Australian Biochemist

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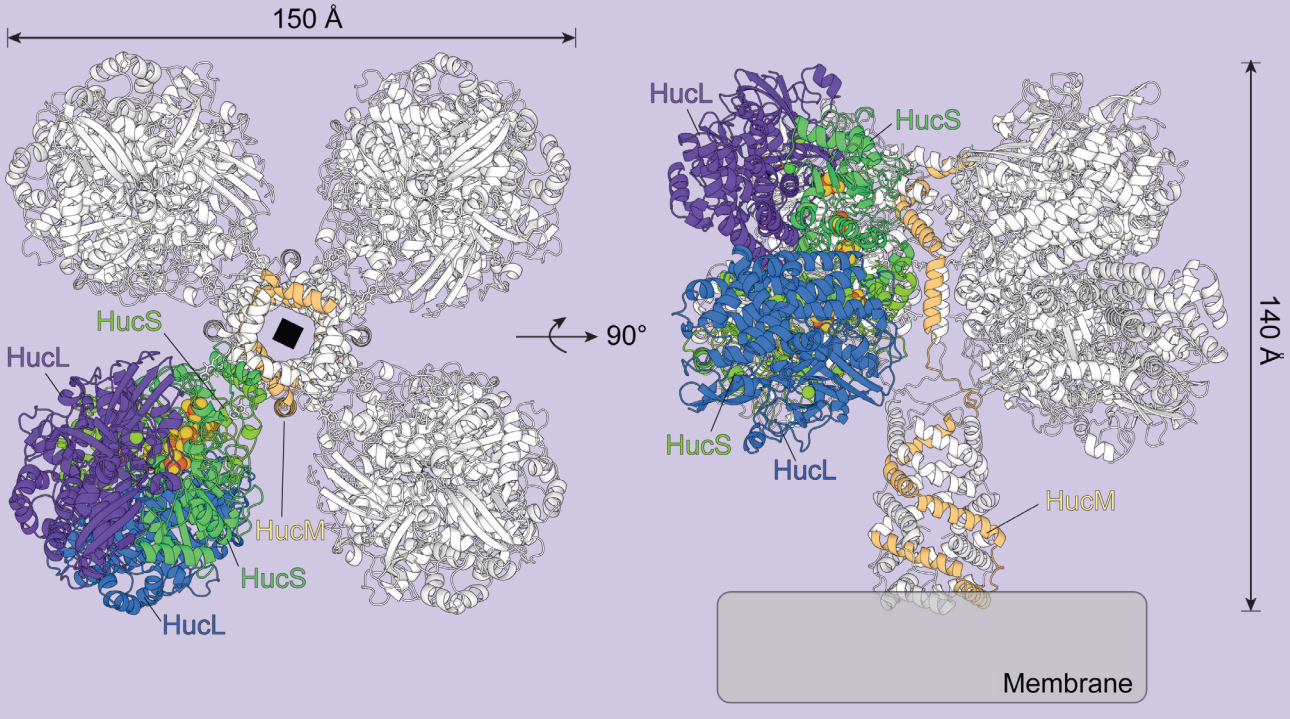

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Editor Tatiana Soares da Costa
Editorial Officer Liana Friedman

Front Cover

The cryoEM structure of the [NiFe] hydrogenase Huc from *Mycobacterium smegmatis*. Adapted from Grinter R *et al. Nature* 2023;615(7952):541-547. Image courtesy of Ashleigh Kropp, Chris Greening and Rhys Grinter, Department of Microbiology, Biomedicine Discovery Institute, Monash University.

Australian Biochemist Editorial Committee

ASBMB 2023 ACT

15-17Nov

ABSTRACTS CLOSE SEPT 4!

15-17 NOVEMBER

The Australian National University

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We invite you to join us in Canberra for ASBMB2023!
This conference will bring together biochemists and molecular biologists from around the country in a friendly atmosphere. Over 2.5 days, we will hear from 2 plenary and 14 keynote speakers, who are all established leaders in their respective fields. Additionally, we will celebrate the annual ASBMB award winners and offer opportunities for EMCRs to present their work. Join us to connect with the Australian biochemistry and molecular biology community in the nation's capital city!

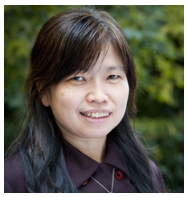
Joel Mackay
Gene Regulation

Andrea Yool
Drug Discovery

John Kuriyan
Plenary Speaker

Seemay Chou
Plenary Speaker

Oliver Rackham
RNA Biology



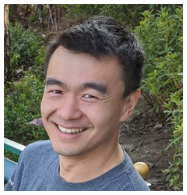
Phoebe Chen
Computation

Wai-Hong Tham
Pathogens

Paola Laurino
Protein & Peptide Engineering & Evolution

Renae Ryan
Membrane Transporter Biology

Magdalena Plebanski
Immunology



Danny Liu
Education

Barry Pogson
Plant & Fungal Biochemistry

Bostjan Kobe
Structural Biology

Kate Schroder
Signalling & Cell Biology

Adam Perriman
Biotechnology

Melissa Davis
Cancer

SBMB 2023 ACT 15-17Nov

Conference Program

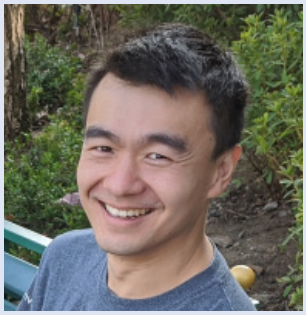
WEDNESDAY 15 NOVEMBER 2023		
09:00 - 09:15	Welcome to Country	
09:15 - 09:30	Conference Welcome	
09:30 - 10:30	Plenary: Prof John Kuriyan (Vanderbilt University, USA)	
10:30 - 11:00	**Morning Tea**	
11:00 - 12:30	**Gene Regulation**	**Drug Discovery**
11:00 - 11:30	Keynote: Prof Joel Mackay (USYD)	Keynote: Prof Andrea Yool (UA)
12:30 - 13:30	**Lunch**	
13:30 - 15:00	**RNA Biology**	**Computation**
13:30 - 14:00	Keynote: Prof Oliver Rackham (Curtin)	Keynote: Prof Phoebe Chen (La Trobe)
15:00 - 15:30	**Afternoon Tea**	
15:30 - 17:00	**Pathogens**	**Protein & Peptide Engineering & Evolution**
15:30 - 16:00	Keynote: Prof Wai-Hong Tham (WEHI)	Keynote: A/Prof Paola Laurino (OIST, Japan)
17:00 - 19:00	**Poster session and networking drinks**	
THURSDAY 16 NOVEMBER 2023		
08:30 - 09:30	Plenary: Dr Seemay Chou (CEO Arcadia Science, USA)	
09:30 - 10:00	ASBMB Eppendorf Edman Award: Dr Pirooz Zareie (Monash)	
10:00 - 10:30	ASBMB SDR Scientific Education Award: A/Prof Maurizio Costabile (UniSA)	
10:30 - 11:00	**Morning Tea**	
11:00 - 12:30	**Membrane Transporter Biology**	**Immunology**
11:00 - 11:30	Keynote: Prof Renae Ryan (USYD)	Keynote: Prof Magdalena Plebanski (RMIT)
12:30 - 13:30	**Lunch**	
13:30 - 15:00	**Education**	**Plant & Fungal Biochemistry**
13:30 - 14:00	Keynote: A/Prof Danny Liu (USYD)	Keynote: Prof Barry Pogson (ANU)
15:00 - 15:30	**Afternoon Tea**	
15:30 - 17:00	**Structural Biology**	**Signalling & Cell Biology**
15:30 - 16:00	Keynote: Prof Bostjan Kobe (UQ)	Keynote: Prof Kate Schroder (UQ)
17:15 - 17:45	**ASBMB Annual General Meeting**	
18:00 - 21:00	**Conference Dinner**	
FRIDAY 17 NOVEMBER 2023		
09:00 - 10:30	**Biotechnology**	**Cancer**
09:00 - 09:30	Keynote: Prof Adam Perriman (Bristol/ANU)	Keynote: Prof Melissa Davis (WEHI)
10:30 - 11:00	**Morning Tea**	
11:00 - 11:45	ASBMB Shimadzu Research Medal: Prof Stephanie Gras (LIMS)	
11:45 - 12:30	ASBMB Lemberg Medal: Prof Michael Ryan (Monash BDI)	
12:30 - 12:40	Fred Collins Award/Fellowship Awards/50 Year Members Award announcements	
12:40 - 13:00	Closing remarks and prizes	

EDUCATION ACTIVITIES at ASBMB2023

Thursday 16 November 2023

The Education symposium will include a keynote presentation from Associate Professor Danny Liu exploring the lessons learnt and ongoing opportunities for biochemistry educators in the impactful times of artificial intelligence. In addition, we will hear from the 2023 ASBMB SDR Scientific Education Award winner, Associate Professor Maurizio Costabile. With opportunities to network with fellow educators, we invite submissions to share practice and advance our teaching. The Education SIG will also hold a writing workshop with *Biochemistry and Molecular Biology Education* Editorial Board member, Professor Susan Howitt.

Contact: Associate Professor Tracey Kuit



Danny Liu is a molecular biologist by training, programmer by night, researcher and academic developer by day, and educator at heart. A multiple international and national teaching award winner, he works at the confluence of learning analytics, student engagement, educational technology, and professional development and leadership. Danny is an Associate Professor in the Deputy Vice-Chancellor (Education) Portfolio at the University of Sydney, where he leads staff across the institution in educational innovation, blended and online teaching, and the effective use of learning analytics and artificial intelligence to improve student learning and experience. He co-chairs the University's AI in Education working group.

Maurizio Costabile is a teaching-focused academic in Clinical and Health Sciences at the University of South Australia. He has held two roles as Interim Dean of Research in Education Futures and UniSA Creative. Maurizio was the Honours coordinator for the Laboratory Medicine Program for over 15 years and has been a higher degree research coordinator since 2016. Maurizio is responsible for teaching Biochemistry and Immunology and closely aligns his practice with educational research. His research interests include creating interactive simulations to enhance student learning of lecture and laboratory content and mind mapping to connect content and 3D-printed objects as learning aids.

