships was intense, and after returning to work half-time in 2014 after 12 months of parental leave, I no longer felt confident to compete at the necessary level. My priorities had changed, and I just wanted a job where I could still be involved in scientific research, but with more stability and not needing to apply for a grant funded salary. It was an easy decision for me, as I felt like I had achieved a lot since finishing my degree and it was the right time to change course. However, I did find it difficult telling my supervisor and co-workers who had invested so much time and funding into developing my career that I wanted to leave and pursue something else.

Amanda Highet.

Once I decided to leave academia, I started getting in touch with people who had previously left research in my department and moved into research support roles. It turned out that I was asking around in the right place, at the right time, because there was a vacancy for a compliance officer that needed to be filled straight away. At the end of 2016, I relinquished the remainder of my fellowship and commenced a position as Research Compliance Officer (Gene Technology) in the Research Services Branch of the University of Adelaide. The role has changed over time, with the coming and going of new rules and regulations, but I am essentially in the same position today as a Senior Research Compliance Officer. I assist researchers with preparing applications to seek approval to work with genetically modified organisms (GMOs) and goods subject to biosecurity control. I oversee compliance of the university's physical containment facilities and liaise with external regulators that enforce the gene technology and biosecurity legislation. I am the Secretary of the university's Institutional Biosafety Committee, which provides expert advice to researchers on gene technology matters and assesses and approves low-risk GMO dealings.

The most useful skill transferred from my research career is problem solving, because regulation of biological organisms and rapidly advancing technologies is rarely straightforward and can lead to complex scenarios. Another great skill that comes from research experience is the ability to understand technical information and review the literature to support decision making. And of course, a good understanding of how a laboratory operates, and how to fit compliance responsibilities into the busy lives of researchers, is also helpful. I am involved in a vast range of research areas and enjoy meeting researchers and learning about their areas of expertise. In my research life, my work became more and more focused until I specialised in one very specific (and very important) placental cell population. When I started working in compliance, it reopened a wide world of biology – plants, animals, insects, fish, viruses, bacteria. University research compliance covers a large range of disciplines, so there is never a dull moment.

Quite a few scientists have said to me that they could never see themselves working in an office job. And when I first started studying science, I certainly had that attitude too. However, as a compliance officer, I venture out of the office frequently to inspect facilities across multiple campuses and meet with researchers, containment facility managers and regulators. Some weeks, it's nice to have some quiet days sitting at my desk catching up on paperwork. I work with a fantastic team of dedicated and caring people and feel very fortunate to have a job that I enjoy doing. I would encourage others who are looking to leave academia to consider how they could use their knowledge and skills to support research in other ways.

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Microbiota with Macro Potential – Patent Protection for Microbiome-related Technologies

Dr Harriet Manley (Patent Scientist), Dr Alex Wong (Patent Scientist) and Dr Sarah Hennebry (Associate Principal) from FPA Patent Attorneys discuss the considerations for patent protection around microbiome-related technologies.

From left: Harriet Manley, Alex Wong and Sarah Hennebry.

Introduction

Human cells are vastly outnumbered in the human body, with 70–90% of cells being bacteria or fungi. This mind-boggling statistic could be considered gross, but from a more optimistic and scientific perspective, this microbial ecosystem represents extraordinary technological potential.

Also known as the body's natural flora, the human microbiome includes the commensal microbes that inhabit the intestines, stomach, skin, mouth, lungs, nose, and genitalia – representing over 100 trillion cells. The dynamic interplay between commensal microorganisms and their human host has a crucial influence on numerous developmental and physiological processes.

Disruption of the microbiome (dysbiosis) can occur where opportunistic pathogens 'overgrow' to cause infections (e.g. candidiasis, *C. difficile* colitis), or where certain commensal microbes are present in higher numbers than others, influencing metabolism and function leading to disease (e.g. inflammatory bowel disease, chronic fatigue, obesity).

With the development of high-throughput sequencing techniques, single-cell omics, gene editing systems, artificial intelligence (AI) and machine learning, our capacity to understand and modulate the microbiome is better than ever. From an improved understanding, comes innovation. This article discusses considerations for patent protection around microbiome-related technologies.

Themes in microbiota technology

From knowledge of the microbiome, three important categories of compositions can be developed:

1. **Prebiotics:** supplements or products that act to stimulate the growth and/or activity of specific normal flora (e.g. non-digestible fibre in food, prebiotics in skin cream).
2. **Probiotics:** compositions comprising live microbes that act to modify the microbiome by influencing the microbial populations that make up the microbiome, and/or inducing biological effects on the normal flora. Probiotics can be intended to maintain a healthy microbiome, or to treat a specific disease or disorder. Probiotics include 'synthetic probiotics', comprising recombinant microbes, and can be engineered to:
   - Produce molecules that enhance the growth or behaviour of commensal species
   - Promote homeostasis
   - Be anti-inflammatory
   - Affect neurological activity.
3. **Postbiotics:** compositions comprising non-viable microbial products that act to alter microbiome activity (e.g. quorum sensing molecules, microbial extracellular vesicles).

Additionally, some naturally occurring antioxidant compounds are implicated in regulating the microbiome. Antioxidants that support the production of anti-inflammatory metabolites by intestinal flora include curcumin from turmeric (1) and sulforaphane from broccoli (2).

Emerging applications

Food, drink and dietary supplements

Prebiotic and probiotic foods, drinks and supplements have been around for a while, and are here to stay. A common example is probiotic yoghurt, or yoghurt drinks such as Yakult®. These are typically developed using live, naturally-occurring *Lactobacillus* and *Bifidobacterium* species, but we anticipate that more synthetic probiotics will arise as research evolves regarding preferred bacterial compositions.

Microbiota with Macro Potential – Patent Protection for Microbiome-related Technologies

Medicine

As the human microbiome is intricately connected with the immune and nervous systems, it is no surprise that modulating the microbiome presents therapeutic opportunities across a vast range of diseases, including infections, autoimmune diseases, neurological disorders, and cancer. Here are snapshots of a few interesting therapeutic applications:

- **Neuropychological disorders.** A field of 'psychobiotics' is emerging to exploit gut microbiota activity in the 'gut–brain axis'. Probiotic therapies are being developed to treat various mental health disorders, including depression and anxiety. Microbial extracellular vesicles could also represent an avenue for delivery of therapeutics across the blood–brain barrier (3).
- **Cardiovascular disease (CAD).** Microbial metabolites in the gut, such as trimethylamine-N-oxide (TMAO), are associated with CAD. Other metabolites may play significant roles in promoting CAD, representing potential therapeutic targets (4).
- **Cancer.** Tumours can have their own microbiome within the tumour microenvironment, as commensal bacteria invade a growing tumour. A growing appreciation for the tumour microbiome, and the crosstalk between cancer and microbial cells, may contribute to new anti-cancer therapeutics (5,6).
- **Neonates.** Birth by Cesarean section (C-section) has been strongly linked to increased risk of the child developing infectious and chronic diseases. A leading hypothesis is that C-section impairs the transmission of natural microbiota from mother to child. Proposed methods to counter this include 'seeding' the neonate with a maternal vaginal microbiota, or maternal faecal microbiome transplantation (7).

Diagnostics

Microbial metabolites and/or population dynamics can be analysed to detect and classify disease e.g. obesity, heart disease, asthma. On-chip devices and organoids can also simulate microbiome environments *in vitro*, to provide preclinical models of disease, and potentially identify targets for microbe-modifying therapeutics.

For example, 'gut-on-a-chip' microfluidic devices can simulate the invasion of enterohemorrhagic *E. coli* into the intestinal epithelia after interacting with commensal gut microbes (8). A 'vagina-on-a-chip' microfluidic device has also been developed to diagnose bacterial vaginosis; where non-optimal, dysbiotic bacterial species are distinguished from optimal protective species by detecting increased pH and inflammatory cytokines (9).

Cosmeceuticals

In the cosmetics arena, there is significant buzz regarding microbiome-focused prebiotic and/or probiotic skincare products, which act without disrupting the body's natural skin microbiome to improve skin health and appearance.

What aspects of microbiome-related technologies may be eligible for patent protection?

The following aspects may represent opportunities for patenting in this technology space:

- Novel microbial strains
- Recombinant microbes
- Recombinant or isolated peptides, polypeptides, nucleic acids
- Probiotic or prebiotic compositions, components and mixtures
- Food, pharmaceutical or cosmeceutical applications
- Methods for:
  - Culturing microbes
  - Modifying microbes
  - Producing microbial proteins or compounds
  - Producing/formulating probiotic products comprising microbes
- Methods for diagnosing diseases/disorders based on microbiome characteristics
- Diagnostic devices
- Methods for treating diseases/disorders influenced by the microbiome

Patentable subject matter considerations

Patentable subject matter requirements are particularly relevant for many of the aspects listed above. As you may recall from our previous articles, to obtain a patent to an invention, the invention must be:

- Novel (new)
- Inventive (non-obvious)
- Supported and enabled, and
- Directed to subject matter that is legally eligible for patentability (in other words, meet patentable subject matter requirements).

Identifying patent-eligible subject matter early, and drafting the patent application accordingly, are important steps for improving the likelihood of obtaining commercially valuable patent protection.

Whilst patentable subject matter requirements differ across different countries, including the major jurisdictions of Europe and the US, here we provide a short summary of the issues that can arise.

Microbiota with Macro Potential – Patent Protection for Microbiome-related Technologies

Naturally-occurring substances (including cells, nucleic acids, proteins, peptides)

Particularly in the US, inventions directed to naturally-occurring substances can be challenging to protect. In some scenarios, it may be necessary to pursue patent claims directed to a recombinant or isolated cell, nucleic acid, protein etc, or claims directed to methods of using said substance in a novel and inventive way.

Methods of diagnosis

Similarly, observing naturally-occurring phenomena in a diagnostic method can encounter patentable subject matter issues. For example, measuring newly-identified microbial biomarkers or measuring the specific proportion of bacterial species in a sample, could represent steps which, on their own, are not patent-eligible methods. Strategies such as combining diagnostic steps with treatment steps, or obtaining claims directed to a diagnostic kit, can be used to address these difficulties.

Methods of medical treatment

Methods of medical treatment are eligible for patent protection in the US and Australia. However, most jurisdictions, including Europe, China and Japan, do not permit claims directed to treating a human being, or claims that involve a step performed on a human being (including obtaining a microbial sample). In these jurisdictions, claims need to be devised that define a novel and inventive use of a composition, without referring to active treatment steps. You patent attorney can advise you regarding suitable claims and limitations, if your invention involves a therapeutic treatment method.

Mixtures of known components

If the composition is a mere mixture of known components where the components are each behaving as per their inherent properties, or the method is a process producing such a composition by mere admixture, then it may not constitute patentable subject matter. This can sometimes be overcome by demonstrating an interrelationship between the elements in a mixture – for example, mixing two known bacterial strains demonstrates an unexpected synergistic effect.

Computer-implemented inventions

Big data bioinformatics may involve developing computer software, artificial intelligence, machine learning and/or algorithms. In several jurisdictions (including Australia), it can be very challenging to obtain protection for an invention that is a computer-implemented method. However, a computer-implemented method may be considered patentable if the method produces a significant tangible effect beyond the computer, and is not simply automating a manual method.

It may also be more appropriate to pursue method claims without specifying that the method is performed using a computer. For example, a claim may recite a method of calculating a value indicating the likelihood of a certain microbiome composition causing an infection, using a new algorithm. The value may be calculated more easily using a computer, but the computer is not a necessary feature to protect the idea.

Conclusion

- The many and varied applications for microbiome-related technologies present ample opportunity for innovation, and for generating IP associated with the innovation.
- Key areas in this space include therapeutics, diagnostics, food and cosmeceuticals.
- Assessing if subject matter is eligible for patent protection in different countries is a significant consideration for patenting in this technology area.
- Your patent attorney will be able to best advise you regarding the available strategies for obtaining patent protection for your invention.

References

1. Scazzocchio B, Minghetti L, D'Archivio M. *Nutrients* 2020;12(9):2499.
2. Marshall SA, Young RB, Lewis JM, Rutten EL, Gould J, Barlow CK, Giogha C, Marcelino VR, Fields N, Schittenhelm RB, Hartland EL, Scott NE, Forster SC, Gulliver EL. *J Funct Foods* 2023;107:105645.
3. Bleibel L, Dziomba S, Waleron KF, Kowalczyk E, Karbownik MS. *Front Microbiol* 2023;14:1211447.
4. Trøseid M, Andersen GØ, Broch K, Hov JR. *EBioMedicine* 2020;52:102649.
5. Chen X, Jin C, Facciabene A, Guo X, Zhang Y. *Front Immunol* 2022;13:897811.
6. Zhou X, Kandalai S, Hossain F, Zheng Q. *Front Oncol* 2022;12:9337407.
7. Fricke WF, Ravel J. *Microbiome* 2022;10:88.
8. Kim J, Hegde M, Jayaraman A. *Lab Chip* 2010; 10:43–50.
9. Mahajan G, Doherty E, To T, Sutherland A, Grant J, Junaid A, Gulati A, LoGrande N, Izadifar Z, Timilsina SS, Horváth V, Plebani R, France M, Hood-Pishchany I, Rakoff-Nahoum S, Kwon DS, Goyal G, Prantil-Baun R, Ravel J, Ingber DE. *Microbiome* 2022;10:201.

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2023 Prime Minister's Prize for Innovation

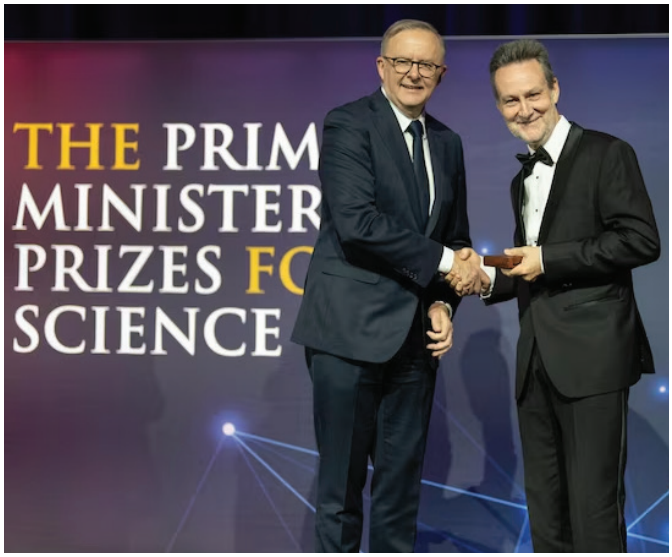
The ASBMB congratulates Professor Glenn King on being awarded the 2023 Prime Minister's Prize for Innovation. On 16 October 2023, seven 2023 Prime Minister's Prizes for Science recipients were recognised by the Prime Minister, the Hon Anthony Albanese MP, and Minister for Industry and Science, the Hon Ed Husic MP, at an event at Parliament House in Canberra.

Professor Glenn King works in the Institute for Molecular Bioscience at the University of Queensland. He was recognised for pioneering using peptides from Australian funnel-web spider venom for sustainable crop protection and potentially human therapeutics.

He first founded the company, Vestaron, which develops safe and eco-friendly insecticides for farmers. This instigated a revolution in crop protection, helping address global food challenges.

He is now the Chief Scientific Officer of Infensa Bioscience, which is developing spider venom therapeutics to help treat strokes and heart attacks. Infensa plans to start Australian-based clinical trials for heart-related therapeutics in 2024.

Professor King's research has impacts in Australia and abroad. Vestaron sells its insecticide products globally, while Infensa continues to create jobs and research opportunities for a new generation of scientists in Australia.



Glenn King receives the 2023 Prime Minister's Prize for Innovation from the Prime Minister of Australia, the Hon Anthony Albanese MP.

Below is a transcript of Glenn's interview with Robyn Williams on ABC Radio National's The Science Show on 11 November 2023.

Glenn King.

"Early on in my career I got interested in how we could protect crops in an environmentally sustainable way. So in the mid-1990s, we began to think about ways to protect crops from insect pests and we decided, why not turn to the best insect killers on the planet, spiders?

What we were searching for were molecules that would kill insects but were completely harmless to humans. Believe it or not, the answer was right here in our backyard. The best molecules were in the venom of the Australian funnel web spider.

In 2005, I founded a company called Vestaron to try and commercialise these discoveries. This Australian innovation is now having global impact with these insecticides around the world. Ten years of working on spider venom made us realise that the venoms had molecules for human therapeutics and that in turn led to the founding of Infensa Bioscience.

Thirty percent of all deaths every year are due to stroke or heart attack and yet we do not have a single drug to protect the brain or the heart. Remarkably, in the venom of an Australian funnel web spider we found a molecule that protects the brain after stroke, the heart after a heart attack, and helps us maintain the integrity of donor hearts for heart transplant.

Infensa plans to start clinical trials for heart attack next year and those clinical trials will be run in Australia. Infensa is truly an Australian story, it's an Australian innovation, it's funded by Australians, it's based in Australia, it's employing Australians, the benefits will feed back into the Australian economy.

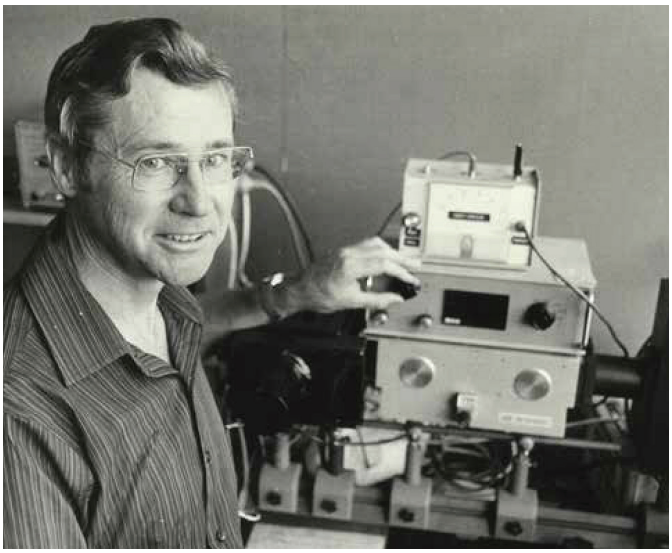
I'm incredibly humbled and honoured to have received the Prime Minister's Prize for Innovation. I hope this will inspire others to push boundaries."

In his acceptance speech, Glenn pronounced, "To those of you who try to create change, who try to push back boundaries, who dare to be different, there will always be naysayers. But remember that the naysayers are not the ones trying to change the world. Try to block out the noise, stay focussed on what you are trying to achieve, and prove them wrong."

In Memoriam

William Hugh Sawyer 1940–2023

William (Bill) Hugh Sawyer was a pioneering researcher in applications of fluorescence techniques to biomembrane biology. He was a former President and Honorary Member of the Australian Society for Biochemistry and Molecular Biology (ASBMB).



Bill with state-of-the-art fluorescence anisotropy equipment at the University of Melbourne.

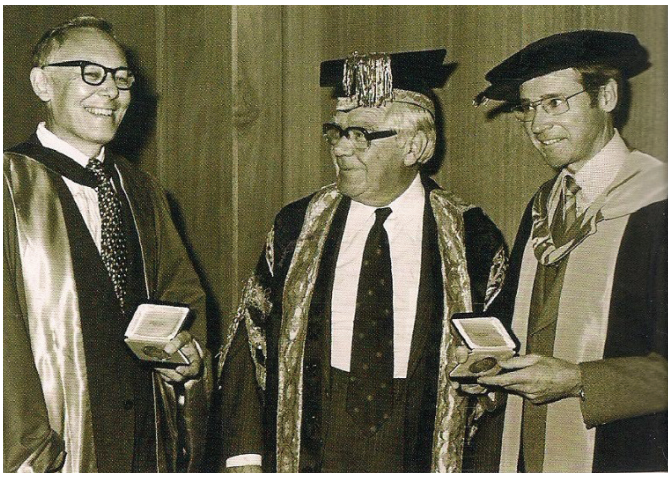
Bill was born in 1940 in Melbourne. His father, Harry, and mother, Hilda, operated the Box Hill Dairy, which instilled in Bill an interest in dairy technology and the science of milk proteins. He undertook an Agricultural Science (BAgrSc) degree at the University of Melbourne, graduating in 1961. As an undergraduate, he secured a scholarship in Dairy Research at CSIRO, where he worked on controlling the viscosity of casein solutions.

Following his interests, Bill travelled to the University of Minnesota for an MSc, where he worked with renowned dairy researcher, Robert Jenness. There, he investigated the formation of disulphide bonds between milk proteins and their role in milk gelling (1), graduating in 1962. He returned to Australia and undertook a PhD in Canberra with Hugh McKenzie at the Australian National University. Here, Bill honed his skills in protein biochemistry and biophysics, continuing his work on milk protein, including a paper in *Nature* on the effect of pH on β-lactoglobulins (2), and expanding to studies of the plant lectin, concanavalin A and bacterial proteins. In Canberra, Bill also met the charming and vivacious Diana Camm, whom he married in 1966. Bill then undertook postdoctoral studies at the Lister Institute of Preventative Medicine in London, working with Michael Creeth.

During these formative years, Bill discovered a deep interest in the structure and dynamics of proteins. He was passionate about applying new physical chemistry theory and biophysical techniques to probe molecular interactions and to understand the biophysical underpinning of protein behaviour and function. He initiated collaborations with Laurie Nichol and Don Winzor, and became convinced of the importance of analysing complex systems from first principles. Bill and Don later co-authored the definitive *Quantitative Characterization of Ligand Binding* (3), about which one reviewer wrote, “The book fills the void between rigorous theoretical discussions of ligand binding … and experimental recipes.”

When Bill was appointed Lecturer at the University of Melbourne in 1968, he took the opportunity to build on his research vision of applying fast reaction photophysics to important biological problems. He acquired, borrowed, or built the most advanced fluorescence and phosphorescence instrumentation available. Further, he developed a series of fluorescent excited state probes. These light-absorbing and emitting chemical envoys were designed to attach to lipids and proteins in membranes to report on the molecular microenvironment and membrane dynamics. Bill was particularly excited about fluorescence anisotropy. When polarised light hits a group of randomly oriented fluorophores, those with dipoles oriented in the same direction are preferentially excited, providing a powerful tool for monitoring the dynamics of biomolecules. In these excited state adventures, the thing that really set Bill apart from other colleagues was his rigorously quantitative approach.

Bill made a remarkable and sustained contribution to our understanding of biological membranes, and the techniques he pioneered have been used by many researchers to interrogate different disease states. His contributions were recognised by the award of the prestigious David Syme Research Prize in 1980.

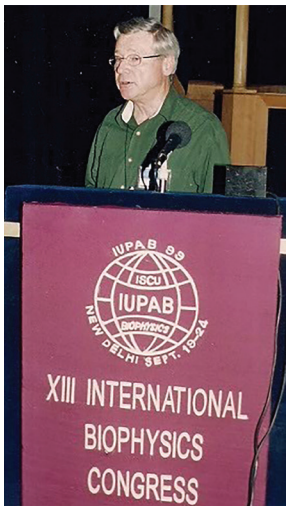


Bill (right) receives the David Syme Research Prize in 1980. Le Roy Henderson (left), Department of Mechanical Engineering, University of Sydney, jointly receives this prize.

In Memoriam

I had the great privilege of working with Bill on the development of fatty acid probes for the assessment of the fluidity gradient of lipid bilayers (4) and the application of phosphorescence anisotropy to studies of lipoprotein receptors (5). His passion for all things fluorescent was contagious and shaped my research vision.

Bill was also innovative in his approach to the teaching of biochemistry, being the first to introduce computer-based exercises at the University of Melbourne. I well remember his third year Biophysical Biochemistry lectures delivered at the uncivilised hour of 8am. It's a good thing he made biophysics so interesting! We students affectionately referred to Bill as Dr Soya (Sawyer)-Bean. I don't think he ever knew, but I am sure he wouldn't have minded. His love of academic life is captured in this quote from Bill, "As research and teaching academics, we are exposed to great minds, and become members of the most exclusive club in the world. Add these intangible assets to the intellectual satisfactions, and you have, I believe, an exceedingly attractive career." Bill's academic contributions were recognised by his promotion to a Personal Professorial Chair in Biochemistry in 1991, and by the award of the title Professor Emeritus from the University of Melbourne in 2001.



Bill presents his work at the 13th International Biophysics Congress, New Delhi, India, 1999.

Later in his academic career, Bill became interested in the translation of biochemistry research outcomes, and completed a Graduate Diploma in Intellectual Property Law. He then served as a member of the university's Patents and Intellectual Property Committees and was appointed a non-executive Director of Rothschild Bioscience Managers Limited, a venture capital trust for the promotion of innovation in science and technology (6).

Bill was an untiring supporter of the scientific community in Australia. He was President of the Australian Society for Biophysics from 1986 to 1988. He served with distinction as President of the ASBMB. During his Presidency (1990–1992), Bill established

Bill (front, third from right) at 16th FAOBMB Symposium, Taipei, Taiwan, 2002.

the Special Interest Groups (SIGs) to organise local meetings on specialist topics and to have input into the programs for the annual Society meetings. In 1990, he and outgoing President, Bruce Stone, presided over the change of name of the Society from the Australian Biochemistry Society to the Australian Society for Biochemistry and Molecular Biology. I remember Bill and Bruce chartering a small private plane in the middle of the pilots' strike to take dedicated colleagues to the ComBio1990 meeting on the Gold Coast. The pilot was kept waiting on the return trip as one of the longest and most fiercely fought Society meetings played out until they wore down everyone, and the name change was accepted. In recognition of his impactful contributions, Bill was awarded Honorary membership of the Society in 1999.

Bill also served as President (1999–2001) of the Federation of Asian and Oceanian Biochemists and Biologists (FAOBMB), which currently has twenty Constituent Members, representing more than 20,000 active scientists (7). Bill was passionate about promoting the science of Biochemistry in the region (8). He fought

Bill (front, far right) with ABS/ASBMB Presidents at the Society's Golden Jubilee celebration at ComBio2005.

hard to try to save the FAOBMB journal, *Journal of Biochemistry, Molecular Biology and Biophysics*, which he saw as instrumental in helping young scientists from the less affluent countries. He also arranged for the ASBMB community to donate biochemistry textbooks to be distributed to other member countries.

In 2001 and 2002, Bill took on a position as an Executive Director of the Australian Research Council (ARC). The Government had recently doubled the funding for the ARC, and Bill had responsibility for overseeing the assessment of all grant applications in Biological Science and Biotechnology, as well as helping to improve the assessment system and institute new programs such as Federation Fellowships and Centres of Excellence.

Bill's time at the ARC made him acutely aware of the difficulties faced by Early Career Researchers (ECRs). From 2004 to 2014, he co-convened workshops to up-skill ECRs. In 2013, with Bill's support, the Department of Biochemistry and Molecular Biology at the University of Melbourne established Bill Sawyer Awards for excellence in the PhD program.

From left: Bill, 2018 Bill Sawyer Award recipient, Jess Bridgford, and Leann Tilley.

Upon his retirement, Bill pursued other passions: carpentry, viticulture and winemaking. He was a keen sailor and rower and hand-built a very beautiful rowing scull. His winery, Wyuna Park, on Victoria's Bellarine Peninsula, specialised in pinot noir and pinot gris wines, including an innovative and award-winning fortified pinot noir. Bill's life was a true partnership with his wife Diana, and he was the very loving and proud father of their two sons, Christopher and Philip.

I benefited directly from Bill's wise guidance, his endless patience and his deep knowledge of scientific principles. I witnessed first-hand the pioneering technologies and scientific rigour that led to his being widely recognised as a world leader in fluorescence-based studies of proteins and membranes. But what particularly impressed me, and many other colleagues, was his gentle nature and the bubbling 'excited state' of ideas that underpinned his quiet determination. It is a great privilege to have had Bill as a mentor and as a friend. Not only was he an innovative and creative scientist, but also one of life's true gentlemen.

References

1. Sawyer WH, Coulter ST, Jenness R. *J Dairy Sci* 1963;46:564-565.
2. McKenzie HA, Sawyer WH. *Nature* 1967;214:1101–1104.
3. Winzor DJ, Sawyer WH. *Quantitative Characterization of Ligand Binding*. 1995, Wiley.
4. Tilley L, Thulborn KR, Sawyer WH. *J Biol Chem* 1979;254:2592–2594.
5. Tilley L, Sawyer WH, Morrison JR, Fidge NH. *J Biol Chem* 1988;263:17541–17547.
6. Flesch J. *Transforming Biology: A History of the Department of Biochemistry and Molecular Biology at the University of Melbourne.* 2015, Melbourne University Publishing.
7. Nagley P, Svasti J, Kikuchi A. *IUBMB Life* 2022; 74:1126–1168.
8. Svasti J, Sawyer WH. *IUBMB Life* 2008;58:280–282.