Susan Howitt is the Director of the Teaching and Learning Centre for the Australian Council of Deans of Science and an Emeritus Professor at the Australian National University. During her career, she transitioned from biochemistry with an interest in membrane proteins to educational research focussing on student experiences of research and peer learning. She has published in a range of higher education and science education journals. Susan is also a former Chair of the ASBMB Education Special Interest Group (2008–2010).

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.

A New Type of Cell-penetrating Bacterial Toxin

Hor L, Pilapitiya A, McKenna JA, Panjikar S, Anderson MA, Desvaux M, Paxman JJ*, Heras B*.
Crystal structure of a subtilisin-like autotransporter passenger domain reveals insights into its cytotoxic function. *Nature Commun* 2023;14(1):1163.
***Corresponding authors: j.paxman@latrobe.edu.au, b.heras@latrobe.edu.au**

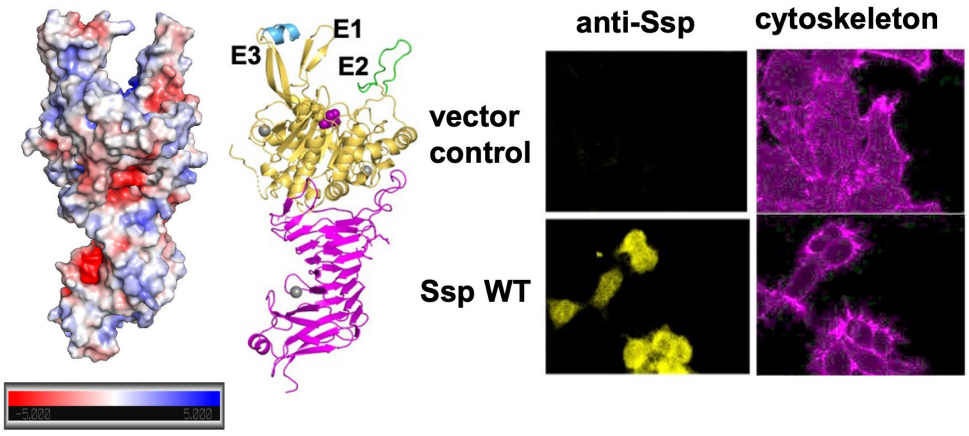
Bacterial virulence factors allow bacterial pathogens to cause infections and disease. Our research looks at revealing the molecular mechanisms of these virulence determinants and their regulators in these processes. Apart from providing detailed information on bacterial pathogenesis and pathogen–host interactions, we used this information to develop new antimicrobials that target virulence processes to 'disarm' rather than kill pathogens. Furthermore, our research also harnesses the molecular properties of virulence factors to create novel medical tools.

The largest group of secreted and surface-bound bacterial virulence factors are the autotransporter proteins, which promote a range of pathogenic processes such as colonisation, biofilm formation, tissue destruction, immune evasion and epithelial penetration. Autotransporters are grouped based on a shared mechanism for the transport of their functional domains to the bacterial surface. However, these domains vary widely with an average of less than 20% shared sequence identity, which can be classified into 16 distinct functional groups. Despite the identification of more than 1500 autotransporters, only a few autotransporters have been functionally and structurally characterised, mostly belonging to just two functional groups.

In this research, we performed the first structure–function analysis of a representative from the large subtilase autotransporter toxin group, Ssp from *Serratia marcescens*. Apart from *Serratia*, subtilase autotransporters are found throughout pathogens, ranging from *Bordetella pertussis, Neisseria meningitidis, Pseudomonas* spp. to *Fusobacterium* spp. These autotransporter toxins have been found to be involved in tissue destruction along with contributing to other roles in bacterial pathogenesis.

In our latest work, we determined the X-ray crystal structure of the Ssp functional domain, which revealed a new toxin framework consisting of an N-terminal subtilisin domain connected to a C-terminal three-stranded β-helix. It has been almost a decade since a new toxin class has been structurally determined. Ssp contains a distinct β-helical scaffold from other autotransporters and even the subtiliase domain was found to be different to other subtilases, through harbouring three active site finger-like protrusions, that we showed were involved in substrate recognition.

S. marcescens is known to have a wide host range from insects to humans. Indeed, our functional characterisation of the Ssp toxin showed that it was active against both human epithelia and in our *Galleria mellonella* (wax moth) model of infection, to cause tissue destruction and death, respectively. We found this cytotoxicity was associated with Ssp entry into epithelial cells that was dependent on its active site subtilase activity.

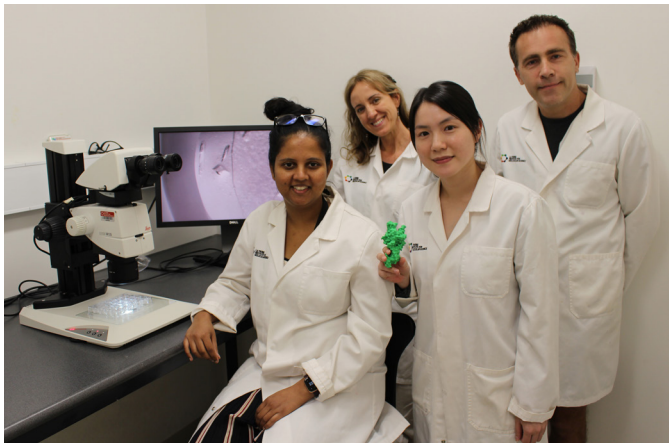


***Left:** Our X-ray crystal structure of the Ssp toxin functional domain. Subtilase domain (yellow) with active site serine (purple spheres) and β-helix (magenta) and active site finger-like protrusions E1–3.*
***Right:** Ssp enters human epithelial cells to cause cell rounding (anti-Ssp antibodies yellow, phalloidin actin stain magenta).*

Publications with Impact

This research provides detailed molecular information into a new class of bacterial toxins. Ssp was also found to exhibit an uncommon broad specificity towards a range of animal tissues, which was consistent with the wide host range of *S. marcescens*. It will be interesting to determine if other toxins in this group also display this feature. Our insights into the molecular mechanism of the Ssp subtilase autotransporter toxin, together with our similar research on other autotransporters involved in bacterial colonisation, biofilm formation, internalisation and cytotoxicity, provide a much-awaited depiction into the different roles these virulence factors play in many aspects of bacterial infection and disease.

Jason Paxman and Begoña Heras
La Trobe Institute for Molecular Science,
La Trobe University



Members of the La Trobe team, from left: Akila Pilapitiya, Begoña Heras, Lilian Hor and Jason Paxman.

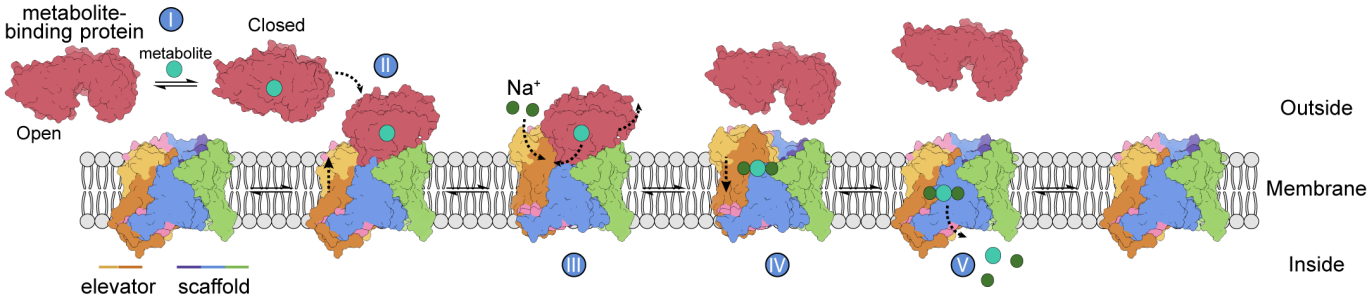
TRAPped in an Elevator: The First High Resolution Structures of a Tipartite ATP-independent Periplasmic Transporter Reveals its Mechanism

Davies JS#, Currie MJ#, North RA#*, Scalise M, Wright JD, Copping JM, Remus DM, Gulati A, Morado DR, Jamieson SA, Newton-Vesty MC, Abeysekera GS, Ramaswamy S, Friemann R, Wakatsuki S, Allison JR, Indiveri C, Drew D, Mace PD, Dobson RCJ*. Structure and mechanism of a tripartite ATP-independent periplasmic TRAP transporter. *Nat Commun* 2023;14(1):1120.
#Contributed equally to this work
***Corresponding authors: rachel.north@dbb.su.se, renwick.dobson@canterbury.ac.nz**

Pathogenic bacteria import metabolites from their environment that are critical for their survival during infection. Specialised transporter proteins embedded within the bacterial cell membrane control this process. We work on **TR**ipartite **A**TP-independent **P**eriplasmic (TRAP) transporters, which are a large family of membrane transporter proteins that have evaded structural characterisation for almost 25 years. TRAPs are only found in bacteria and archaea, not in eukaryotes, and because some homologues import essential metabolites, this opens an avenue for antimicrobial design against pathogens that use TRAPs during infection.

TRAPs are unique in that they are secondary transporters that use a secreted metabolite-binding protein, similar to that of an ATP-binding cassette (ABC) importer. But instead of hydrolysing ATP to drive transport across the membrane, TRAPs use energy in the form of a Na^+ ion gradient. In our paper, we present high-resolution cryo-EM structures and mechanistic insight for a TRAP that imports host-scavenged sialic acids.

Our structures enabled us to describe TRAPs as elevator-type transporters that comprise a rigid scaffold domain anchored in the membrane and a transport domain that traverses up and down through the



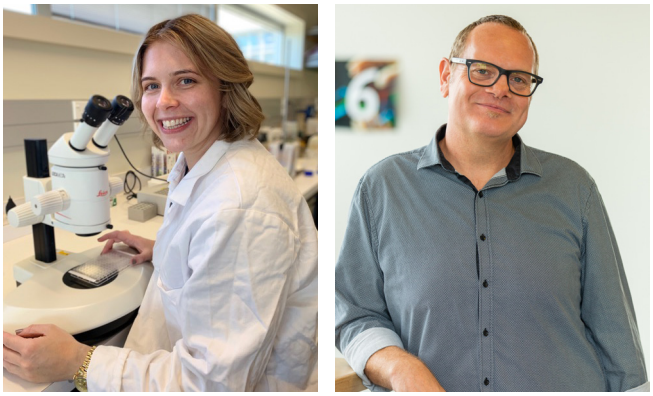
The elevator-with-an-operator mechanism.

membrane to deliver scavenged metabolites to the inside of the bacterial cell. Our structures show that TRAPs have an extended scaffold domain not seen in other elevator-type transporters that enable them to function as monomers (as opposed to the typical oligomers seen for other elevator-type transporters).