Leann Tilley
Department of Biochemistry and Pharmacology
University of Melbourne

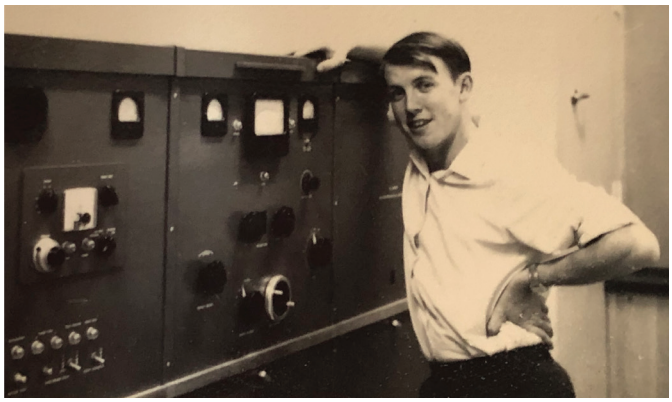
Bill loved the water and was a keen sailor. In retirement, he hand-crafted his own boat – a rowing skull.

In Memoriam

Geoffrey John Howlett 1947–2023

Geoff Howlett had a distinguished career as a physical biochemist. During his career, he made major contributions to understanding protein structure and function, particularly in relation to amyloid formation.

Geoff was born in 1947 in Moe, Victoria. His father was a bank accountant, and his family (parents and five children) moved around regional Victoria every three or four years. Geoff attended three country high schools (Camperdown, Hamilton and Euroa) and completed Year 12 at Melbourne High School. He then went to the University of Melbourne, where he completed a Bachelor of Science (Honours) in Biochemistry in 1969 and a PhD in 1972. His project was on the sedimentation equilibrium of lysozyme and was supervised by Laurie Nichol and Bill Sawyer. During the final year of his PhD, Laurie Nichol accepted a chair in Physical Biochemistry at the John Curtin School at the Australian National University. Geoff spent two years in Canberra, completing his PhD and as a postdoctoral fellow.



Geoff with the Model E analytical ultracentrifuge, 1969.

This experience laid the foundation for Geoff's interest in using analytical ultracentrifugation to analyse interacting macromolecules. At that time, the only instrument available to carry out this approach was the Beckman Model E analytical ultracentrifuge, which was about the size of three fridges next to each other. It was developed after the Second World War and was based on jet engine design and capable of very high rotational speeds (up to 60,000 rpm). Geoff further advanced his knowledge of this technology during his postdoctoral research with Howard Shachman at the University of California Berkeley from 1973–76, where he studied changes in the structure of the highly regulated 12-subunit enzyme, aspartate transcarbamylase, which catalyses the first committed step in pyrimidine biosynthesis.

Geoff returned to Australia in 1976 for a research fellowship at La Trobe University, and in 1979, he was appointed as lecturer in the Department of Biochemistry at the University of Melbourne, where he remained until his retirement in 2013, and subsequently as an Honorary member of the department. In the 1980s, given that few biochemistry departments had the space or interest to house a Model E ultracentrifuge, Geoff turned his attention to learning techniques in molecular biology, a field that was beginning to take off in the US, but was still nascent in Australia. In 1982, he spent a sabbatical in the Biochemistry Department at Stanford University with George Stark, where he developed bacteriophage rat cDNA libraries – not a trivial feat at the time. He brought these libraries back to Melbourne and distributed them to whoever asked him without requesting co-authorship, a testament to his generosity. In collaboration with Gerhard Schreiber and their PhD students, he cloned various serum proteins, including apolipoproteins, that carry lipids in the bloodstream.

His interest in ultracentrifugation was rekindled during a sabbatical at the NIH in Washington, USA, with Allen Minton, where he had access to a new, more compact, and easier-to-use analytical ultracentrifuge, the Beckman ProteomeLab XL-A. The international ultracentrifugation community was very excited about this equipment, and his department acquired one of the first in Australia. With widespread interest in this new model, Geoff developed many collaborations with colleagues analysing the molecular masses and heterogeneity of proteins and protein complexes. He became one of the world's leading exponents of this technology and its ability to provide key information about protein structure and function.

He co-founded a group, Reversible Associations in Structural and Molecular Biology (RASMB), that focused on analytical ultracentrifuges, and he hosted a very successful meeting of the group in Melbourne in 1994. He then began to study the structure of lipoproteins and how the protein components formed amyloids, aggregates of misfolded fibrillar structure. Geoff pioneered studies using the analytical ultracentrifuge to understand the heterogeneity of fibril sizes and their formation kinetics. This research on amyloid sustained his career until his retirement in 2013.

Geoff (front, sixth from left) at the second Lorne Protein Conference on Protein Structure and Function, 1977.

In Memoriam

Geoff Howlett.

Geoff undertook several sabbatical visits to outstanding scholars in the UK and the US during his career. Such trips reflected his international perspective on research – building networks with leading thinkers in the field. Geoff attended the second Lorne Protein Conference in 1977 and became enamored with the scope and quality of the meeting. He then attended 35 annual meetings in a row and played key roles on the Organising Committee between 1980 and 2010. Geoff was a member of the ABS/ASBMB for many years. He inspired bright thinkers in his laboratory. His legacy is in the people he trained and the ethos of his trainees. He inspired bright thinkers in his laboratory. Many of his former PhD students or postdocs have gone on to their distinguished careers, including Cait MacPhee, Mike Griffin, Matt Perugini, Ben Atcliffe, Danny Hatters, Cameron Stewart, Chris MacRaild, Leanne Wilson, Chi Pham, Yee-Foong Mok, Tim Ryan, Menachem Gunzberg and Katrina Binger.

Geoff is survived by his wife, Barbara, and daughters, Lisa and Melanie, as well as four grandchildren.

Danny Hatters
Department of Biochemistry and Pharmacology
University of Melbourne
Barbara Howlett
School of BioSciences
University of Melbourne

Competition: RWDCORSSO

Presenting the latest competition for members of the ASBMB. Unscramble the crossword clues, then unscramble the shaded letters to find the mystery word. Submit your solution to the Editorial Officer by 29 January 2024 to enter the draw to receive a gift voucher. With thanks to Joe Kaczmarski.

DOWN

1. epteipt
2. ehem
3. ropin
4. slakf
6. ogvesl
8. nntaltoirsa
10. ocntssdeoyi
11. rliva
13. oatm
14. tnvoels
15. shdiinite
16. sasya
17. tcarihomn
21. iorosbem
22. pdlii
23. ronisecet
26. haeacar
27. rncooeminbita
28. lecl
29. lompayrese
32. efnnmotteiar
33. hsoeyitsbsni
34. erstionon
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ACROSS

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20. ufecersleonc
23. isbtiustoutn
24. opaisstop
25. nlgaid
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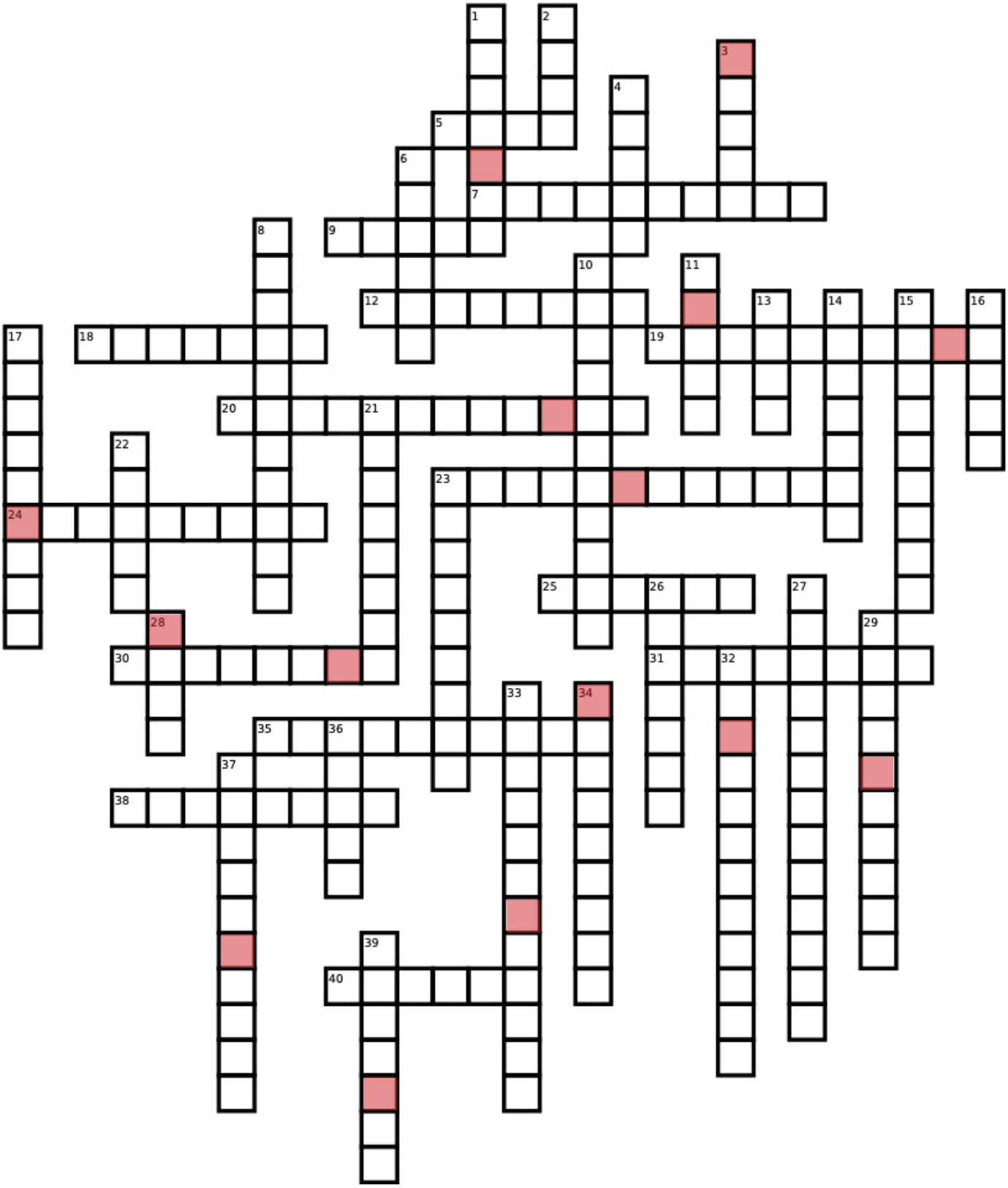

My Story for LGBTQIA+ Visibility in the Life Sciences

I grew up in rural southeastern Australia, which is an area of stunning natural beauty. Our house was set in natural bushland with lots of space to ride motor bikes and go exploring. I was fortunate to have parents who instilled in me a sense of discovery and of nature.

I was fascinated by the natural life-forms around me – especially the things I could get up close to. I caught small bugs and critters with my net to keep in an aquarium. In the nearby creek, I found fossils of small crustaceans and ferns that got me interested in evolution. I became obsessed with the ideas of continental drift and the ancient supercontinent of Gondwanaland. I was one of those kids who had every type of pet – guinea pigs, mice, aquarium fish, frogs, chickens – and I had my own little rainforest-themed garden. I was always interested in the science of biology, and I was good at school.

These were the key factors that gave me direction, and I ended up a professor in biochemistry.

An integral part of me, as of everyone, is my sexuality. I knew I was gay at a young age – probably around 11 or so, but it is hard to pin down the exact time I put two and two together. The world was blatantly homophobic back in the mid-1980s to early '90s – it was the peak of the AIDS epidemic – but I was always sure that the way I felt was fundamentally normal despite a culture that pushed other ideas.

I was confronted from a very young age with the reality that the default templates for how to live life did not fit me. I was expected to marry a woman and have kids. And though my parents, friends and teachers were kind and sympathetic, they lacked firsthand experience of being gay, so even if they'd known, they couldn't have provided me with alternatives.

For me, being gay was, as it probably was then for most gay teenagers, something to be kept totally secret. I knew no one who was openly gay. I lived in a rural region before the internet and with no gay support groups I knew of. Prevailing attitudes portrayed LGBTQIA+ people as nonexistent, sick or to be mocked. I was on my own, trying to imagine what my life might be like ahead.

Grappling with this isolation dominated my mind during my teenage years. By the age of 15, I no longer could stay silent, so I found the courage to talk to two people at school I trusted: a friend and a teacher. They encouraged me to come out to my parents. That was the hardest thing I have ever done in my life. Thankfully, those people at school and my parents were wonderful. Coming out was a big deal, but it didn't change the fundamental issue of being on my own trying to learn about how to live my life.

After I finished school, I finally was in a position to begin to learn how to live as a gay man. Attending university meant moving to a big city where, for the first time, I met other LGBTQIA+ people.

During orientation week of 1993 at the University of Melbourne, I sought out the GaySoc society's stall and encountered a group of enthusiastic students. I remember Bronski Beat was playing on a portable stereo in the background. I was so nervous to approach the stall, but the three people I talked to, Cameron, Marina and Damien, were just so warm and welcoming. They invited me to attend the regular lunchtime discussion groups they ran at the student union. It was the beginning of a new world, and it is no exaggeration to say I was like a kid in a candy shop from that moment on.

Danny Hatters.

Lacking a template for living meant I had unbridled freedom to explore. I believe this freedom is a special privilege of our LGBTQIA+ community, but it took me more than a decade to work out how to harness it to be able to live my most rich and rewarding life. With so much choice, combined with my inexperience and a lack of role models, I didn't know how to build meaningful connections beyond the shared experience of sexuality. I also felt a disconnect between what the gay world offered and my own personal interests – such as becoming a scientist.

In the academic world of biomedical sciences, we are lucky to work with educated and enlightened colleagues who generally have no problems with LGBTQIA+ people. But the lack of visible LGBTQIA+ scientist role models left me feeling alienated and fueled imposter syndrome during my graduate student and postdoc years.

The institute where I did my postdoc often hosted esteemed visiting scientists for seminars, and these visits included a lunch or dinner where postdocs could meet the guests in an informal setting. The institute worked hard to provide a diverse program of visitors,

My Story for LGBTQIA+ Visibility in the Life Sciences

including many women and scientists from ethnic minority groups. The informal meetings led to fascinating discussions about many topics, especially personal perspectives on lives and careers. It was actually a very good program. But never were any of the guests openly LGBTQIA+.

People sometimes ask why sexuality matters in the context of life science research, considering our research is about testing hypotheses that generally are unconnected to the researchers' sexuality. My answer is that it doesn't matter at the direct level the questioner asks – but the lived experience of being gay creates a deeper imprint on self-identity that permeates all aspects of a person's life, including their work life. Social discussions with colleagues occur through the prism of heterosexual assumptions as people talk about their wives or husbands or kids. Such small things form the social bonds that are important in networking and in career discussions about work–life balance. If I do bring up my partner in social discussions – even just very casually – the fact that my partner is male too often becomes the point of the discussion. Sometimes I am OK with that, but other times it is kind of tedious and can make me reluctant even to bring up the gender of my partner.

I am not setting a gay agenda by being assertive about this – indeed, I am uncomfortable about having to assert my sexuality anywhere, because it is a very personal thing. Rather, I am asking non-LGBTQIA+ people to think about the assumptions they might be making on topics they normally might not need to think too hard about. For example, assuming that a person they meet for the first time will have a partner of the opposite sex when asking social questions sets up barriers for people who are gay.

When an institution is establishing policies and a scope of inclusion is relevant, a well-intentioned inclusion policy that leaves out a minority group (either in wording or by action) can make the feeling of exclusion worse than if there were no policy at all. I have felt that many times in my life.

In my younger years, particularly in my early 20s to early 30s, I would have felt more comfortable and more a part of the scientific community if I had known more about others like me. My personal development would have benefited from having role models who shared my experience and whose example resonated with the whole of me – particularly LGBTQIA+ scientists who had successful careers and were inspiring and confident in their own skin without needing to be in the closet. Sure, I knew great gay people in the LGBTQIA+ community, and I knew great scientists – but I felt those two realms were generally parallel worlds. I know they shouldn't be and are not really. I hope to provide a beacon to others who hunger for role models.

The world has become so much better in so many ways for the LGBTQIA+ community over the last two decades. I am writing this as Australia is abuzz with WorldPride celebrations in Sydney. The world definitely has come a long way, especially in the last decade. But we still can work to create beacons of visibility that showcase a wide variety of people who are scientists – this is relatively easy to do if you put yourself out there. The sexuality of many LGBTQIA+ people is invisible unless they put their hands up.

And thus, here I am – a full professor running a lab on the mechanisms of neurodegeneration. This is my story for visibility.

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Australian Society for Biochemistry and Molecular Biology Inc
PUBLICATION SCHEDULE FOR *AUSTRALIAN BIOCHEMIST*, volume 55, 2024

Issue	ASBMB Content	Copy Deadline	Issue Date
April 2024 55(1)	Profiles of medal, award and fellowship winners Nominations for Executive/Council	Monday 5 February	Tuesday 2 April
August 2024 55(2)	Nominations for medals, awards and fellowships Notice of AGM/proposed constitutional changes	Monday 3 June	Monday 29 July
December 2024 55(3)	Annual reports ASBMB meeting report	Monday 7 October	Monday 2 December

News from the States

Australian Capital Territory

Contributed by Christina Spry

Canberra Protein Group

The Canberra Protein Group (CPG), chaired by Dr Megan Outram (CSIRO), hosted several events over the year, including meetings on Alphafold, High-throughput Methods, as well as Protein Engineering and Tools. All sessions were well attended by students and staff from across the ANU campus and CSIRO. The highlight of the year was the EMCR Showcase held in July where four early career researchers were selected from abstracts to present a 15-minute talk for an opportunity to represent the CPG at ASBMB2023. The Showcase also included five-minute flash talks and poster presentations. Lani Davies (Nitsche Group, Research School of Chemistry, ANU) was awarded the ASBMB2023 speaking slot. Ciara Wallis (Corry lab, Research School of Biology, ANU) took away the People's Choice Prize for her five-minute flash talk and Elaine Tao (also Corry lab) was awarded the Poster Prize.

The Australian Biochemistry Lunch Seminar Series

The Australian Biochemistry Lunch Seminar Series, initiated by Professor Thomas Huber (Research School of Chemistry, ANU) and now coordinated by the CPG, continued over the summer of 2022–2023. This series, entitled Making Futures, featured the work of outstanding EMCRs planning to submit fellowship applications in the field of biochemistry. Nineteen speakers from across Australia shared their research in weekly Zoom seminars. A list of past speakers, and recordings of past presentations, can be accessed here.

ANU ASBMB Awardees

The 2022 ANU ASBMB Prize for the ANU undergraduate student who achieves the two highest average marks in three of four courses with a biochemistry and/or molecular biology focus, was awarded to Riley Furbank.

Canberra Protein Group EMCR Showcase awardees, from left: Elaine Tao, Sancia Gracias (Beckman Coulter), Ciara Wallis and Lani Davies.

ASBMB2023 Conference

The ASBMB2023 organising team, Professor Colin Jackson (Chair), Dr Christina Spry (Co-Chair), Associate Professor Kate Quinlan and Dr Xiaoxiao Zhang (Treasurers), Dr Emily Furlong (Program Organiser), Dr Joe Kaczmarski (Trade Organiser), Associate Professor Tracey Kuit (Education), Dr Rebecca Frkic (Social Media), Dr Simon Williams (Venue and Catering), Dr Joe Brock (Website and Registration), Dr Kai Chan (EMCR Representative – Biology), Associate Professor Christoph Nitsche (EMCR Representative – Chemistry), Zaka Yuen (Social and EMCR Representative – Medical), worked hard to put together a stellar conference.

New South Wales

Contributed by Laura Sharpe

I am pleased to report on the activities and awards that were sponsored by ASBMB NSW this year. We continue to reward our excellent undergraduate and high school students across NSW.

Charles Sturt University – ASBMB Biochemistry Prize

This was awarded to Christopher Colla for outstanding results in Biochemistry subjects at Charles Sturt University.

University of Newcastle – ASBMB Prize for Biomedical Science

This was awarded to Georgia Cook as the student with the best overall performance in the Bachelor of Biomedical Science program at the University of Newcastle.

NSW Science Teachers Association Young Scientist Awards

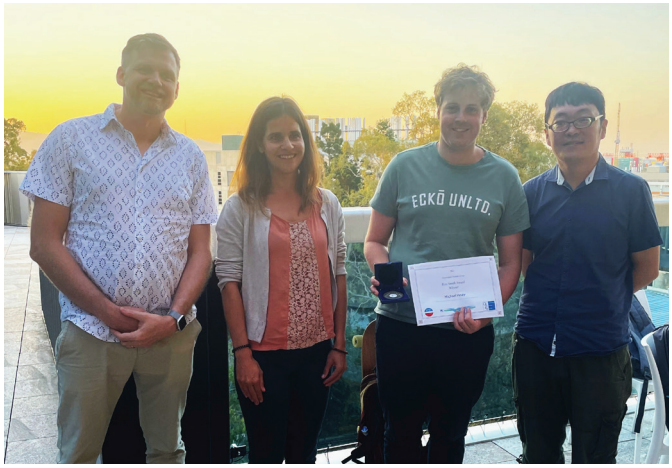
ASBMB NSW has sponsored this award for several years. The ASBMB Award is given for the best high school student project with a biochemistry or molecular biology theme. Our involvement in schemes like this helps encourage our future scientific stars and ignite their passion for research.

Queensland

Contributed by Michael Landsberg

ASBMB Queensland has continued to support biochemistry and molecular biology outreach and activities over the past 12 months. The ASBMB supports the annual Queensland Science Contest, organised by the Science Teachers Association of Queensland (STAQ). In 2023, we funded three competitive bursaries, which were awarded to Matilda Lockhart Walsh (Graceville State School), Myah McGregor (Marymount College) and Juha Oh (Queensland Academy of Science Maths and Technology). Congratulations to the winners and thank you to the ASBMB judges, Dr Conan Wang, Dr Rebecca San Gil, Dr Adam Walker and Associate Professor Michael Landsberg.

News from the States



Ross Smith ECR Medal winner, Michael Healy, with organisers of the Ross Smith EDR Award Symposium (from left): Thomas Ve, Larissa Dirr and Kevin Chen.

The Griffith University ASBMB prize for academic excellence in biochemistry was awarded to Sarah Lena Rein. We also sponsored the University of Queensland Research Student Symposium held in November, which was attended by approximately 100 Honours, Masters and PhD students in biochemistry and molecular biology.

Together with the Queensland Protein Group, we co-hosted the annual Ross Smith ECR Award Symposium, which was held on 17 October on the rooftop of the Queensland Brain Institute. The Ross Smith ECR Medal was awarded to Dr Michael Healy (University of Queensland), while Ada Quinn (University of Queensland) took home the QPG award for the best student presentation.

South Australia

Contributed by Michael Roach

The SA branch of the ASBMB has supported several events throughout 2023 for primary and secondary school students, as well as our amazing community of undergraduate, postgraduate and EMCR researchers.

Oliphant Science Awards

The Oliphant Science Awards are an annual competition for Reception to Year 12 students across South Australian schools. The SA branch of the ASBMB continued its sponsorship in 2023. There were many winning and highly commended projects with a biochemistry or molecular biology theme this year, and the level of talent in this next generation of scientists is astounding. We congratulate Emily Papacharalambous (St George College) on receiving the ASBMB-sponsored award for her game project, Photosynthesis Survival.

Barossa Meeting: Cell Signalling to Cancer Medicine

After an extended hiatus due to COVID, the Barossa Meeting on Cell Signalling to Cancer Medicine was held again this year. This four-day symposium featured talks from high-profile international and interstate speakers in the heart of one of Australia's best wine regions. The SA branch-sponsored best poster prize was awarded to Daniel Reed from the Garvan Institute for his poster, Dual epithelial and stromal targeting in triple negative breast cancer using ROCK2 inhibition.

Centre for Cancer Biology Awards

The SA branch continued its support of the annual Centre for Cancer Biology (CCB) Achievement Awards. These awards recognise the research that the CCB postgraduate and EMCR researchers have achieved in the year prior, including best publication, best publication by a student, ECR award (sponsored by the ASBMB), commended PhD theses and best scientific image. The ASBMB congratulates the ECR awardee, Dr Barbara McClure, and all CCB awards winners for 2023.

Oliphant ASBMB awardee Emily Papacharalambous (left) and ASBMB SA Representative Michael Roach.

Winner of the ASBMB-sponsored best poster prize at the Barossa Meeting, Daniel Reed (left) and ASBMB member, Briony Forbes.

ASBMB South Australia Representative Michael Roach (left) and CCB ECR awardee, Barbara McClure.

News from the States

Adelaide Protein Group 2023 AwardsFest winners, from left: Susanna Grigson, Xavier Montin, Alison Roennfeldt and Ibrahim Javed.

Adelaide Protein Group

The SA branch works with the Adelaide Protein Group (APG) to put on several events throughout the year to support our amazing community of biochemists and molecular biologists. The APG decided to shake things up this year by hosting its annual end-of-year Proteins in the Pub networking event in July. This featured a talk by Professor Colin Jackson (Australian National University), as well as the usual icebreaker games and refreshments.

The combined student and ECR AwardsFest symposium took place in August. This is the APG's premier event for recognising and supporting our researchers. It featured guest talks by Associate Professor Michael Lazarou (WEHI and Monash University) and Dr Adrienne Sullivan (ACE and SAiGENCI), as well as student and ECR talks and posters. We congratulate our winners for 2023: Dr Ibrahim Javed (ECR award), Alison Roennfeldt (student award), Susanna Grigson (people's choice), Xavier Montin (poster award) and Daniel Doherty (poster award).

Lastly, our APG Quiz Night was a resounding success with a sell-out crowd. This event provides an excellent, casual format for networking, and a fun way to unwind after a long year of research. We look forward to continuing this night as a regular event into the future.

Adelaide Protein Group 2023 Quiz Night.

Victoria

Contributed by Laura Osellame

The ASBMB Victoria branch has continued its commitment to a wide range of scientific events for all researchers at all stages of their career. ASBMB Victoria sponsored the following events in 2023.

Monash University Biochemistry Student Symposium

The Monash University Biochemistry Student Symposium is run by the Biochemistry Graduate Student committee and represents around 270 PhD students. This annual symposium attracts around 200 registrants from Monash Biochemistry and Molecular Biology. ASBMB Victoria was once again a Silver Sponsor for this event, supporting one of the morning or afternoon tea sessions. The event took place on 25 October at the Clayton campus.

Networking at the Monash University Biochemistry Student Symposium 2023.

Melbourne Protein Group ECR and Student Symposium

The MPG Student symposium was held in conjunction with the Royal Australian Chemical Institute of Victoria at RMIT from 24–26 October. ASBMB Victoria once again sponsored this event, which aims to strengthen ties between young biochemists and chemists of Victoria. There were three exceptional keynote speakers in the MPG session, Dr Rhys Grinter (Monash University), Dr Jai Rautela (Founder and CEO, oNKo-Innate) and Dr Sarah Hennebry (FPA Patent Attorneys). The student posters and talks were all of great quality, with the Tilley Award for best oral presentations awarded to Jordan Crameri (Bio21) and Kaiseal Sarson-Lawrence (WEHI). Fabian Munder (Monash University), Phoebe Lemming (Bio21), Minal Chaturvedi (RMIT) and Imesha Hettige (MIPS) were awarded poster prizes.

Austin Medical Research Foundation Research Fest

ASBMB Victoria was excited to sponsor a new event for 2023 – the Austin Medical Research Foundation Research Fest 2023. This event aimed to bring together basic and translational scientists from the Austin precinct with clinical scientists at teaching and research hospitals across Melbourne. This event was held at the Austin Heidelberg campus from 2–5 October. ASBMB

News from the States

Victoria sponsored the Working Better Together session designed to encourage collaboration between basic and translational scientists in research institutions and hospitals across Melbourne.