We resolved the metabolite and Na^+ ion binding sites in the TRAP and confirmed this assignment using structural homology and mutagenesis experiments. We also show that lipids are important for TRAP function, the metabolite-binding protein is essential for transport, and by modelling the whole complex (metabolite-binding protein with the membrane transporter component) we were able to predict hotspots of interacting amino acid partners between these two proteins. Mutagenesis and transport assays confirm that many of these hotspots contribute to the recognition and/or allosteric modulation of the metabolite-binding protein to release the metabolite to the transporter component for import.

Together, we used our data to propose a new 'elevator-with-an-operator' mechanism of transport. Here, the loaded metabolite-binding protein (step I in the figure) is the operator that triggers the motion of the elevator (orange/yellow domains) to move into the up position and receive the metabolite (steps II and II). The metabolite is then moved across the membrane with the help of a Na^+ ion gradient (steps IV and V). Teasing apart the intricacies of this mechanism and how these two proteins are conformationally coupled is ongoing.

Rachel North
University of Sydney
Renwick Dobson
University of Canterbury, New Zealand



Rachel North (left) and Renwick Dobson.

The Antifungal Crocodile Defensin CpoBD13 Kills *Candida albicans* in a pH-Dependent Manner

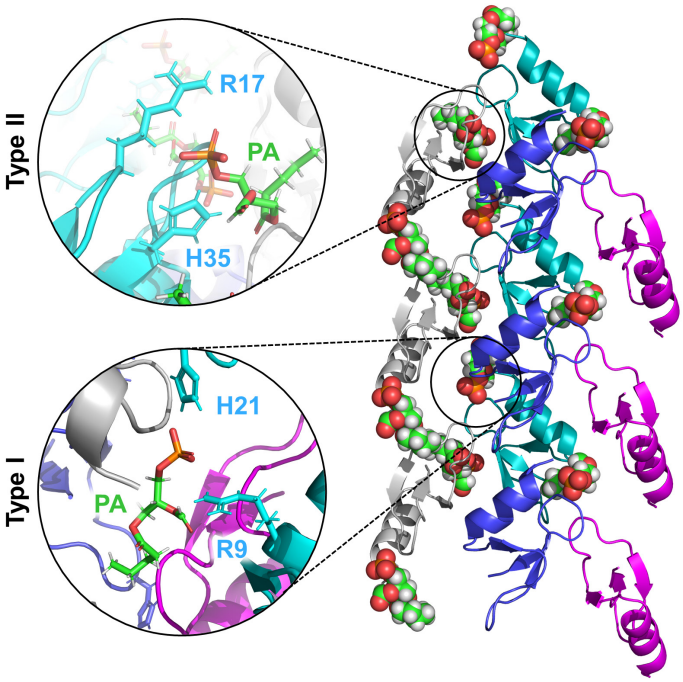
Williams SA, Lay FT, Bindra GK, Banjara S, Poon IKH, Phan TK, Kvansakul M*, Hulett MD*. Crocodile defensin (CpoBD13) antifungal activity via pH-dependent phospholipid targeting and membrane disruption. *Nat Commun* 2023;14(1170).
Corresponding authors: m.hulett@latrobe.edu.au, m.kvansakul@latrobe.edu.au

Fungal disease is an increasing threat to human health worldwide. Severe mycotic disease has disproportionally affected the elderly and immunocompromised patients in the past, however, cases in relatively healthy individuals are becoming more common. Due to the widespread development of resistances against our limited arsenal of antifungal drugs and the emergence of inherently resistant pathogenic species, new effective antifungal therapies are urgently needed.

In the search for potential drug candidates, our attention turned towards the potent immune system of the Australian saltwater crocodile. These ancient reptiles inhabit microbe laden waterways and riverbanks yet, despite receiving open wounds during territorial disputes, they rarely develop systemic infections. Defensins, a class of cysteine rich cationic host defence peptides, contribute to the innate immunity of all eukaryotes. These peptides, which permeabilise microbial cell membranes through the direct binding of negatively charged phospholipids, have been well characterised in humans and plants, however, the defensins of reptiles are poorly understood.

In our study, to better define the structure–function of crocodilian defensins, we identified *Crocodylus porosus* (saltwater crocodile) β-defensin 13 (CpoBD13) in the animal's genome. CpoBD13 was specifically chosen due to the unusual abundance of histidine in the defensin's mature sequence; a phenomenon unseen in the β-defensins of humans. Recombinant CpoBD13 (expressed in the methylotrophic yeast, *Pichia pastoris*) was shown to effectively inhibit the growth of the human pathogenic fungus *Candida albicans* (IC50 of 4.1 μM) through the permeabilisation of the plasma membrane. To investigate the mechanism behind the defensin's membranolytic activity, we performed phospholipid-binding experiments to see if the ability to bind lipid had been evolutionarily conserved with humans and plants. CpoBD13 was found to specifically bind the membrane lipid phosphatidic acid (PA) and form large supramolecular sheet like structures (determined by transmission electron microscopy). We proposed that these structures are oligomeric membrane disrupting complexes, similar to the protein–lipid fibrils previously observed in the studies of plant defensins.

Publications with Impact



X-ray crystallographic structure of the CpoBD13–phosphatidic acid oligomeric complex (PDB ID: 7T9R). CpoBD13 utilises arginine and histidine residues to bind PA in two independent binding sites, termed the Type I (R9 and H21) and Type II (R17 and H35) binding sites. The antifungal activity of CpoBD13 is regulated by the charge state of the PA binding histidine residues, with the peptide functioning optimally in acidic pH when H21 and H35 carry a positive charge.

To gain insight into how the protein and lipid interacted at the atomic level, the protein structure of CpoBD13 in complex with PA was determined using X-ray crystallography. The complex structure (which resembled a continuous left handed helix) revealed that protein–lipid interactions were mediated by arginine and histidine residues. The presence of histidine as a binding residue was interesting for several reasons. Firstly, previous characterised defensins have been found to primarily utilise arginine and lysine residues for electrostatic interactions with anionic lipids. Additionally, the relatively low pKa of histidine (~6.0) compared to the other basic residues enables modulation of its charge at physiological pH levels. Membrane permeabilisation assays conducted at a range of pH (5.5–7.5) showed that the antifungal activity of CpoBD13 was greater at pH <6.0 due to the increase in charge, and therefore the affinity for PA, accredited to the protonation of the peptide's histidine residues.

These results indicate that the membrane-targeting mechanism, established in the studies of human and plant defensins, has been evolutionarily conserved in the crocodilian defensin CpoBD13. Furthermore, elucidation of the CpoBD-13 structure showed for the first time that the family-defining β-defensin fold is conserved between mammals and crocodiles. This study also uncovered that the ability of CpoBD-13 to bind PA and permeabilise fungal cell membranes is regulated by changes in pH, a function which has not been observed in other defensins. Collectively, these data may be helpful in the development and peptide engineering of future defensin-based antifungal therapeutics.

Scott Williams and Mark Hulett
La Trobe Institute for Molecular Science,
La Trobe Universty

From left: Mark Hulett, Scott Williams and Fung Lay.

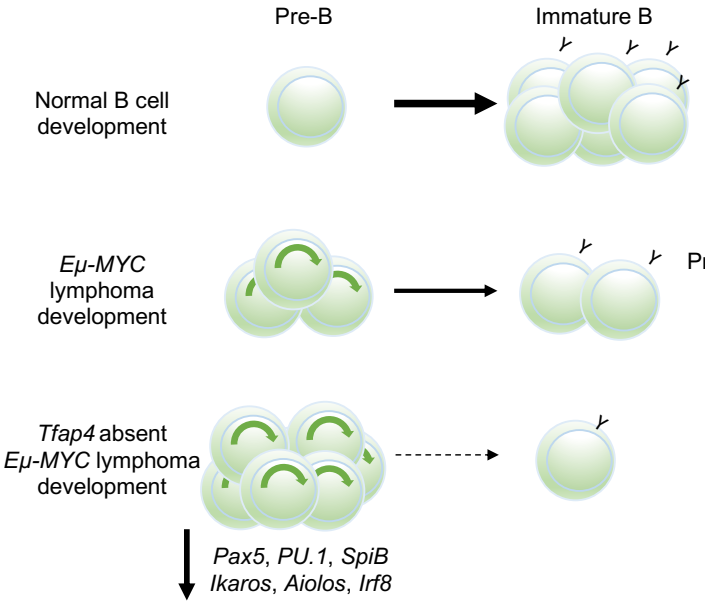
The Transcription Factor TFAP4 Differentiates Itself in MYC-driven Lymphoma Development

Potts MA, Mizutani S, Garnham AL, Li-Wai-Suen CSN, Kueh AJ, Tai L, Pal M, Strasser A, Herold MJ*. Deletion of the transcriptional regulator TFAP4 accelerates c-MYC-driven lymphomagenesis. *Cell Death Differ* 2023;30(6):1447-1456.
***Corresponding author: herold@wehi.edu.au**

The Herold lab is interested in functionally identifying and validating tumour driving genes in blood cancers using CRISPR technologies *in vitro* and *in vivo*. We employ the *Eμ-MYC* mouse model of B cell lymphoma that mimics Burkitt lymphoma as well as other MYC-driven malignancies. Of note, the MYC oncogene is abnormally highly expressed in approximately 70% of human cancers.

Previously, our lab identified the transcription factor *Tfap4* as a candidate tumour suppressor gene in

Publications with Impact



In wildtype mice, B cells differentiate normally from pre-B cells to immature B cells. Conversely, Eμ-MYC *mice have a pool of highly proliferative pre-leukemic pre-B cells that transform into pre-B and immature B cell lymphomas. Deletion of TFAP4 further impairs B cell differentiation in* Eμ-MYC *mice at the pre-B cell stage due to failure to upregulate transcription factors driving B cell differentiation and transform into pre-B cell lymphoma only.*

Eμ-MYC lymphoma development in a genome wide *in vivo* CRISPR/Cas9 knockout screen. TFAP4 represents an attractive hit, as it is directly regulated by MYC and is involved in many MYC regulated processes. Furthermore, approximately 9.7% of human Burkitt lymphoma patient samples carry inactivating mutations in TFAP4. While there are many studies on the roles of TFAP4 in solid malignancies, not many studies investigated TFAP4 in lymphoma development.