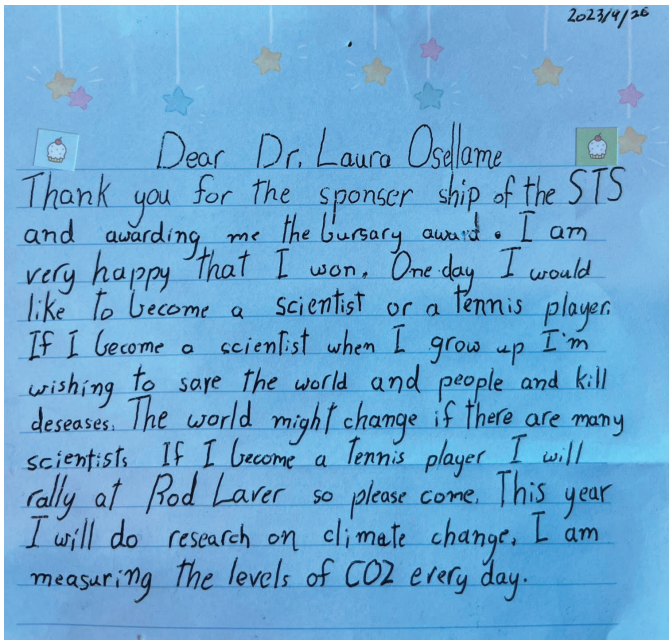
Science Talent Search Victoria

ASBMB Victoria was once again a gold sponsor of the Science Talent Search Victoria, supporting ten awards for primary and secondary school students. This year's theme was Innovations: Powering Future Industries. Some winning experiments being undertaken in the classroom and at home this year included 'A replacement for ammonia-based fertilizer', 'Producing energy through anaerobic digestion' and 'How do onions effect bacterial growth?' Prize presentations will take place online on 5 December, where some of the winning students will present their work.

This will be my last contribution as the Victorian State Representative. While the COVID years were a challenge for all Victorians, it was so wonderful to see the Victorian and Australian biochemistry and molecular biology communities bounce back to vibrant and successful in-person meetings at ComBio2022. Thank you to all our Victorian ASBMB members, I have enjoyed working with you and supporting many diverse events over the last three years!

Melbourne Protein Group Tilley Award winners, from left: Kaiseal Sarson-Lawrence, Chris Langendorf (MPG President) and Jordan Crameri.

Melbourne Protein Group poster award winners, from left: Fabian Munde, Minal Chaturvedi, Chris Langendorf (MPG President), Phoebe Lemming and Imesha Hettige.



Thank you letter to ASBMB Victoria from a Science Talent Search 2022 major bursary winner.

Western Australia

Contributed by Alyssa Van Dreumel

In 2023, there was heavy re-engagement in attendance to both national and international conferences for many students, academics and researchers in Western Australia, particularly in the latter half of the year.

The ASBMB WA branch's main form of outreach is through sponsorship of research communication prizes for best talks or poster presentations at various events, with a focus on students, and early- and mid-career researchers. One such event is the Perth Protein Group (PPG) Annual General Meeting (AGM). The fourth PPG AGM was held on 3–5 November at the UWA Albany campus. The meeting received strong sponsorship support and included a keynote presentation from Dr Gavin Knott, a workshop from industry partner Cytiva, and oral and poster presentations by early career researchers, and Honours and Masters students. At the beginning of 2023, Dr Mark Agostino took on the role of PPG Chair from Professor Josh Mylne. At the 2023 AGM, the group's committee had several role changes including Secretary, Convenor and Events Officer and sought to ensure there was representation from across all institutions in WA on the committee in filling these roles. We look forward to seeing what the group will achieve in 2024.

In addition to sponsorship of research communication prizes at local ASBMB Special Interest Group and institutional events, the WA branch is keen to invest in initiatives within the education space, at both secondary and tertiary levels. This year we set about establishing an award, like those given in other states, to recognise and reward outstanding academic achievement of

undergraduate students in biochemistry and molecular biology focused areas of study. For the 2023 academic year, two second-year UWA undergraduate students whom demonstrate academic excellence across core biochemistry and molecular biology major units are to receive the inaugural award after results are finalised and released. Moving forward, this award may be offered at other WA institutes where appropriate discipline specific units/areas of study are taught.

Finally, we note, along with colleagues from across Australia, representatives in WA have participated in preliminary discussions and tasks of the recently established National Biochemistry and Molecular Biology Core Concept project working group led by Dr Amber Willems-Jones. We look forward to seeing the progress of the group's effort to achieve national agreement on Core Concepts for the Discipline of Biochemistry and Molecular Biology undergraduate learning outcomes.

ASBMB SDR Scientific Education Award Report

Improving Academic Skills and Academic Achievement Across Continents

I had the privilege of receiving the ASBMB SDR Scientific Education Award, which provided me with the opportunity to present at the International Academic Forum held in Hawaii in 2023. The 8th International Academic Forum (IAFOR) International Conference on Education in Hawaii (IICE2023) brought together over 700 scholars from more than 50 countries, celebrating the interdisciplinary, intercultural and international aspects of academia. Founded in Nagoya, Japan, in 2009, IAFOR aims to facilitate interdisciplinary discourse, promote cross-cultural understanding and advance global exchange. It operates as a research institution, conference coordinator and publisher, with a primary focus on fostering international collaboration and academic research.

I chose to participate in this conference because I had previously presented my academic research at a local level and desired to share my knowledge with an international audience while gaining insights into global academic endeavors. I was particularly drawn to IAFOR's inclusive and diverse interdisciplinary conferences, which offered valuable networking opportunities. As a result of my participation, I established collaborations with academics in Ghana and incorporated elements of their assessment methods into my teaching. I have also learned that a similar exchange occurred on their end.

Below: Lois and her daughter, Paige, on their way to Honolulu. Right: Butterfly garden.

Our journey took us to Honolulu from 5–8 January 2023. My 30-minute presentation, titled Improving Academic Skills and Academic Achievement in a Diverse Student Cohort, focused on the implementation and validation of a continuous scaffolded assessment for formal scientific report writing.

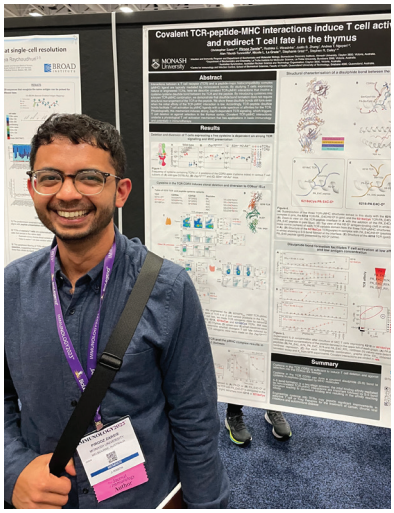
In addition to my professional commitments, I am the primary caregiver for my 6-year-old daughter. Fortunately, I was awarded an Athena Swan Advancement Subsidy for women in STEMM by Edith Cowan University, which allowed my daughter to accompany me and receive care while I presented at the conference. This trip marked her first flight, and during our time in Honolulu, we had the opportunity to explore a butterfly enclosure, visit the Pearl Harbor USS Arizona Memorial, explore waterfalls, enjoy the beaches and parks, and immerse ourselves in the local culture.

Dr Lois Balmer is a Senor Lecturer and researcher at Edith Cowan University, Perth.

Eppendorf Edman ECR Award Report

Immunology from Beltway to Broadway

They say, “There’s no Business Like Show Business,” but they clearly haven’t been to the American Association of Immunologists (AAI) annual conference. The AAI IMMUNOLOGY meeting stands as one of the premier immunology focussed meetings globally, drawing in renowned leaders in the field and attracting thousands of international delegates. This year, IMMUNOLOGY2023 was held at the Walter E Washington Convention Center in Washington, DC, USA.



Pirooz Zareie presents his research during a poster session at IMMUNOLOGY2023.

A few members from our laboratory were fortunate to secure some funding to attend the same conference, which was great! We decided to get an Airbnb near the conference centre for the trip. The first day of the conference started in the late afternoon, which made it a bit easier to overcome the jet lag. Naturally, we left the house early to see the iconic sights of DC before heading to the conference. This included the White House, the Washington Monument and the Lincoln Memorial. IMMUNOLOGY2023 is the largest conference I have ever attended. The program boasted numerous distinguished speakers in more sessions that one could realistically attend. One of the highlights was a plenary lecture titled ‘Pandemic Preparedness and Response: Lessons from COVID-19’ by Dr Anthony Fauci, the former director of the NIAID and NIH, and former chief medical advisor to US President Biden. His insights into the situation in the US during that critical time were very interesting. The program was packed with very high-quality research from a range of PhD students, postdocs and lab heads. Conferences like this always get me excited to get back to the lab!

After the conference finished up, I hopped on a train from Washington DC to New York City to visit the Memorial Sloan Kettering Cancer Centre (MSKCC). The next day, I made my way to the upper east side of NYC where the institute was located. I had the pleasure of meeting with Professor Andrea Schietinger and Professor Joseph Sun, who very kindly hosted my visit. I gave a one hour talk about my research to a friendly and engaging audience. Professor Schietinger and Professor Sun were fantastic hosts and they allocated lots of time for me to meet their postdocs and see their facilities. I also had the wonderful opportunity to have one-on-one meetings with them as well as several of their postdocs who shared their unpublished work with me. It was an enjoyable and engaging visit, which I think has led to truly long-lasting connections. After spending the whole day at the MSKCC, I was able to spend the evening with old friends who now live in NYC. Although it was a short trip, I had a wonderful time and returned to Melbourne with a lot of motivation and excitement to do my research. It is an absolute honour to be awarded the 2023 Eppendorf Edman ECR Award from the ASBMB, which generously supported me to have this enriching experience.

Dr Pirooz Zareie is undertaking postdoctoral research in the Department of Microbiology and Immunology at the Peter Doherty Institute for Infection and Immunity, Melbourne.

ASBMB Fellowship Report

Cachexia, Castles and Kilts

I was very fortunate to be a recipient of a 2023 ASBMB Fellowship, which supported my travel to the 7th Cancer Cachexia Society meeting held in Edinburgh, Scotland. Cancer cachexia is a condition defined by the loss of bodyweight that leads to profound weakness and frailty experienced by individuals with cancer. Understanding the aetiology of cancer cachexia is an ongoing challenge that is largely being advanced by fundamental researchers with a strong foundation in biochemistry and molecular biology.

The 7th Cancer Cachexia Society meeting was held at the Surgeons Quarter.

The Cancer Cachexia Society (CCS) brings together a fantastic mix of preclinical researchers, many with a strong background on skeletal muscle biology and clinical researchers who are currently conducting trials in the cachexia space. This was the first meeting of the CCS since the pandemic and provided a unique opportunity to learn about the newest work being undertaken in the field.

I arrived a day before the meeting and took this time to meet with a collaborator and do a little exploring of Edinburgh, which has a phenomenal history. The highlight was visiting Edinburgh Castle, which was constructed in the 10th century and has witnessed countless sieges, occupations and reoccupations. It even served as a prison during the Second World War.

The meeting was held in a particularly historical location, the Surgeons Quarter, operated by the Edinburgh Royal College of Surgeons, linked to the Medical School which was established in 1726. Over the three days, there were sessions focused on the intracellular and extracellular control of proteostasis, inflammatory signalling, immunometabolism, tumour biology, transcriptional regulation and metabolomics, all under the context of cancer cachexia in preclinical and clinical settings. We also heard about the latest clinical trials being conducted in the field, as well as a very insightful session focused on patients, providers and caregivers. The keynote presentation was delivered by Professor Denis Guttridge from the Medical University of South Carolina. Professor Guttridge's impressive career has focused on the inflammatory response, particularly NF-κB signalling, and how this regulates cellular differentiation and tumorigenesis in the context of muscle wasting disease including cancer cachexia.

With a keen interest on the molecular mechanisms that drive cachexia, my attention was primarily focused on the fundamental and preclinical research. The presentations that I found particularly interesting focused on the role of E3 ubiquitin ligase activity and how this is a continuing area of interest for the field, the emerging role of the microbiome in the pathogenesis of cachexia and the intricate crosstalk between tissues in cachexia. Importantly, we saw the use of single nuclei RNA sequencing featuring in many talks. It is clear that this technique will continue to be particularly useful to the field.

The meeting was a great opportunity to network, socialise and talk science with some of the leaders in the field. The non-scientific highlight was the cèilidh, a traditional Scottish dance party held after the conference dinner. Many attendees took to full Scottish tradition, donning kilts and dancing the night away.

After the meeting ended, I stayed in Edinburgh for a few extra days to explore more of the city with a longtime friend and collaborator. We took a day tour to the Highlands to check out the Scottish countryside. I was also able to go on a tour of the underground vaults

A day trip to the Scottish Highlands.

of Edinburgh, located under one of the main bridges in the city. These vaults date back to the 1700s and were originally commissioned by merchants to store goods. However, the vaults soon became refuges for the less fortunate who endured horrific living conditions in them, out of fear of being persecuted in the streets above. The vaults later became a home for witches before being used as a fascinating and somewhat spooky tourist attraction today. I also indulged in some whiskey tasting, learning a lot about the differences based on the regions in which the whiskey is produced.

I'm sincerely grateful to the ASBMB for providing me the opportunity to attend a fantastic meeting, to meet up with old friends and collaborators and see a new part of the world!

Dr Adam Hagg is a postdoctoral researcher in the School of Biomedical Sciences at the University of Queensland.

Drinking Healing Water and Discussing Cell Death

I was honoured to be awarded an ASBMB Fellowship, which supported me to travel to Italy and attend the 13th European Workshop on Cell Death (EWCD) from 4–9 June 2023. Hosted in the historic town of Fiuggi, this conference brought together junior researchers and leading international experts in the field of cell death. The EWCD focuses on the development of early career researchers. Uniquely, this conference has no invited or keynote speakers. All selected speakers, irrespective of career stage, have equivalent speaking time.

The view of surrounding mountains from old Fiuggi.

Across the four days of the conference, we heard from PhD students, postdoctoral researchers and laboratory heads who spoke on topics such as cancer, inflammation and cell death. In a testament to the collaborative and cordial environment promoted by the organisers, speakers shared a range of projects at various stages of completion. Amongst these talks, I was thrilled to share my research in the 'Poking Holes' session that focused on proteins that mediate the disruption of cell membranes. It was fantastic to receive interesting experimental suggestions and new questions on my research during question time.