To elucidate the role of TFAP4 in MYC driven lymphomagenesis *in vivo*, we deleted *Tfap4* in *Eμ-MYC/Cas9* doubly transgenic primary haematopoietic stem and progenitor cells (HSPCs) with an sgRNA targeting *Tfap4*. These cells were transplanted into irradiated recipient mice and monitored for lymphoma onset. We observed significantly faster lymphoma development in mice reconstituted with TFAP4-deficient HSPCs compared to mice reconstituted with control HSPCs. Immunophenotyping of fully transformed TFAP4 deficient lymphoma cells revealed an exclusive pre-B cell phenotype, which is in contrast to control lymphomas that developed into pre-B, B cell or mixed B cell lymphomas. We next assessed the different blood cell lineages in pre-leukemic mice. Mice transplanted with TFAP4 deficient HSPCs showed an increased proportion of pro-/pre-B cells and a reduced proportion of further differentiated immature B cell subsets. Together, these results suggest that TFAP4 might regulate B cell differentiation during MYC-driven lymphomagenesis.

Indeed, RNA sequencing of TFAP4 deficient pre-leukemic pre-B cells demonstrated dysregulated expression of genes that orchestrate early B cell differentiation, including *Ikzf1, Ikzf3, Spi1, SpiB* and *Pax5*. Bioinformatic analysis of public data revealed that all these genes are direct targets of TFAP4 and MYC. Therefore, we propose that loss of TFAP4 leads to a failure to upregulate genes critical for B cell differentiation. Lack of differentiation, in combination with high MYC expression, increases the pool of highly proliferative pre-leukemic pre-B cells, which acquire additional mutations that drive transformation into malignant pre-B cell *Eμ-MYC* lymphomas. Interestingly, a separate study found that *TFAP-low/MYC-high* expression correlates with significantly poorer rates of survival in patients with paediatric B progenitor cell acute lymphoblastic leukaemia (B-ALL). Therefore, restoring TFAP4 or one of its direct target genes identified in our study could restore B cell differentiation into less proliferative mature B cells, and serve as a novel therapeutic approach to treat MYC driven malignancies.

Margaret Potts and Marco Herold
Walter and Eliza Hall Institute of Medical Research, University of Melbourne and Olivia Newton-John Cancer Research Institute

Clockwise from top left: Maggie Potts, Marco Herold, Lin Tai and Andrew Kueh.

Publications with Impact

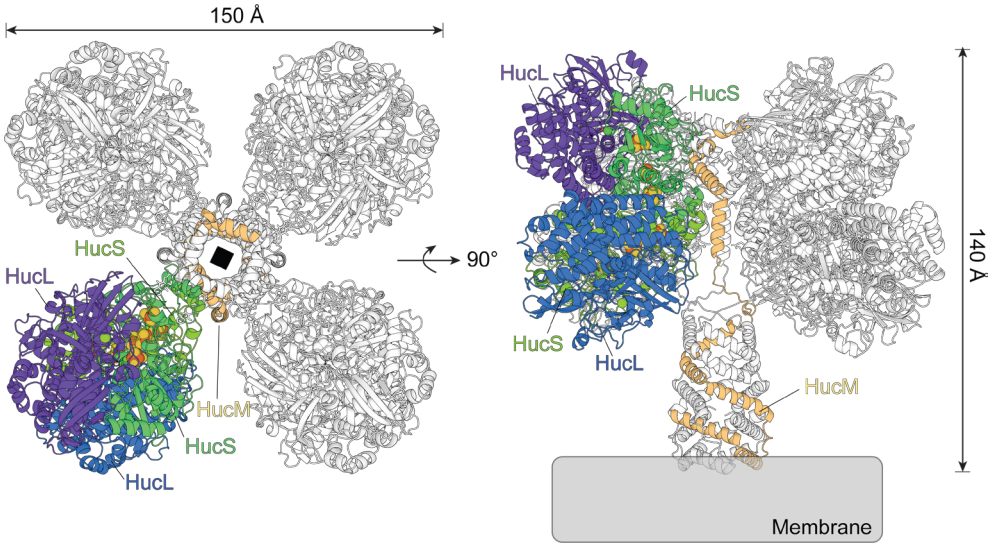
Living on Thin Air: the Structural Basis for Atmospheric Hydrogen Scavenging by Bacteria

Grinter R[#*], Kropp A[#], Venugopal H, Senger M, Badley J, Cabotaje PR, Jia R, Duan Z, Huang P, Stripp ST, Barlow CK, Belousoff M, Shafaat HS, Cook GM, Schittenhelm RB, Vincent KA, Khalid S, Berggren G, Greening C*. Structural basis for bacterial energy extraction from atmospheric hydrogen. *Nature* 2023;615(7952):541-547.
[#]Contributed equally to this work
***Corresponding authors: rhys.grinter@monash.edu, chris.greening@monash.edu**

Microorganisms are the most abundant and diverse life forms on earth, and have colonised almost every habitat imaginable. Within these microbial communities, competition for resources is fierce, and as a result, many bacteria are starved of the energy required for growth and exist in a dormant, but viable, state. In this state, bacteria require a small amount of energy to remain viable. Work by the Greening lab and others over the past decade has demonstrated that soil bacteria overcome starvation by using the trace quantities of hydrogen (H_2) in the atmosphere (air contains 0.00005% H_2) as a source of energy. Bacteria harvest this H_2 using specialised members of the [NiFe]-hydrogenase family of enzymes. Atmospheric H_2-oxidising hydrogenases are widespread in soil bacteria and pure culture experiments show they are important for survival during energy starvation. Furthermore, this process shapes the composition of our atmosphere, as soil bacteria remove 60 million tonnes of hydrogen from the atmosphere every year, representing 75% of all hydrogen removed.

The goal of our current work was to understand how atmospheric H_2-oxidising hydrogenases work on a structural and biochemical level. To achieve this, these enzymes must have an extremely high affinity for H_2 and be resistant to inhibition by oxygen, properties not observed in any previously characterised hydrogenase. We worked with the model soil bacterium, *Mycobacterium smegmatis*, which produces a [NiFe]-hydrogenase named Huc, in order to oxidise atmospheric H_2 when it is starved for other sources of energy. [NiFe]-hydrogenases are complex enzymes, composed of two core subunits, which contain a catalytic [NiFe] cluster and a series of iron-sulphur clusters for electron transfer. These catalytic subunits often associate with additional subunits to form the mature enzyme. This complexity makes them difficult to produce recombinantly, so we isolated native Huc from *M. smegmatis* cells by engineering a chromosomally-encoded affinity tag. The yields from this purification strategy were modest. For each expression batch, we grew *M. smegmatis* in 16 L of carbon-limited media, which yielded only 500 μg of protein. However, with a lot of work on Ashleigh Kropp's part, this provided enough enzyme for structural and biochemical characterisation.

Our first striking observation was that, despite only being predicted to contain two catalytic subunits (HucS and HucL), Huc is an oligomer with a molecular weight of approximately 800 kDa that associates with the cell membrane. We also discovered that Huc contains a third previously unidentified protein subunit, which we designated HucM. Using a genetic knockout and native-PAGE, we showed that HucM is essential for



The cryoEM structure of the [NiFe] hydrogenase Huc from M. smegmatis. *Adapted from Grinter R* et al. Nature *2023.*

the formation of the Huc oligomer. Next, we performed biochemical analysis on the Huc complex, showing that it is totally insensitive to inhibition by oxygen and is capable of oxidising hydrogen well below atmospheric concentrations, making it the highest affinity hydrogen oxidising catalyst identified to date. Moreover, using electrochemistry, we showed that Huc can use traces of H_2 in the air we breathe to generate an electrical current.

We determined the structure of the Huc oligomer at 2.19 Å using cryo-electron microscopy (cryo-EM). This showed that Huc is shaped like a symmetrical four-leaf clover and is composed of eight HucS, eight HucL and four HucM subunits. The HucM subunits form a central tetrameric scaffold that supports the HucS and HucL subunits and attaches the complex to the membrane, providing evidence for the essentiality of oligomerisation Next, we performed a focused refinement on one of the four lobes of the Huc complex obtaining a resolution of 1.52 Å, a record for a cryo-EM enzyme structure. This allowed us to analyse the structure of the HucS and HucL at near-atomic resolution, resolving the positions of many hydrogen atoms in the structure, and providing insight into how Huc oxidises atmospheric H_2. This showed that the gas channels leading to the Huc [NiFe] active site are much narrower than other [NiFe]-hydrogenases, and as a result, they help to prevent oxygen from entering the enzyme active site. Further, structural and spectroscopic data showed that Huc has an unusual configuration of three [3Fe-4S] clusters in its small subunit, which likely contributes to its high affinity for hydrogen.

Altogether, these results show Huc can produce energy from small amounts of hydrogen in air and reveal the structural basis for these findings. These findings may allow us to develop Huc-containing fuel cells that efficiently and robustly generate electricity from low, even atmospheric, concentrations of hydrogen.

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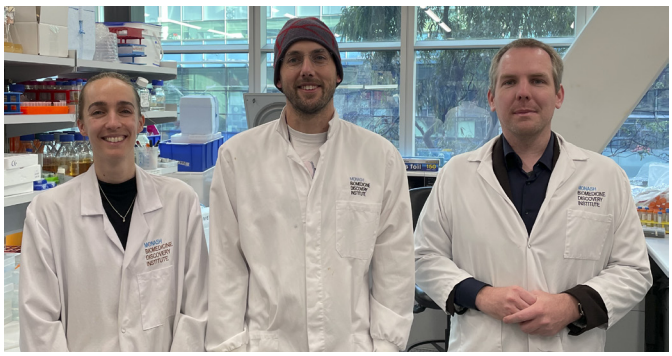

From left: Asleigh Kropp, Rhys Grinter and Chris Greening.