Fiuggi, a municipality in the region of Lazio in central Italy, is famous for its Acqua di Fiuggi (Fiuggi water) which flows from the natural springs and mountains of the area and has renowned healing properties. The town originally gained fame in the early 14th century when Pope Boniface VIII claimed his kidney stones had been healed by the Fiuggi waters. This was just one of interesting facts we learnt when participating in an organised guided tour of the historic town. Whilst navigating the cobbled laneways of the medieval fortified village, we also observed many of the recent artworks of town history painted on the building exteriors. Standing at 760 meters above sea level, upper or old Fiuggi provided stunning views of the surrounding mountains, an ecosystem historically unchanged by humans that contains ancient volcanic deposits.

The conference held at a standalone hotel in lower Fiuggi, creating ample opportunities to meet and network with attendees over breakfast, lunch and dinner. It wouldn't have been a successful conference in Italy without lots of delicious food. Breakfast included a table of freshly baked cakes, and lunch and dinner comprised of several courses and featured three different pasta dishes a day! Of course, we also ventured to a local restaurant to get a customary slice of Italian pizza and sample the local wine. As one of the attendees who travelled the furthest, I greatly appreciated the sociable conference atmosphere, and it was fantastic to have the opportunity to foster new research collaborations and make friends with our European colleagues.

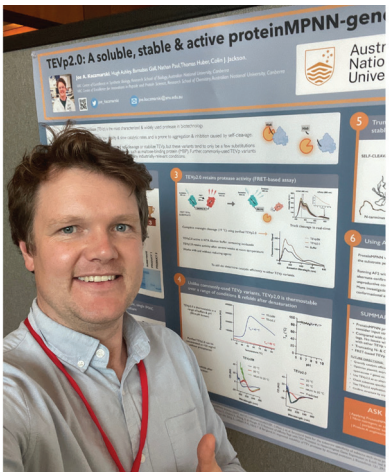
I would like to thank the ASBMB for providing this incredibly rewarding experience. It was an invaluable opportunity for me to present my research at an international conference and network with the cell death community.

Dr Sarah Garnish is a postdoctoral researcher in the Inflammation Division at the Walter and Eliza Hall Institute for Medical Research.

ASBMB Fellowship Report

Exploring the Forefront of Protein Engineering and Design in the Boston Area

I recently returned from a fantastic trip to Boston, where I attended two top-notch conferences on emerging ideas and techniques in protein science and engineering. I am very grateful to have received an ASBMB Fellowship that helped to support this trip. The Fellowship was from a few years ago, so a special thanks to the ASBMB for letting me still use these funds post-COVID and other delays!



Joe presents his poster at the 37th Protein Society Annual Symposium.

The trip kicked off with the 37th Protein Society Annual Symposium (PS37), hosted in the South Boston Waterfront area. I was happy to have finally made it to a ProtSoc meeting to hang out with fellow protein enthusiasts. I'd been eyeing this meeting off for a few years now and I certainly wasn't disappointed! The meeting was a fantastic opportunity to catch up with old friends and colleagues, meet people whom I had only ever crossed paths with online or via admiring their work, and hear about a tonne of exciting (primarily unpublished) research in topics ranging from cryoEM of massive protein complexes, bispecific antibody engineering and the evolution of enzyme function.

During the conference, I presented our work using proteinMPNN to generate stable, soluble and active enzyme variants (specifically, a TEV protease). I was pleased to receive plenty of positive and helpful feedback. People seemed particularly interested to hear more about our experiences using proteinMPNN to generate optimised protein sequences. Other than the talks, highlights of PS37 included a surprisingly fruitful workshop on career development for EMCRs, a tour of the Gingko Bioworks waterfront laboratories (I was jealous of their dog-friendly offices, well-stocked snack bars and automated workflows) and the ASAPbio flash presentations (where authors of pre-prints discussed their work and were interviewed about their findings).

The second conference I attended, the Gordon Research Conference in Protein Engineering, was a much more focused and specialised meeting. There was an impressive lineup of attendees and presenters, especially as it was the inaugural Protein Engineering GRC. I appreciated the balance of academic research labs and industry representatives in attendance – it was exciting to hear more about the recent growth in the protein engineering industry and the myriad of new companies that are popping up in this space. The talks were great, but the best parts of the meeting were the discussions had during mealtimes. There's something so special and productive about meetings where everyone is living and eating in the same place and there's plenty of spare time for science chats between sessions. It was a perfect environment for EMCRs like myself to meet, mingle and be inspired by some of the big names and emerging leaders in our field.

An overwhelmingly common theme of the talks at GRC was the increasing use of machine learning (ML) to help design, engineer and optimise protein structures and sequences – my guess is that more than half of the posters were ML-related! I was pleased by the positive interest that my poster on proteinMPNN received.

During the week between conferences, I was keen to make the most of my time in the protein engineering hotspot that is Boston, so I organised to visit some of the local research groups and commercial labs. I was particularly impressed by the work being done at AI Proteins, a company using AI-based design to create mini therapeutic proteins. It was great to tour the facilities and meet with their head of protein engineering, Ben Meinen; we had a great discussion about their workflows and the future of protein engineering.

Getting inspired during a tour of the Gingko Bioworks lab.

While in Boston, I also had the opportunity to visit the biophysics lab of Professor Eugene Shakhnovich at Harvard (via my connection with ex-ANU colleague, Dr David Thorn, whom I ran into at PS37), caught up with colleagues from the Okinawa Institute of Science and Technology over dinner in Harvard Yard, and also had a great meetup with Chun-Chen Jerry Yao from the Polizzi protein design group at Harvard Medical School.

The highlight of the whole trip was spending time

ASBMB Fellowship Report

getting to know Dr Sergey Ovchinnikov, who is behind the ColabFold and ColabDesign notebooks that have helped to make protein structure prediction and design so accessible to researchers and students from around the world. Sergey and his group were super generous and welcoming. It was so special to spend this time discussing the field with him over several meals and wanders.

Joe with Sergey Ovchinnikov on the spot where the Havard commencement speech is given each year.

I am very grateful to the ASBMB (and ARC Centre of Excellence in Synthetic Biology) for the opportunity to attend these conferences and to explore the protein engineering delights of the Boston area. The trip was an invaluable experience that helped me gain a fresh perspective on my own research in protein engineering and build connections that I am sure will lead to some fruitful collaborations in the future.

Dr Joe Kaczmarski is undertaking postdoctoral research with the ARC Centre of Excellence in Synthetic Biology and is based at the Australian National University's Research School of Biology.

Decoding Poxviruses

It was an immense honour for me to receive an ASBMB Fellowship, which helped me to attend the XXIV International Poxvirus, Asfarvirus, and Iridovirus Conference held in Hotel Land Gut Höhne, Mettmann, a town in Dusseldorf, Germany, from 2–6 September 2023. This biennial meeting is the most prominent event in the field of pox virology, attracting leading researchers, clinicians, experts, ECRs and students from around the world. This year's conference focused on recent advancements, breakthroughs and challenges in the study of poxviruses, Asfavirus (African swine fever virus), Iridovirus and viral diseases.

The five-day conference featured ten engaging plenary sessions, including keynote presentations by renowned virologists. Topics ranged from emerging infectious diseases to the latest advancements in antiviral therapies, including virus entry, gene expression and proteomics, DNA replication, virus assembly and release, immunity and immune evasion, virus-host interactions, pathogenesis, vaccines and antivirals, diagnostics, virus vectors and virus oncolytics. Each plenary session comprised between four and six speakers per session, followed by two poster presentation sessions to allow participants to continue their discussions.

As an ECR working on the molecular mechanism underpinning poxvirus-mediated apoptosis inhibition and poxvirus replication-associated protein interactions, the plenary sessions were notable for their diverse and well-represented research topics from the leading researchers in the field. They covered a broad spectrum of cutting-edge subjects, showcasing the depth and breadth of research in virology today. From discussions on emerging infectious diseases to the latest breakthroughs in antiviral therapies and diagnostic techniques, the plenary sessions effectively captured the multifaceted nature of virology research. It really inspired me to witness how researchers from different subfields came together to share their expertise and contribute to the collective knowledge base. This well-rounded representation of research topics truly enriched my conference experience and left me with a comprehensive understanding of the current state of virology research.

Chathura Suraweera.

One of my favourite sessions at the conference was undoubtedly the one dedicated to Viral Gene Expression and Replication, which is closely aligned with my current research program and provided a deep dive into the intricate mechanisms by which poxviruses multiply and propagate within their hosts. Professor Wim Burmeister spoke about the structure and flexibility of the DNA polymerase holoenzyme of vaccinia virus, and I was fascinated to learn about the molecular intricacies and strategies these viruses employ to hijack cellular machinery. The session not only showcased the remarkable adaptability of poxviruses, but also

underscored the critical importance of this knowledge in developing innovative antiviral therapies and vaccines.

I had the privilege of presenting my research on the monkeypox virus inhibition of apoptosis during the dedicated plenary session on Emerging Poxviruses. I also presented a poster, which allowed me to share our work and receive positive feedback from experts in the field, which will be instrumental in refining my future research program. Following my presentation, I had the opportunity to talk with Professor David Evans, a world-leading pox virologist from the University of Alberta. This enabled us to share ideas and to discuss possible future collaboration with his research group.

The conference concluded with a gala dinner on the Rhine River Cruise. The experience was enhanced by the picturesque surroundings around the Rhine River. Live music and entertainment added a festive atmosphere to the event, keeping attendees engaged and entertained throughout the evening. The relaxed ambience of the cruise provided an excellent environment for networking and socialising. I had the opportunity to converse with fellow conference participants, including speakers and organisers, fostering new connections.

My attendance at the Poxvirus Conference has provided me with valuable insights into the latest developments in poxvirus research. I plan to integrate these insights into our ongoing research projects, particularly those related to my monkeypox virus research. Furthermore, I have identified potential collaborators and resources that could aid our team in achieving our research goals in this field.

I would like to express my gratitude to the ASBMB for providing the opportunity to engage in this exceptionally fulfilling experience.

Dr Chathura Suraweera is a postdoctoral researcher at the John Curtin School of Medical Research, Australian National University.

The perfect way to relax and unwind – a dinner cruise banquet on the Rhine River.

ASBMB Annual Reports

President's Report

ASBMB President Ross Hannan.

Dear ASBMB members,

I write to you from the traditional lands of the Ngunnawal and Ngambi people in the Canberra region. I pay respect to their Elders past, present and emerging, and particularly welcome all First Nations people in our Society. I note with some dismay the outcome of the Voice to Parliament and remind myself we still have a significant way to go to improve the life of the Indigenous community.

Managing the Society: Those That Do All the Work

I want to firstly thank the immediate Past President of the ASBMB, Jacqueline Matthews, who has been on the Executive for the past three years and continues to support the ASBMB admirably. I also give my thanks to all on the current Council – especially the indomitable Secretary, Dominic Ng, whose tireless work keeps it all together. Special thanks also to our superb Treasurer, Kate Quinlan, and of course, Liana Friedman and Tatiana Soares da Costa (and in her parental leave absence, Doug Fairlie), for continuing to capably steer the *Australian Biochemist* magazine.

The transition from Sally Jay Conferences to WaldronSmith Management (with over 28 years of experience in managing associations and societies) for the management of our Society has been relatively smooth. Particular thanks to Sarah Parsons from WaldronSmith who liaises with our membership and helps Dominic and the rest of the team manage the Society in the background. I would also like to particularly take this opportunity to thank Sally for all her support of our organisation in the past.

Conferences Immediately Past, Present and Future

With COVID behind us (almost; I caught it for the sixth time on my most recent trip to the USA…), the enormous success of ComBio2022 in Melbourne in the wake of the pandemic was very reassuring. Many thanks to Jackie Wilce and her team and Sally Jay Conferences in their last year managing the meeting.

This year, we continue the trial of a standalone ASBMB meeting on the alternate years to ComBio. This year's ASBMB2023 meeting was held in my home town, Canberra, and I particularly want to thank Colin Jackson (ANU) and his remarkable team for their efficient organisation and stimulating program ranging from synthetic biology, through membrane transporters, plant and fungal biochemistry, DNA and genes, computational biology, drugs, drug resistance and therapeutics, RNA and cancer biology and much more. This has proven to be a herculean effort, given the absence of professional conference organising support.

I also very much anticipate ComBio2024: Biomolecular Horizons 2024, a special ComBio meeting to be held in conjunction with the 26th IUBMB Congress and the 17th FAOBMB Congress, at the Melbourne Convention and Exhibition Centre from 22–26 September 2024. The superb organisation is a great credit to the ongoing hard work of the organising team lead by Convenor, Leann Tilley, and Deputy Convenors, Frances Separovic and Christina Mitchell. The program, put together by Andy Hill, Wai-Hong Tham and Stephanie Gras, looks truly spectacular and I encourage all to attend for what promises to be a major conference event of the decade for the ASBMB. The ASBMB is also partnering with our Korean counterparts (KSBMB) to hold a joint satellite meeting at Bio21 coinciding with the main congress. I express my thanks to Victor Anggono for driving this initiative.

Casting an eye to the future, the good news is that Tracy Bryan and Mark Larance have tentatively agreed to co-chair ComBio2026 at the International Convention Centre Sydney.

Membership

Pleasingly, our membership across ordinary, student and Sustaining Members, is healthy, with numbers largely holding steady since 2019–2020, aided in part by the introduction of three-year memberships packages. But as competing interests rise, we need to keep an eye on this and make sure we remain relevant. Some of the smaller states continue to struggle for membership. In particular, I wish to thank Adele Holloway for single-handedly keeping the Tasmanian branch of ASBMB alive with support from our Treasurer to stimulate activities.

Special Interest Groups (SIGs) remain strong and very important to the ASBMB, but as expected, some may outgrow the relationship with time. Archa Fox has informed me that the RNA SIG will move away to form its own independent society, supported by ASN Events, and will have an annual conference on RNA. We welcome growing the broader community and would hope the RNA society might contribute to future iterations of ComBio.

Awards

It is important to recognise those who contribute to our ecosystem and I congratulate all our current awardees of the ASBMB prizes and fellowships for research education and community support.