The Origami of Viral Proteins

Sethi A#, Rawlinson SM#, Dubey A, Ang CS, Choi YH, Yan F, Okada K, Rozario AM, Brice AM, Ito N, Williamson NA, Hatters DM, Bell TDM, Arthanari H, Moseley GW*, Gooley PR*.
Structural insights into the multifunctionality of rabies virus P3 protein.
***Proc Natl Acad Sci USA* 2023;120(14):e2217066120.**
#Contributed equally to this work
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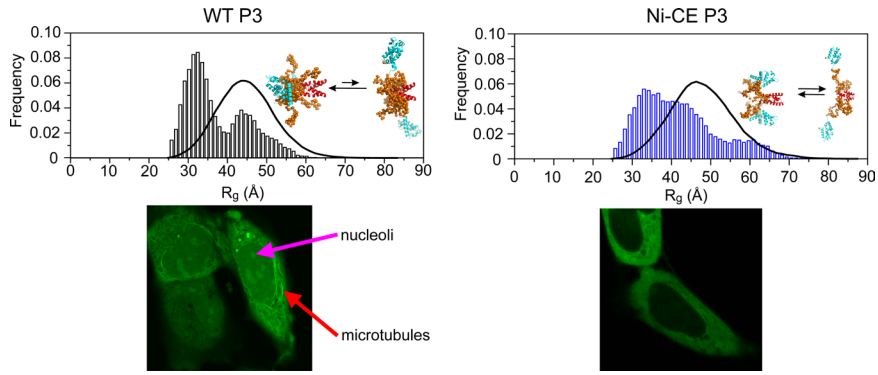
Negative-strand RNA viruses (NSVs) include highly lethal pathogens such as rabies, Nipah and Ebola viruses. These viruses have small genomes that express as few as five proteins but nevertheless can mediate viral replication and assembly, as well as exerting potent control over the biology of the infected cell, including anti-viral immune processes, to create an environment conducive for efficient viral replication. To accomplish these diverse processes, NSVs have evolved proteins with remarkable multifunctionality, such as the rabies virus P protein, that are able to interface with multiple cellular components to hijack and manipulate cellular processes. In the conventional model of protein multifunctionality, we think of a protein comprising a linear sequence of domains, each of which has one or more distinct functions. Thus, truncation or deletion of one of the domains would result in loss of those functions. However, studies of P protein indicate that this is not the case, and truncation can result in the extensive gain of new functions involving multiple regions of the protein, suggesting that properties beyond the simple complement of functional domains are important.

Rabies virus has only five genes, but increases its coding capacity by expressing five isoforms of P protein, called P1-5, that differ in cellular localisation and function. The full-length protein, P1, has critical functions in replication through interaction with viral N and L proteins, and has a potent N-terminal nuclear export sequence, causing it to localise in the cytosol, where replication occurs in viral 'factories' called Negri bodies, which are liquid–liquid phase separated membraneless organelles (MLOs). The P3 isoform is truncated, removing sequence essential to replication function and nuclear export. However, P3 demonstrates a remarkable gain in function including profoundly

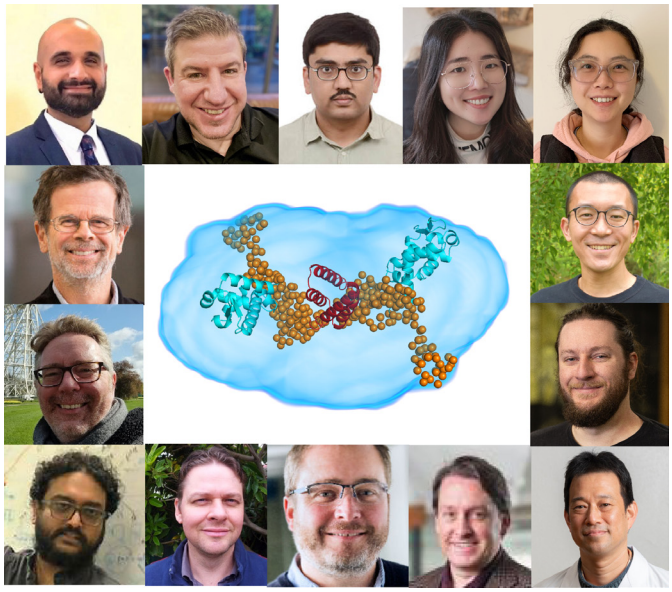
Publications with Impact



P3 multifunctionality derives from higher order conformational organisation. Ensemble pptimised method analysis of small angle X-ray scattering data (upper panels), together with cross-linking mass spectrometry and NMR data, show wildtype P3, from a pathogenic rabies strain, shows preference for a closed state, where the C-terminal domain interacts with the intrinsically disordered domains. In contrast, P3, from the attenuated Ni-CE strain prefers an open state with reduced interdomain interactions. These complex intramolecular interactions correlate with phenotype (lower panels) where live cell imaging shows P3 from pathogenic P3, but not Ni-CE rabies virus localises to nucleoli and microtubules, which underlies unique functions in regulation of ribosome biogenesis and immune evasion. Adapted from Sethi A et al., Proc Natl Acad Sci USA *2023.*

enhanced nuclear import, association with host cell MLOs such as nucleoli and other nuclear bodies, and bundling of microtubules, which impart novel functions including in immune evasion. These differences in function appear to require interactions between domains and regions that are distant within the P protein sequence. Notably, despite containing the full P3 sequence, P1 lacks these functions.

With collaborators in Japan, we are characterising the structures, interactions and functions of P1 and P3 from a pathogenic strain of rabies called Nishigahara, and a non-pathogenic derivative called Ni-CE, which contains several mutations in its P protein that contribute to the attenuation. In our publication, we compared the structure, cellular localisation and phenotype of P3 from Nishigahara (wt-P3) and Ni-CE P3. The P proteins are dimers, comprising two disordered and two structured domains, making it challenging to determine their structure. Using an integrated structural biology approach by combining size exclusion chromatography in line with small angle X-ray Scattering (SEC-SAXS, performed on the SAXS beamline at ANSTO), Cross-linking Mass Spectrometry and NMR spectroscopy (NMR and MSPF at Bio21 Institute), we showed that individual domains of wt-P3 interact with each other, especially the structured C-terminal domain (CTD) with the two disordered domains. We envisaged the functional protein to be an equilibrium between 'closed' (where domains interact) and 'open' conformations. Ni-CE P3, however, is much more open, with apparent loss of all interactions between the CTD and the first disordered domain. Importantly, using techniques including live-cell and super-resolution imaging, we found that these differences in higher order structure correlate with phenotype, whereby Ni-CE P3 loses characteristic interactions with MLOs, microtubules and the nucleus. We further showed that wildtype P3 undergoes phase separation *in vitro*, whereas Ni-CE P3 cannot, suggesting that this may underpin P3 interaction with host-cell MLOs. Thus, our research indicates that higher order organisation, distinct from the simple presence or absence of domains, appears critical to P3 isoform's unique gain-of-functions. These findings advance understanding of multifunctionality by showing that while individual domains can contribute discrete functions to multidomain proteins, intricate and complex interactions between the domains can generate additional functions. Such phenomena show how a virus (or indeed other biological entities) with a limited number of proteins can expand its functional repertoire.



Clockwise from top left: Ashish Sethi, Steve Rawlinson, Abhinav Dubey, Yoon Hee Choi, Fei Yan, Kazuma Okada, Aaron Brice, Naoto Ito, Nick Williamson, Danny Hatters, Toby Bell, Hari Arthanari, Greg Moseley and Paul Gooley.

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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).

Inclusive Laboratory Practice: Perspectives of a Second-year Undergraduate Student

Amber Willems-Jones and Alexander Rey (University of Melbourne) talk to undergraduate Biochemistry student Michael Blyth

Universities nationwide affirm that students experience education opportunities equally and inclusively. At the University of Melbourne, the Diversity and Inclusion Strategy 2030 states, "Diversity and inclusion… is about opening the intellectual enterprise to people who may be prevented from attending because of broader social inequities, by creating space, opportunities, ….. and support for underrepresented students and staff." Furthermore, the university's Disability Inclusion Action Plan indicates that the university aspires to "become a champion and an exemplar of disability inclusion and accessibility" through the removal of "barriers to participation in university life that are faced by people with disability."

To this end, when designing the state-of-the-art teaching facility of the Western Edge Biosciences precinct, teaching spaces were tailored to be suitable for all students irrespective of accessibility needs. Wet lab teaching facilities were designed with adjustable height laboratory benches and height appropriate handwash stations to facilitate the needs of wheelchair-user students. We had anticipated that we met the needs of our students, but did we really get the balance right?

Amber Willems-Jones and Alex Rey recently sat down with second year Bachelor of Science student, Michael Blyth, to get his insights into the Techniques in Molecular Science laboratory class in the Department of Biochemistry and Pharmacology at the University of Melbourne.

Can you tell us a little about yourself and your history with disability?

My name is Mike, I'm 28 years old, I'm a mature age student. I am a manual wheelchair user, the result of a mountain biking injury in 2013. Following my injury, I spent a couple of months in rehab at the Austin Hospital, followed by a few years in a bit of a mental rut. It took me some time, but I eventually got my license, a job – all that type of stuff – which in time, led to enrolling into university.

While study currently takes up most of my free time, I have outside interests including music/sound production. I'm also a disability advocate and I help local music venues around Melbourne improve the accessibility experience.

What made you choose to come to university?

After getting my license, I managed to tee up employment at a disability equipment supplier. Prior to my injury, I was employed as a bike mechanic, so the skillset carried over pretty naturally. At the disability equipment supplier, I worked with wheelchair users, their physios and OTs, an experience that led to my current job at the Royal Children's Hospital. I now support kids in rehab with assistive technologies to enable them to use everyday consumer devices, such as eye and head-tracking for iPads, laptops, Xbox, etc (i.e. for kids that don't have the hand dexterity for keyboards, touch screens). Being in a medical environment as a person with a disability, interacting and helping these kids learn to adjust to their disabilities is a profound experience. This provided me with the motivation to pursue medicine, which meant enrolment in a science degree first.

Michael Blyth performing a practical experiment in the second year subject, Techniques in Molecular Science.

Given your accessibility needs, did you have concerns about choosing to study a science degree?

There was some hesitancy. I firstly had to wrap my head around whether studying medicine was something viable I could do from the chair (I do realise there are certain fields that are logistically more complex than others). Because I finished high school in 2012 and had never been to university, I had to go through alternative application routes. I was aware that there would be hands-on practical classes, and I wasn't sure how that would work out, but I felt well-supported from the start. It was a matter of asking the right questions and finding support groups, but I managed to find my way around and I reached out to the right people, for example, the SEDS (Student Equity and Disability Support) team.