ASBMB Annual Reports

Self-reflection as President

I must admit I feel somewhat like an absentee landlord, having not achieved as much as I would have liked this year, in particular using the ASBMB as a platform for advancing the cause for EMCRs. Funding and career prospects for EMCRs continues to worsen. As I write this, ARC Discovery Project funding results have been announced and the trend is not good, with $275 million awarded in 2023 versus $387 million in 2020; lower number of projects funded, 421 in 2023 versus 660 in 2020; and the lowest success rate to date at 16.3% in 2023 versus 23.0% in 2020. With academic careers in STEM becoming increasingly difficult, the responsibility is on those of us teaching, supervising and mentoring students and EMCRs to broaden opportunities for them to participate in alternative career pathways to academia such a biotech/industry. One mechanism to facilitate this is for PhD students to undertake three- to six-month industry engagements and internships as part of their HDR training through programs such as the National Industry Research Program. However, uptake is low and placements notoriously difficult to find, despite the Australian biotechnology ecosystem including health, agriculture, marine, industrial and environmental sectors being worth more than $8 billion in annual revenue. More needs to be done and we, the ASBMB, should be more involved. Our conferences are ideal vehicles for discussion of exemplars of biotech/industry as a viable career alternatives. We should also unashamedly use our membership to lobby state and federal bodies for further investment in career pathways for our scientists. I welcome thoughts on how we can do more in this respect.

Professor Ross Hannan, President
ross.hannan@anu.edu.au

ASBMB Annual Reports

Treasurer's Report

ASBMB Treasurer Kate Quinlan.

Relevant summaries of the filed annual return (1 July 2022 to 30 June 2023) should be read in conjunction with this statement. The final audit has been completed and will be submitted shortly, and the summary statements on which the report is based were provided by our auditors.

The overall position of the Society has substantially improved compared to the 2021–2022 financial year. We recorded an operating profit of $34,984 in 2022–2023 compared to a profit of $7,540 in 2021–2022. This surplus was strongly driven by the success of ComBio2022, which returned a net profit of $96,271. Following profit-sharing with other ComBio2022 societies, ASBMB received $48,554 in ComBio2022 profits. We would like to thank the ComBio2022 Organising Committee and our partner societies for running a scientifically stimulating, successful and profitable meeting.

The major sources of income for the ASBMB are membership revenue, ComBio profits and bank interest. There was $5,055 of advertising income, which was similar to the $4,990 income in the previous period. Corporate support for our named awards remains strong and on behalf of the Society, I thank their support of these awards. I would also like to thank Sally Jay for her tireless efforts in securing continuing sponsorship of our awards. Interest on our accounts was higher in the 2023 financial year, at $5,266 compared to $780 in 2021–2022, driven by increased interest rates. Further increases in interest income are expected in the next financial year, driven by rising bank interest rates.

Net expenditure in 2022–2023 financial year was up $14,756 compared to the previous period, largely due to increased expenditure on conference support, Council expenses and renewal of affiliate memberships. The distribution of funds to the state branches and Special Interest Groups in 2022–2023 was equivalent to that in 2021–2022.

We are fortunate that Sally and Chris Jay managed the ASBMB National Office with a high degree of effectiveness, while keeping their costs relatively stable, and for their assistance in transitioning our National Office to WALDRONSMITH Management at the start of 2023. National Office costs have remained relatively stable during this transition, with $47,026 expenditure in 2022–2023 compared to $44,621 in 2021–2022. We thank WALDRONSMITH Management for its role in managing the National Office transition and for its efficient management of the Society throughout 2023.

Our flagship publication is the *Australian Biochemist* and it is available to members as a PDF. Tatiana Soares da Costa as the Editor of the *Australian Biochemist*, along with Editorial Officer, Liana Friedman, are to be commended for their work in putting the magazine together.

The overall financial position of ASBMB has improved in 2022–2023. After accessing cash reserves in 2019 ($100,000 was used), we have been able to return a significant amount of this to our reserves for investment in the subsequent years. Our cash reserves are $510,216 at the end of the 2022–2023 financial year, up from $504,481 at the end of the 2021–2022 financial year.

In my role as the ASBMB Treasurer, I have many people to thank. I would like to acknowledge Marc Kvansakul, who was ASBMB Treasurer throughout 2018–2022, including half of this current financial reporting period. Mark expertly steered the ASBMB through the very financially challenging years of the pandemic, allowing our Society to emerge relatively unscathed. I was lucky enough to inherit a financially stable Society from Marc. I also appreciate Marc helping me to step into the role of ASBMB Treasurer through a detailed handover and a transition period. I would also like to thank the members of the ASBMB Executive, Sally and Chris Jay (ASBMB National Office 1991–2022), WALDRONSMITH Management (ASBMB National Office 2023), Ian Price (ASBMB bookkeeper), Priestleys (ASBMB accountants) and Mark Andreassen (ASBMB auditor) for their support of the ASBMB, and for being patient with me as I learn the ropes.

Associate Professor Kate Quinlan, Treasurer
kate.quinlan@unsw.edu.au

Executive Officers' Report

Your Executive Officers submit herewith the financial statements of the Association for the year ended 30 June 2023, together with the Auditors' Report thereon and in accordance with Section 73 of the Associations Incorporation Act 1991 report as follows.

PRINCIPAL ACTIVITIES

The principal activity of the Association in the course of the financial year was the advancement of the science and profession of both biochemistry and molecular biology.

ASBMB Annual Reports

Executive Officers' Report

EXECUTIVE OFFICERS

The Executive Officers throughout the year were: Professor Ross Hannan (President Elect to 31/12/22, President from 1/1/23); Professor Jacqui Matthews (President to 31/12/22 Past President from 1/1/23); Professor Dominic Ng (Secretary); Professor Marc Kvansakul (Treasurer to 31/12/22); Associate Professor Kate Quinlan (Treasurer from 1/1/23); Dr Tatiana Soares da Costa (Editor and Chair of Communications); Associate Professor Nirma Samarawickrema (Education Representative to 31/12/22); Associate Professor Tracey Kuit (Education Representative from 1/1/23); Associate Professor Terrence Piva (FAOBMB Representative to 31/12/22); Associate Professor Nirma Samarawickrema (FAOBMB Representative from 1/1/23).

OPERATING RESULTS

During the year, the Association produced an operating profit of $34,984 (2022: operating profit $7,540).

STATEMENT BY EXECUTIVE OFFICERS

In the opinion of the Executive Officers the financial statements, consisting of the Statement of Profit and Loss and other Comprehensive Income, Statement of Financial Position, Statement of Changes in Equity, Statement of Cash Flows and Notes to and forming part of the Financial Statements:

(a) Presents a true and fair view of the financial position of the Association as at 30 June 2023 and its performance for the year ended on that date in accordance with Australian Accounting Standards – Simplified Disclosure Requirements.

(b) At the date of this statement, there are reasonable grounds to believe that the Association will be able to pay its debts as and when they fall due.

Signed in accordance with a Resolution of the Executive Officers.

Professor Ross Hannan, President
Associate Professor Kate Quinlan, Treasurer

Independent Auditor's Report

REPORT ON THE FINANCIAL STATEMENTS

We have audited the financial report of the Australian Society for Biochemistry and Molecular Biology Incorporated (the association) which comprises the statement of financial position as at 30 June 2023, the statement of profit or loss, statement of comprehensive income, statement of changes in equity and statement of cash flows for the year then ended, notes comprising a summary of significant accounting policies and other explanatory information, and the certification by members of the committee on the annual statements giving a true and fair view of the financial position and performance of the association.

AUDIT OPINION

In our opinion, the accompanying financial report of the Australian Society for Biochemistry and Molecular Biology Incorporated is in accordance with the Associations Incorporation Act 1991 including:

(i) giving a true and fair view of the association's financial position as at 30 June 2023 and of its performance for the year then ended; and

(ii) that the financial records kept by the association are such as to enable financial statements to be prepared in accordance with Australian Accounting Standards – Simplified Disclosure Requirements.

BASIS FOR OPINION

We conducted our audit in accordance with Australian Auditing Standards. Our responsibilities under those standards are further described in the Auditor's Responsibilities for the Audit of the Financial Report section of our report. We are independent of the association in accordance with the ethical requirements of the Accounting Professional and Ethical Standards Board's APES 110: Code of Ethics for Professional Accountants (the Code) that are relevant to our audit of the financial report in Australia. We have also fulfilled our other ethical responsibilities in accordance with the Code.

We believe that the audit evidence we have obtained is sufficient and appropriate to provide a basis for our opinion.

EXECUTIVE OFFICERS' RESPONSIBILITIES

The committee of the association are responsible for the preparation and fair presentation of the financial statements in accordance with Australian Accounting Standards – Simplified Disclosure Requirements, the Associations Incorporations Act 1991 (ACT) and for such internal control as the committee determine is necessary to enable the preparation of the financial report that gives a true and fair view and is free from material misstatement, whether due to fraud or error.

MC Andreassen (Partner)
Priestleys Chartered Accountants

AUSTRALIAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY INCORPORATED

STATEMENT OF FINANCIAL POSITION AT 30 JUNE 2023

	2023 $	2022 $
CURRENT ASSETS		
Cash and cash equivalents	510,216	504,481
Trade and other receivables	58,383	80,379
Other current assets	2,500	286
TOTAL CURRENT ASSETS	**571,099**	**585,146**
NON-CURRENT ASSETS		
Property, plant and equipment	-	-
TOTAL NON-CURRENT ASSETS	**-**	**-**
TOTAL ASSETS	**571,099**	**585,146**
CURRENT LIABILITIES		
Trade and other payables	122,885	171,916
TOTAL CURRENT LIABILITIES	**122,885**	**171,916**
TOTAL LIABILITIES	**122,885**	**171,916**
NET ASSETS	**448,214**	**413,230**
EQUITY		
Retained surplus	448,214	413,230
TOTAL EQUITY	**448,214**	**413,230**

STATEMENT OF CASH FLOWS FOR THE YEAR ENDED 30 JUNE 2023

	2023 $	2022 $
CASH FLOWS FROM OPERATING ACTIVITIES		
Receipts from members	71,084	109,868
Conference revenue	77,778	19,267
Other income	5,586	12,750
Payments to suppliers and employees	(151,251)	(95,032)
Interest received	2,538	780
Net cash provided by/(used in) operating activities	**5,735**	**47,633**
CASH FLOWS FROM INVESTING ACTIVITIES		
Net increase/(decrease) in cash held	5,735	47,633
Cash at the beginning of the financial year	504,481	456,848
Cash at the end of the financial year	**510,216**	**504,481**

REVENUE

	2023 $	2022 $
Operating activities		
Administration Fund		
Subscriptions – ordinary, student, retired and Sustaining Members	87,168	78,571
Conference revenue *(see note)*	48,554	19,267
Advertising in proceedings and magazines	5,055	4,990
Other Income	7,500	7,500
	148,277	**110,328**
Non-operating activities		
Interest received – Administration Fund	5,266	780
Donations	25	260
	5,291	**1,040**
Total Revenue	**153,568**	**111,368**

EXPENSES

	2023 $	2022 $
Other expenses from ordinary activities		
Affiliate memberships	5,774	3,288
Awards and medals	11,800	13,305
Conference support – other conferences	9,159	145
Council expenses	7,260	3,512
Insurance	750	-
National Office costs	47,026	44,621
Magazine costs	8,458	11,168
Other costs	5,236	4,496
State allocations	8,482	8,000
Remuneration of auditor		
- audit or review services	3,334	2,950
- other services	1,985	2,200
ASBMB Fellowship – Research Fund	9,357	10,143
	118,584	**103,828**

CASH AND CASH EQUIVALENTS

	2023 $	2022 $
Cash at bank – Administration Fund	510,216	504,481
	510,216	**504,481**

TRADE AND OTHER PAYABLES

	2023 $	2022 $
Current		
Accrued expenses – Administration Fund	10,400	172
Conference receivables	15,283	44,507
Advances to state committees	32,700	35,700
	58,383	**80,379**

RETAINED SURPLUS

	2023 $	2022 $
Administration Fund		
Retained surplus at beginning of the year	413,230	405,690
Net surplus (deficit) attributable to the Fund	34,984	7,540
Retained surplus at the end of the year	**448,214**	**413,230**

All sums given in Australian Dollars.

Note
Conference revenue represents the Association's share of the net profits generated by ComBio2022.

Our Sustaining Members

ASBMB welcomes the following new Sustaining Member:

Solve Scientific

Wasserlab, a Spanish company established in 1998, brings over 25 years of expertise in Water Purification Systems. Specialising in designing and manufacturing high-quality water purification systems, Wasserlab offers Ultra Pure (Type I), Pure Water (Type II) and Osmotic Water (Type III) solutions for laboratories, hospitals, and various industries.

With a commitment to delivering the highest quality water purification systems, Wasserlab ensures competitive pricing without compromising on quality. Wasserlab water purification systems utilise a sequential process combining filtering, reverse osmosis, resin deionization distinguishing them from conventional distilled water.

Wasserlab caters to diverse requirements by providing off the shelf and customised solutions, tailored to the laboratory needs of universities, research facilities, hospitals, food production, pharmaceuticals, industrial applications, agriculture, and environmental sectors. A Wasserlab key advantage is the use of a pressurised storage tanks which reduce the frequency of consumable replacements. Wasserlab systems include:

- Type I (Ultra Pure Water)
- Type II (Pure Water)
- Type III (Osmotic Water)

Wasserlab's dedicated research and development team continuously innovates and ensures systems meet international standards and verifiable parameters. Additionally, Wasserlab systems are user-friendly, easy to maintain and adaptable to evolving laboratory needs.

For more information, contact **Capella Science** on 02 9575 7512 or enquiries@capellascience.com.au

Cayman Chemical Introduces a New Tool to Study Protein–Lipid Interactions

Cayman Chemical, a leading supplier of bioactive lipids, has developed Cayman LipiDOT Strips™ as a research tool for the rapid identification of protein-lipid interactions. This new tool allows researchers to maximise the information gained from early protein–lipid interaction screening campaigns, giving researchers greater insight into protein–lipid interactions while being simple to perform, low cost, and easily completed in a single day.

Cayman LipiDOT Strips™ can be used to identify one or more lipids interacting with a protein of interest, assess a protein's relative lipid-binding specificity, and/or identify protein candidates for in-depth lipid-binding analysis. By identifying new lipid–protein interactions, researchers can better understand the important roles of lipids in modulating protein function and gain important insights into the biology of diseases and biological processes, which may prove useful in the pursuit of new therapeutic avenues.

Cayman LipiDOT Strips™ – PIPs Plus is the first introduction to Cayman's new product group. It includes 22 biologically relevant lipids arranged in a preconfigured panel. Cayman LipiDOT Strips™ – PIPs Plus contains several types of lipids, such as phospholipids, a variety of phosphatidylinositol phosphate (PIP) species, lysophospholipids, and cardiolipin, as well as cholesterol and sphingolipids.