What has your experience been like so far at university, in terms of inclusivity?

Really good. When I started with SEDS, I was set up with an academic adjustment plan that meant I had access to academic support workers (third year or Masters students) in practical classes to assist me. For example, if I needed to move any large bits of glassware around etc, which happened quite a bit in first year Chemistry.

I've always felt I have had a choice of how much I want to be involved in my practical classes, with teaching staff being flexible and supportive. Though it has been on me to reach out for support, to contact subject coordinators and to arrange times to discuss my needs. While this is acceptable for me as I'm pretty comfortable advocating for myself, I think this could be an area of improvement to help students make those first connections with subject coordinators.

How have you found your experience in the wet lab biochemistry space this semester?

It has been great. When I first came in to discuss my requirements with the subject coordinator, Amber, and the technical team before semester started, seeing the height adjustable benches built into the laboratory was pretty cool. In my first year in other subjects, there were height adjustable tables that were slid into/tacked onto the benches, but they protruded out, which made it a bit difficult to move around. Whereas in this space, the built-in design is so neat, it fits into the rest of the lab. I'm a big believer that accessibility shouldn't stick out like a sore thumb, and the way that accessibility is designed into this space just smoothly blends in with everything else in the lab.

I have felt really supported in this class, by both staff and students. The lab bench has been well set up with items I need easily accessible; and fellow students have been happy to help out whenever I have needed assistance. My demonstrator, Alex, was always aware

of what was going on around our group and made sure I got to participate in everything we were doing. For instance, a few times he moved shared equipment (e.g. gel tanks, etc) to my lower bench, as well as ensuring I got to have the best look I could at some other elevated immovable equipment (e.g. centrifuges). Having a lowered hand washbasin in the lab, plus accessible toilets on the same floor, has also been great.

Did you find it difficult to learn the practical aspects of biochemistry in this class?

Not really. Although there were some instruments that were used that were elevated (e.g. large centrifuges), I didn't feel like I was missing out because there were smaller microfuges that the demonstrator used to explain the underlying principles.

While this next point wasn't really an issue (but rather something I became aware of in the practical exam) I realised I needed to be more vocal when working with a lab partner. In terms of challenges, I found that sometimes we were working at different speeds and on different parts of experimental protocols. A recommendation to others with a disability working with a lab partner: make sure you clearly verbalise what your needs are.

Would you recommend taking a lab class to others with the same accessibility requirements as you?

For sure. Absolutely. After my first year lab class experience, I anticipated that there would be more moving around of large items which would mean I would be extremely reliant on my lab partner or support worker, but it wasn't like that. It was all molecular biology and biochemistry experiments at the bench, and I had everything I needed with enough space to perform the experiments myself (with all my equipment accessible and clearly laid out) without a support worker. I felt comfortable to work independently and found it to be a great experience.

Without doubt, the lab space is exceptional. For me though, the most important part of accessibility is ensuring people with disabilities are included in the conversations, and that their concerns are listened and responded to.

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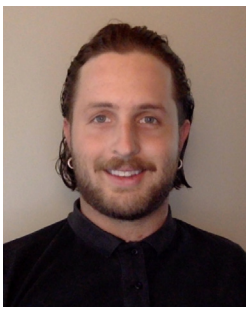

ChemBraille: 3D Chemical Models for the Vision Impaired

Aaron Oakley, University of Wollongong

In 1865, German chemist August Kekulé famously described a dream about a snake eating its own tail as the inspiration for the now-accepted hexagonal ring structure of benzene. This emphasises the importance of visuospatial thinking in chemistry. Molecular models can be used to inform visuospatial thinking and represent an important learning aid for students. While commercially available chemical models typically use colour to represent different elements, this visual stimulus is not accessible to those who are visually impaired. To further enhance accessibility of chemistry models to the blind and vision impaired, I developed 'ChemBraille' – tactile chemistry models inspired by my involvement with two visually impaired students in second-year university chemistry subjects I taught.

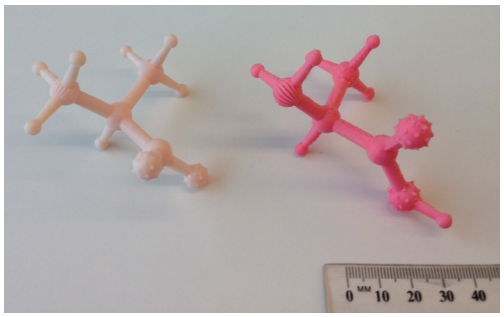

Fig. 1. *Printed ChemBraille models of L-alanine. Ruler shown for scale.*

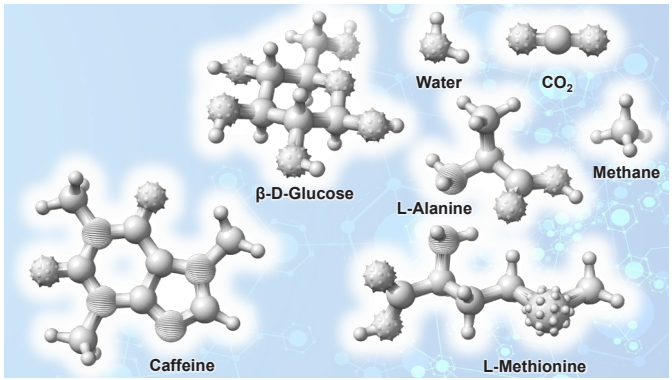

Fig. 2. *Computer rendering of ChemBraille models of biologically relevant compounds.*

Using widely available chemical structure files, the ChemBraille system is flexible in that any organic compound can, in principle, be converted to an inexpensive tactile 3D molecular model. Chemical data in the form of 'chemical table files' (a family of text-based chemical files) is used as a starting point for the generation of models. These files contain information about atoms, bonds, connectivity and the coordinates of molecules. Using a newly developed Python script, sdf2scad, to convert chemical table files to OpenSCAD scripts, the OpenSCAD then acts as a 3D compiler that takes the script generated by sdf2scad and renders the model. The model is output as a STL file, which is widely used in computer aided design (CAD) and can be imported by 3D-printer software for model production.

In the physical ChemBraille models, spheres represent atoms and rods represent bonds. For the elements boron, carbon, nitrogen, oxygen, fluorine, phosphorus, sulfur, chlorine, bromine and iodine, distinctly textured atoms are produced, each with their own unique 'feel'. Bond order is encoded by the profile of the connecting bridges between atoms. Single bonds have a circular profile, double bonds a square profile and triple bonds a hexagonal profile. Thus, through touch alone, a ChemBraille model conveys information about elements, molecular shape and bonding. An example of a 3D-printed model for L-alanine is shown in **Fig. 1**.

For biochemical education, I have produced models of relevant molecules including amino acids, nucleic acid bases and simple sugars. Some designs are shown below in **Fig. 2**.

I have produced a set of ChemBraille models for high school and university teaching. The 'functional group set', available from the Harvard Dataverse, contains model compounds comprising common functional groups of organic chemistry (aldehyde, ketone, ester, amines, etc).

Feedback from students has been positive. One visually impaired second year student noted, "I wish I'd had these in first year." It should be noted that the use of ChemBraille models is not necessarily restricted to blind students; the tactile information encoded in such models is readily apparent to sighted chemistry students and can be used for the same learning purposes. A natural advantage of the ChemBraille system is that models can be printed on the most common (and economical) 3D printers, which are invariably restricted to one colour. An advantage over systems based on fixed sets of bonds and atoms (as exemplified by most available chemistry model sets) is that the number of models is not limited to what can be created by the number of parts provided.

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Open-book and Open-AI Mindset: Strategies to Redesign Final Exams in Response to Generative AI and the Potential for Academic Misconduct

Eduardo Araujo Oliveira and Sarah Frankland, University of Melbourne

During the COVID-19 pandemic, the potential for academic misconduct was heightened when final exams had to be held online rather than in invigilated in-person settings. More specifically, being able to complete exams in a largely unsupervised online form afforded students the opportunity to cheat by using search engines and other online tools to seek answers to questions (1,2). In addition, the emergence of ChatGPT in 2022 raised concerns in academia due to the platform's ability to generate largely accurate, well-structured and original texts in response to simple prompts that can be submitted by students as their own work (3). In this article, we reflect on an example of how an online final exam worth 60% of the overall grade was modified to reduce the risk that students would engage in cheating and plagiarism using online tools.

Redesign of Software Design and Architecture final exam

Software Design and Architecture is a core subject in the Master of Software Engineering degree at the University of Melbourne with 80–100 enrolments. Between 2012–2019, the final exam was an invigilated in-person written exam worth 60% of the subject grade (4). The exam, 2-hours in length, featured several short answer and open-ended questions predominantly related to definitions and concepts covered in the subject, but was not really designed to challenge students to apply their knowledge in authentic ways (5). Motivated to improve the design of the exam due to the transition to an open-book online exam format during COVID, and to focus more on authentic assessments rather than the memorisation of facts, the teaching team reimagined and refined the exam to encourage knowledge application while also minimising problems involving academic misconduct. A practice exam was delivered through Gradescope in Week 11 to better prepare students for the new final exam format (and for them to become familiar with Gradescope).

As shown in Table 1, the original exam questions asked students about well-known software engineering principles that can be easily memorised or found through search engines on the internet. In similar contexts, generative AI technologies like ChatGPT would have no difficulty in creating answers for these types of questions as these large language models were trained with huge data available on the internet. In contrast, the refined exam questions made it difficult for students to cheat using AI or the internet because questions were based around subject-specific (and sometimes imaginary) scenarios with unique problems that did not exist online or in ChatGPT's training material (**Table 1**). In the new questions, students were asked to evaluate, synthesise, or apply concepts to solve novel real-world problems, limiting the potential use of AI or internet -based search tools for cheating or plagiarism. The new final exam was fully aligned with topics and scenarios covered in the students' projects (worth 40% of subject grade), which they received feedback on as part of four deliverables between weeks 1 and 11.

The new exam format proved difficult for ChatGPT to generate high scoring answers and allayed the teaching teams' concerns that students would be able to use online tools or generative AI to construct their answers.

Though it is an investment of time to craft the new application and higher-order-thinking questions, the consequential advantages of evaluating student learning in a deeper way than the previous recall-based questions, as well as security of exam assessment outweigh such negatives. Moreover, there were no significant changes in overall student results between this exam and previous years, showing similar distributions. While foundational knowledge is fundamentally important to all disciplines and underlying principles and facts must still be remembered and recalled, testing the understanding of this knowledge through evaluation/synthesis style questions is more applicable to high-stakes final assessment.

While this example is of a particular discipline-based exam, the design process is applicable and adaptable to educators in other disciplines, and is one novel approach to ensuring academic integrity, and encouraging students not to cheat.

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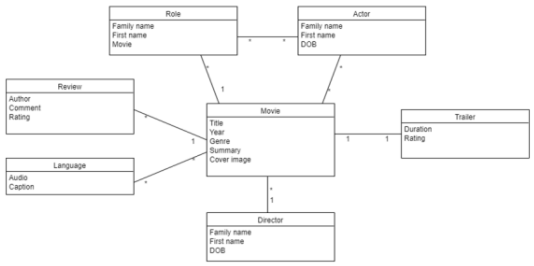
Table 1. *Example of a question about software performance in the original and new final exam.*

Original exam Question on software performance (focus on memorisation) ChatGPT score: 8.5/10	Content Delivery Networks (CDNs) are distributed networks of servers that host data and allow for local caching. ***Describe*** two important properties of data that make it beneficial to be cached, and why poor caching algorithms may have negative consequences on performance. *In this question format, we ask students to describe well-known concepts in software engineering. And we name them to students.*
New exam Explanation of new scenario for question on performance	You have been hired as an enterprise architect for a new company that develops software for an online movie streaming service called Flix. Flix reached 100,000 users in its first month, and the number of subscribers continues to increase. Users can browse a large selection of movies. The domain model diagram of Flix is shown below.  Flix is looking to improve its user experience as subscribers are complaining of extremely slow response times when loading and browsing through the selection of movies. After looking into the system's implementation, architects have identified the following issues: 1. The details of each movie in the selection list are loaded sequentially (i.e. one at a time). 2. Multiple fine-grained requests are made over the network to retrieve all the details related to each movie and display them. 3. The current implementation loads all the trailers in the displayed list, which is inefficient as users don't necessarily watch them all. Subscribers' behaviour has also been studied and Flix has found that users are more likely to watch movies that are popular in their area and in their language. The company wants to take advantage of this information to improve performance.
New exam Question on performance (focus on analysis, evaluation, and application of related knowledge) ChatGPT score: 2/10	***Identify*** four design principles or patterns discussed in the subject that could help in improving the performance of this system. ***Justify*** your answer by explaining how each principle/pattern can improve performance in the context of the system. ***Support*** your explanations with diagrams when appropriate. *In this question format, we ask students to identify four design principles or patterns discussed in the subject. They also need to justify their answers and to support explanations with diagrams when appropriate (in this case, it would be very hard to explain their answers without the support of diagrams).*

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Science Meets Parliament 2023

Science & Technology AUSTRALIA

Megan Outram reports on Science Meets Parliament 2023

Science Meets Parliament (SMP), first created in 1999 and run annually by Science & Technology Australia (STA), is an event designed to facilitate and connect STEM researchers with our country's key policy decision makers. Firstly, SMP offers tailored training to give STEM experts the skills and knowledge to effectively engage with the media and policymakers. Secondly, SMP builds on this training by providing a platform to connect STEM experts and policymakers. For 2023, SMP was run as a hybrid event, and I was fortunate to be supported by the ASBMB to attend both online and in-person events.

SMP online promised to "deliver world-class Science Meets Parliament training, professional development and inspiring speakers online," and it certainly did. The online section was jam-packed, and over the course of the three days (7–9 March), we heard from a stellar line up of about 50 speakers from scientific, policy/political and media backgrounds. I found all the sessions engaging, both because of the speaker's enthusiasm and topics, but also the capacity to participate with other delegates and the panel members through the chat. All sessions were also recorded so there was the added benefit of revisiting talks or watching them in your own time.

I started the first day doing just that – listening to the pre-recorded session How to Get Science into the Media. We heard from the panel, Patricia Karvelas, Katharine Murphy and Dr Jackson Ryan, their own perspectives on the best ways to engage the media, from knowing when it's a good time to make contact to getting your point across concisely and having a key hook for your research. The first day officially started with an enthusiastic welcome to SMP from STA President, Professor Mark Hutchinson, and STA Chief Executive Officer, Misha Schubert, and a welcome to country from Ngunawal Elder, Uncle Wally Bell, before jumping into the keynote speaker Professor Terence Tao, dubbed the 'Mozart of mathematics'. Professor Tao shared his insights into how maths can help solve the complex problems we face in the real world, and that tackling these problems isn't necessarily just about "being the smartest or the fastest – but about patiently accumulating knowledge."

We then had three panel-based sessions, the first a refresher recapping all things related to the political system and how sharing our STEM expertise can work into the policy process. This led nicely into a panel on effective engagement with policymakers and this session was a particular highlight for me, with many great insights not just in engaging with policymakers but also more broadly for communicating research in general. There were several great tips, including a reminder from Dr Subho Banerjee that media personal and policymakers are busy people with many and varied things on their plate at once, so ensure you are "pertinent, clear and relevant." This same sentiment was echoed by Professor Paul Young, not only with respect to engaging with policymakers but in all facets of research, such as grant writing: "The elevator pitch is key: it's a hook that gets you attention. Then you build a story around the impact your science will have." The concept of storytelling and connection led nicely into the final panel session of the day on the importance and wealth of Indigenous knowledge, and application in modern STEM and society. Closing off the first day, Professor Chris Matthews urged us all to "break open the boxes that (we) situate ourselves in" and to think "deeply about the impact of our work, both on people and Country," which really embodied the theme of this year's SMP – putting science front and centre in our society.

Day two started with another major highlight and fitting for International Woman's Day - hearing from Professor Katalin Karikó, whose incredible research on mRNA and delivery of mRNA in nanoparticles to fight disease played and continues to play a crucial role in vaccine development, including those against COVID-19. While fascinating from both a scientific perspective, Professor Karikó also gave great advice on being resilient in science, including a reminder that we can only control our own responses to setbacks and perhaps the most important advice of the day to "love what you're doing, and to be happy and healthy." I particularly enjoyed her reminder to researchers to "poke holes in their own hypotheses" and really push scientific boundaries!

We then moved into panel sessions focussing on effective advocacy, telling the hard truths in science – where acknowledgement of past wrongs and building trust lends itself to a platform of change moving forward, and finally how to navigate geopolitics in an ever-changing environment.

The focus of the third day of SMP online was preparing delegates to meet with their designated parliamentarian. The first of these preparatory sessions involved perfecting your pitch, which was great preparation for the in-person

Science Meets Parliament 2023

networking we were also soon to do! In this session, we heard from Dr Lila Landowski, Dr Mike Todorovic and Tanya Ha, three stellar communicators, who each gave some phenomenal suggestions to hone our elevator pitch, including "flipping the narrative" to start off with the "why care" to get people hooked onto our research. As scientists, we often think we need to give all the intricate details and are used to speaking to our colleagues that way, but we learnt how important it is not to go down the rabbit hole too far and lose people in the nitty gritty details. This was nicely summarised by the one-line pitch formula from Dr Lila Landowski, "I tackle (this problem) by seeking (this solution) by looking at (this process)." And importantly Tanya Ha reminded us that our pitch is just "a taster – so leave them wanting more." Building on this, the next panel session focussed on preparing us to make the most of the opportunity to meet a parliamentarian, and how to get your message most effectively across in a short time, as things can change very quickly in parliament! The consensus was to get to the main point quickly, share your enthusiasm and make it a memorable and fun experience!

A highlight from the Australian Parliament Geology Tour – the green Cipollino pillars in the Marble Court represent the Australian eucalyptus trees.

A couple of weeks later, we moved to the in-person segment of SMP, aptly called On the Hill. While I am now based in Canberra, I had not yet had the opportunity to make my way inside Parliament House, and it was an exciting start to the day passing through security with David Pocock MP behind and hearing the casual conversation of rugby and politics between him and the security personal. We kick-started the day with a welcome to country from Ngunnawal Custodian, Serena Williams, and an energetic welcome from STA President, Professor Mark Hutchinson. We then jumped straight into the first panel session of the day, led by Misha Schubert with Dr Cathy Foley and ANU Vice Chancellor Brian Schmidt. Both made important points surrounding how crucial science communication is, particularly during this point in time where the world has never "relied so much on science" and encouraged us to continue to push the frontiers of science and adopt new technologies, such as AI and machine learning, to augment scientific research. In the second panel session, Forging a New Golden Era for Australian Science, we heard from Professor Sharath Sriram, Sally-Ann Williams, Dr Anita Goh and Dr Jane Fitzpatrick about the importance of cooperation, collaboration and trust for the theme of the day "seizing the future of Australian science."

Following on from the panel sessions, we had the option to select a tour, and I was fortunate to be a part of the Australian Parliament House Geology Tour. While a little bit out of my area of expertise, it was fascinating to learn about the architecture of Parliament House. We started our tour inside the Marble Court, learning that the green Cipollino marble from Italy was selected to represent eucalyptus trees, and that the limestone floors hold a treasure trove of sea life fossils – be sure to ask about "Sean the Prawn" on your next visit! We then moved on to the members hall to see the Reflective Pool, made from a single piece of South Australian Black Imperial granite. We then returned to the front of the building where we admired the stunning possum and wallaby dreaming mosaic by Aboriginal artist Kumantje Jagamara that serves as a reminder of the continual importance and connection of Indigenous peoples to this land.

We finished the day off with the Welcome Reception and National Gala Dinner in the Great Hall at Parliament House, where everyone was encouraged to "dress fabulously," all 450 of us certainly met the brief. We were welcomed by Misha Schubert, followed by a Welcome to Country from Ngambri Elder, Paul Girrawah House, including a performance on his glass yidaki created at the Canberra Glassworks! We were treated to a wonderful meal and dessert, interspersed between talks from Shaun Jenkinson (ANSTO Chief Executive Officer), the Hon Ed Husic MP (Minister for Industry and Science), the Hon Richard Marles MP (Deputy Prime Minister and Minister for Defence) and the Hon Karen Andrews MP (Shadow Minister for Home Affairs) and the Hon Paul

Deputy Prime Minister, the Hon Richard Marles MP, addresses the SMP National Gala Dinner.