For more information, contact:
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https://www.caymanchem.com/news/cayman-lipidot-strips-for-rapid-screening-of-protein-lipid-interactions

BEYOND WESTERN BLOTTING AlphaLISA® *SureFire*® *Ultra*™: One Well, No-Wash, Quantitative Assay

Numerous technologies have been developed for studying signalling pathways and screening compound libraries in search of agents to modify kinase activities. Western blots suffer from limited sensitivity and low throughput. **AlphaLISA® *SureFire*® *Ultra*™** assays measure endogenous levels of phosphorylated and total cellular proteins. The assay is a homogeneous, bead-based technology that utilises two antibodies in a sandwich assay format. One antibody recognises a specific phospho-epitope on the analyte, while the other antibody is directed towards another, non-phosphorylated epitope. One of the antibodies binds to a Donor bead and the other to an Acceptor bead, so that in the presence of a phospho-protein or total protein, the two beads are drawn into close proximity. Excitation of the Donor bead at 680 nm results in energy transfer to the Acceptor bead yielding a sharp emission signal at 615 nm. The amount of light emission is directly proportional to the amount of phosphorylated/total protein present in the sample. **AlphaLISA® *SureFire*® *Ultra*™** assays are quantitative alternative to Western Blotting, automation-friendly, easy to miniaturise, and detect both endogenous and recombinant proteins. For more information and queries, contact salesau@revvity.com

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MCE® MedChemExpress

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MedChemExpress Featured Products – Antibody–drug Conjugates

The antibody–drug conjugate (ADC) is a humanised or human monoclonal antibody conjugated with highly cytotoxic small molecules (payloads) through chemical linkers. ADCs increase the cell-killing potential of monoclonal antibodies (mAbs), and confer higher tumor selectivity. ADCs have emerged as a novel therapeutic format in the fields of oncology and hematology.

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Mutate With Confidence! Tips and Tools for Successful Site-directed Mutagenesis

Site-directed mutagenesis allows scientists to precisely modify discrete DNA sequences with insertions, deletions, or substitutions. This ability to intentionally introduce targeted alterations at specific sites unlocks potential in a wide range of studies – from elucidating protein structure-function relationships, to enhancing enzymatic functionalities, to screening mutations for desired properties, or investigating disease mechanisms. Site-directed mutagenesis is also useful for domestication of plasmids with its ability to introduce or remove restriction endonuclease sites upstream of cloning experiments.

If you're diving into site-directed mutagenesis experiments for the first time, or if you've been doing them for years but are looking to update your workflow, you may not be aware of various tools available to simplify the process and enhance your efficiency. From kits and enzyme mixes to web tools and streamlined protocols, we have the answers that will have you acing your site-directed mutagenesis experiments from start to finish!

Visit www.nebiolabs.com.au/nebinspired-blog/mutate-with-confidence-tips-and-tools-for-successful-site-directed-mutagenesis-experiments to learn more about:

- Effective primer design strategies for substitution, insertion or deletion
- Amplification with optimised PCR conditions
- Re-circularisation of your PCR product and removal of wildtype background
- Securing your target clone with efficient transformation and screening

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Phasefocus Livecyte T Cell Killing Assay Tracks Cancer Cells and Quantifies T Cell Interactions

What is the problem we are solving?

T cell killing assays are primarily used to investigate the efficacy of engineered T cells in killing target cancers. To gain meaningful insight, there is a need for accurate segmentation and tracking of target cells throughout an experiment to quantify the dynamics and history of cell killing interactions.

Why is that a problem?

Most solutions on the market focus on population-level analysis such as quantifying total apoptotic material, or average distances between target and effector cells. They don't quantify the effector-target cell interactions on a single-cell level, which means they offer limited direct insight into T cell efficacy.

How does Livecyte solve this?

Livecyte uses advanced segmentation and tracking algorithms to automatically segment effector T cells and target cells. In addition, Livecyte can accurately track target cells over time to quantify effector-target interactions from the start of the experiment building up a unique interaction profile until target cell death.

Livecyte automatically compiles metrics based on these killing interaction profiles into its Dashboard view, providing a wealth of information summarising T cell cytotoxicity and target cell recognition, in addition to Livecyte's standard phenotypic data. This enables Livecyte to specifically quantify T cell–target cell interactions and behaviour independently from cytotoxicity, yielding greater depth of insight into how T cells find and kill their targets.

Contact us to learn more or to request a guided demo.

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Fisher Biotec is one of Australia's leading laboratory equipment suppliers. With 20+ years of experience under our belts and backed by ISO 9001:2015 certification, we've got the expertise to deliver quality, cost-effective and timely solutions to the scientific community.

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Our extensive product line spans a wide spectrum, encompassing fundamental laboratory necessities such as plastic lab consumables, pipette tips, PCR seals, custom solutions and buffers, whilst also extending to advanced equipment and machinery such as centrifuges, biosafety cabinets and gel documentation systems.

To get in contact with our friendly team, please don't hesitate to call 1800 066 077, email info@fisherbiotec.com or visit our website www.fisherbiotec.com. We look forward to working with you!

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Why Flow Injection Analysis With FIAlab?

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- Small Footprint: Saves critical bench space
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- Spectrometer Capabilities: broaden your sample concentration range, reduce noise, and collect even more data
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TECAN.

Uno Single Cell Dispenser™

The simplicity of single cell isolation at your fingertips

Tecan's Uno Single Cell Dispenser is an automated benchtop instrument designed for ease of use, efficiency, and precision in single cell workflows. Uno empowers a wide range of single cell applications across the "-omics" landscape, including MS-based single cell analysis, iPSC libraries, 3D cell research, cell line development, and beyond.

With Uno, you can achieve accurate, viable, and precise single cell dispensing, managing reagent volumes from picolitres to microlitres within minutes.

Tired of spending hours on manual single cell isolation with limited success? Struggling with the shortcomings of conventional FACS methods, which leads to decreased cell viability and altered cell function post-sorting?

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- **Simple and accessible benchtop solution for labs of any size**
  Integrate intuitive software and compact hardware at a competitive price without compromising on performance.
- **Fast and precise dispensing saves reagents with picolitre level accuracy**
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- **Reliable dispensing process for reproducible results**
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- **Gentle single cell dispensing to preserve cell integrity**
  Maintain a robust 90% cell viability (1) for downstream analysis. Works with a wide range of cells and reagents.

(1) <1 hour post-dispense

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Scitech
imaging specialists

Azure Cielo™ Real-time PCR System

The Azure Cielo™ real-time PCR system from Azure Biosystems is a qPCR system designed to provide high-quality data through high-performance optical technology, broad-spectrum detection capability, exceptional specificity, precision, fast run times and reproducible qPCR data. Applicatons include quantitative and qualitative gene expression analysis, miRNA analysis, genetic mapping, genetic fingerprinting, NGS library quantification, pathogen quantification and 6-channel multiplexing.

The Cielo™ is designed for multiplex experiments involving up to six different targets. With the ability to scan 16 wells simultaneously, an entire 96-well plate can be scanned for all six detection channels in 9 seconds. It uses fiber optics to deliver light to each individual well with precision, which reduces background excitation and the need for passive reference dyes.

With the option of three or six fluorescent channels, the CieloTM 3 (with 3 detection channels) and the Cielo 6 (6 detection channels) can detect up to 6 different fluorophores per well and provides the ultimate flexibility for experimental design. High sensitivity and superior resolution save time, money and samples, and the Cielo™ comes with a 12-month standard warranty.

qPCR is used to detect specific DNA sequences in bacterial, viral, and parasitic pathogens. For accurate pathogen detection, assays need to be able to detect very low amounts of genetic material. This has been especially true with SARS-CoV-2 where early detection and diagnosis is important. When tested, the Cielo™ was able to detect as little as 0.625 copies of RNA per uL of sample meaning it can be used for reliable and rapid detection of SARS-CoV-2.

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Get 20% off mexec jobstrategy™ program in 2023 with code '2023jobstrategy'.

A well-developed job search strategy can make the difference between getting a job offer or not. It can help to unlock your full potential, gain an advantage over other candidates, and help you secure your next role.

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- Do you have a networking strategy?
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Your CV is what will open the door to interviews. Understanding and presenting your capabilities clearly in your CV shows how you align to a role. Showcase your achievements and give context as to how they were actually achieved.

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Treat your job search like you are planning an experiment, with you now as the research question! Think about your skills, values and interests. Career planning must start well before you are ready to move.

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https://www.mexec.com/mexec-jobstrategy-program/

qPCR Offer From Genesearch

PCR is one of the modern molecular biologist's workhorses, and qPCR has several advantages including rapid, sensitive, high-throughput detection, quantitation of target sequences, and the ability to measure gene expression.

But one of its disadvantages can be cost. You might be aware of ABclonal as a supplier of a wide range of quality, economical antibodies and ELISA kits. But did you know they also have a growing range of molecular biology products including PCR?

We are happy to be able to help your budget with a special price on qPCR mixes of only $40 per ml for ABclonal's 2X Universal SYBR Green Fast qPCR Mix (#RK21203) and Genious 2X SYBR Green Fast qPCR Mix (RK21204), both available in 1, 5 and 25 ml sizes.

Or if it is RT-qPCR you need, try our ABScript II One Step SYBR Green RT-qPCR Kit (#RK20404: 10 reactions for $40 or 100 reactions for $300) or ABScript III One Step RT-qPCR Probe Kit with UDG V5 (#RK20412: 50 reactions for $100 or 250 reactions for $400).

For more information visit: www.genesearch.com.au

Note: prices available until end 2023 and are before GST; shipping extra on orders < $250.

GREINER BIO-ONE – VACUETTE® CAT Serum Fast Separator Tube

The VACUETTE® CAT Serum Fast Separator Tube offers a significant time advantage by achieving complete clotting of whole blood samples in just 5 minutes, compared to traditional serum tubes. This innovation combines the benefits of heparinized plasma for immediate use in emergencies and the necessity of serum in emergency departments. The tube allows for rapid clotting, shortening the preanalytical process considerably.

Reducing the turnaround time (TAT) is crucial for assessing a laboratory's efficiency, and the VACUETTE® CAT Serum Fast Separator Tube excels in this aspect. With a quick clotting time of 5 minutes followed by 5 minutes of centrifugation, key clinical chemical parameters can be analysed within 10 minutes, yielding reliable results promptly. This translates to a potential 30-minute reduction in TAT per sample, facilitating swifter and more targeted treatment initiation.

The interior of the shatter-proof tube is coated with a mixture of blood clot activator and thrombin, while a gel creates a stable barrier between the serum and solid components. The presence of thrombin accelerates the clotting process in the blood sample, making it an efficient and time-saving tool in clinical settings. Note that actual time savings may vary depending on centrifugation conditions.

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Spectroscopy Instruments From JASCO

The JASCO suite of spectroscopy instruments are well suited for biochemical applications, ranging from reaction kinetics, quantitative analysis to more complicated structural determination, protein folding and protein interactions. The J-1000 series circular dichroism instrument is a staple analytical tool in any biochemistry lab. It has unmatched performance and capability which is supported by the wide range of sampling accessories available and the Spectra Manager software suite.

Spectra manager is the parent software which operates all spectroscopy instruments within the JASCO range. This cross-platform flexibility is one of the biggest advantages for the JASCO instruments. It allows users to import data from different instruments to perform more complex data analysis through some of the optional software that JASCO can provide.

JASCO has recently released an app ebook, which showcases the utilisation of the J-1000 series instruments for therapeutic antibody discovery (Application eBook – Therapeutic antibodies | JASCO Global).

For more information, please contact
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MP Biomedicals

MP Biomedicals is committed to providing scientists and researchers with innovative tools and exceptional service to support their pursuit of groundbreaking discoveries.

Our product catalog encompasses a wide array of offerings in the fields of life sciences, fine chemicals, and diagnostics. Among our featured products are the FastPrep-24™ 5G bead beating grinder and lysis system, the MPure™ automated magnetic bead-based nucleic acid extraction system, and an extensive range of high-performance purification kits including the Magbeads range for microbiome research.

Our MPure™-32 and MPure™-96 aNAP Systems are fully automated magnetic bead-based nucleic acid extraction systems tailored specifically for medium to high volume microbiome research. The systems accommodate throughput from 32 to 96 samples per run.

Partnered with MP Biomedicals' range of Magbeads DNA/RNA extraction kits for diverse and complex microbiome samples, MPure™ Systems are the only automated systems specifically designed with microbiome researchers in mind.

MPure-32™ aNAP System efficiently processes up to 32 complex microbiome samples simultaneously, delivering results in a short timeframe (typically 40 to 60 minutes). Beyond its capacity for high-purity and high-yield nucleic acid extraction, the MPure-32™ aNAP System boasts user-friendliness, eliminating the potential for human error and cross-contamination.

Key features of the MPure-32™ Automated Nucleic Acid Extraction Platform include:

- Exceptional purity and yield
- High flexibility with customisation options
- Streamlined workflow
- Rapid and consistent outcomes

Users have the flexibility to assemble the required reagents and consumables for cost-effectiveness or opt for pre-assembled reagent kits for ultimate convenience.

Contact us at www.mpbio.com or on 1800249998 to discuss your research requirements and learn more about our newest products.

AXT

AXT Appointed CELLINK Bioprinter Distributors in Australia

CELLINK are recognised as world leaders in the field of 3D bioprinting. With increased growth around the world, they have recently appointed AXT as their distributor in Australia and New Zealand. AXT will look after sales and service of instruments as well as supply of consumable such bioinks.

CELLINK boast a range of light and extrusion-based bioprinters. Today CELLINK boast over 1600 installations (including several in Australia) in over 60 countries and are featured in more than 1200 publications. Their portfolio of bioprinters is supported by a range of bioinks that allow researchers to push the limits of medical research.

CELLINK's product lineup is headlined by the **BIONOVA X**, a high-throughput system powered by Digital Light Processing (DLP) technology that allows printing of high-resolution complex structures at high-speed and multimaterial printing. The **LUMEN X** DLP bioprinter offers users precision and versatility. For researchers looking for extrusion-based bioprinters, the modular **BIO X** series allow simultaneous printing using up to six bioinks and offers multimaterial and coaxial printing capabilities. The popular **INKREDIBLE** extrusion bioprinters round out their range at a cost-effective price point.

With the addition of CELLINK's bioprinters to their portfolio, AXT are now the premiere supplier of bioprinters in Australia and NZ.

For more details, visit www.axt.com.au/products/lumascopes/ or email info@axt.com.au.

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