Science Meets Parliament 2023

Science & Technology AUSTRALIA

Megan Outram and AJ Mitchell (Nuclear Physics and Accelerator Applications, ANU) at the SMP National Gala Dinner.

Fletcher MP (Shadow Minister for Science). It was great to hear the importance of science for our nation being recognised, with Richard Marles commenting, "We need to change the conversation and put science front and centre in this nation."

One exciting take-home message for me was that SMP2023 had seen the greatest ever number of parliamentarians (more than 40%) engaging in the program – it's fantastic to see the impacts of STEM in policy, and the willingness of policy makers to engage with STEM working toward that "front and centre" goal. Unfortunately, the parliamentarians designated to sit at our table were unable to attend. However, it was fascinating to meet a variety of people working in so many different facets of STEM, and trying out my elevator pitch, as there was plenty of time to network in between courses and speakers.

SMP2023 exceeded my expectations and I would like to thank the ASBMB for supporting my attendance and my professional development. I feel optimistic about the future of Australian research and particularly the interplay between STEM and policy. I'll remember the words from Shadow Minister for Science, the Hon Paul Fletcher MP, "Your work as scientists is enormously respected and valued across the political spectrum." We as scientists must not lose sight of that. I strongly encourage others to attend SMP2024!

Dr Megan Outram is a postdoctoral researcher at CSIRO and Chair of the Canberra Protein Group, an ASBMB Special Interest Group.
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SDS Page: Short Discussions for Students Page

How I've Started Utilising ChatGPT

George Ashdown

Walter and Eliza Hall Institute

Artificial intelligence (AI) continues to integrate and reshape various aspects of research. One such model, ChatGPT, developed by OpenAI, was trained on a diverse range of internet text sources, using a supervised / reinforcement method and consisting of 175 billion parameters. It has a tested verbal-linguistic IQ of 147.

GPT stands for Generative Pretrained Transformer: the transformer is the part that distinguishes which sections of the input (your text) are most important and which sections it can mostly ignore. This lets it generate human-like responses to text inputs, giving potential value for scientific research.

Some of the capabilities of ChatGPT 3.5 include:

1. **Knowledge extraction:** ChatGPT can summarise literature, enabling researchers to extract relevant information swiftly. **Beware:** it makes up references, and if you ask it to summarise your own paper (yes, I tried this) it does a terrible job.
2. **Assistance in experimental design:** The model can help formulate experimental design, suggesting variables, methodologies or controls.
3. **Hypothesis generation and validation:** Pulling on the vast training data to generate hypotheses from existing knowledge.

SDS Page: Short Discussions for Students Page

4. **It can write code:** including languages such as Python, R, Java, C+ and others. See example below.
5. **Literature review:** Through the use of previous research, it can identify gaps – helping us find those all-important niches!
6. **Writing emails:** Including changing tone – this can be particularly powerful for non-native speakers.

Sounds great, doesn't it? However, there are some important caveats I've noticed:

1. **Lack of understanding:** ChatGPT sometimes generates responses that may appear accurate, but lack contextual understanding. Essentially, it makes responses up, so always cross-reference answers.
2. **Reliance on pre-existing data:** Responses are based on training information, which primarily comprises text available on the internet from 2021 which could already be out-of-date.
3. **Ethical considerations:** As with any AI model, ethical considerations are crucial. These include the environmental impact of using such technologies.

Taking all these points on board I was keen to try it out for myself, so I asked ChatGPT 3.5 to write some code in Python to analyse live-cell fluorescent microscopy images. I wanted it to write code which could segment the cells from background and track them through time. On the surface it seemed to do a good job, generating code which imported the correct libraries, loaded the imaging data, segmented using the Otsu method and attempted to track cells. I knew the function of all these steps because it also annotated the code for me, letting me know what each step was meant to be doing. This makes checking and editing the code (which you will need to do) easier. It also builds on the conversation you're having – taking previous text within the same 'chat' into account when generating follow-up responses.

There are things it didn't do well, for example:

- **Maths:** I've found mathematical errors of an order of magnitude in its code, reinforcing the fact it's a text-based platform, not a mathematical one.
- **Be logical/creative:** when trying to fix errors in its own code, ChatGPT will have a couple of suggestions to try, but that's it. After you've exhausted these options, you're on your own.
- **Finish its own sentences:** When it generates large amounts of text, or code, it sometimes just stops halfway through a response. While obvious, it's annoying having to ask ChatGPT to finish its own sentences.

Bearing this in mind, ChatGPT should be seen as an accelerator – researchers still need a fundamental understanding of what they're asking it to do and knowing the right question to ask. But it can be incredibly useful for providing frameworks (such as some foundational code) for users to work and build on. It has also become a go-to for answering specific questions or error solving, instead of trawling through Stack Overflow.

ChatGPT 3.5 can offer potential in knowledge extraction, experimental design, hypothesis generation and literature reviews. However, caution should be exercised, and its responses validated. With responsible and thoughtful integration into research workflows, ChatGPT 3.5 can serve as a valuable tool for accelerating scientific discoveries and transforming the landscape of biochemistry and molecular biology research. It should be noted that ChatGPT 4 represents a huge step forward from many of the limitations found using ChatGPT 3.5, and, upon release, ChatGPT 5 will move the AI landscape forward again.

The use of AI to support scientific work is particularly timely as Google's Bard has just been released. This has several apparent advantages over ChatGPT, including internet access, image processing and responses, plugins and better coding potential.

Future AI iterations could assist with drug discovery and development, predicting the efficacy and safety of drug candidates, protein engineering by suggesting modifications to enhance protein stability, functionality, or binding affinity. For personalised medicine, it could be used to analyse patient data and medical literature, identifying genetic markers and/or predicting drug responses based on individual patient characteristics. With data analysis from large-scale omics data, the model can help identify correlations, biomarkers and novel molecular pathways.

Overall, our creativity, logic and collaboration mean we're not going to be replaced by AI just yet. And one thing large language models can't do is the practical work, so keep your pipetting skills up! Researchers are safe, at least for now.

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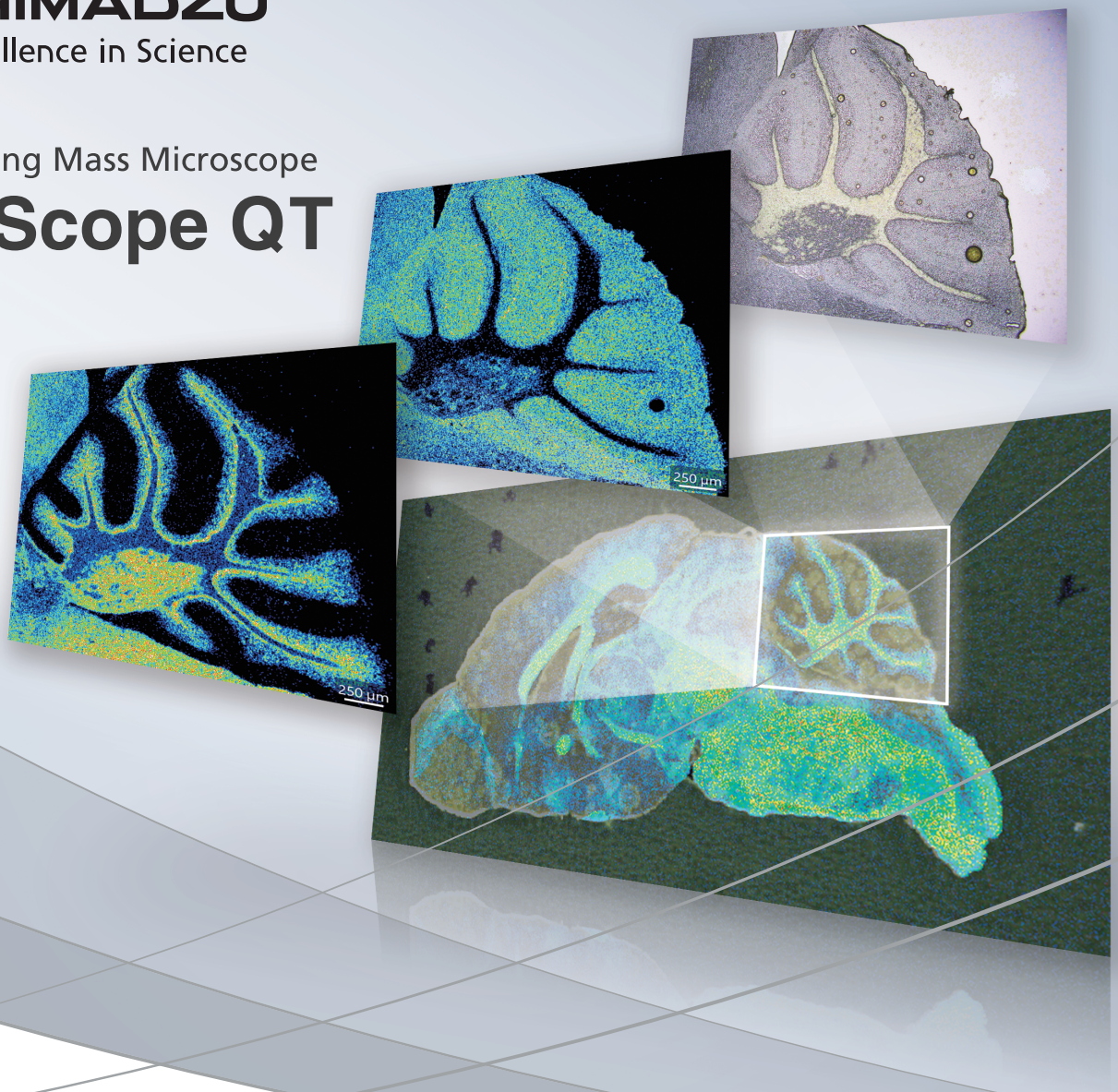

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Education: an ASBMB Special Interest Group

Hello from the Education Special Interest Group (SIG) of ASBMB. It has been a while since we provided a profile for the *Australian* Biochemist, and what a few years it has been! We have all experienced major disruptions to the way we teach Biochemistry and Molecular Biology globally due to the COVID-19 pandemic. Our community rose up and met them head on, with some fantastic achievements along the way. Over the past three years, the Education SIG has:

1. Created an Education Committee to support SIG activities
2. Added educational resources to the ASBMB website to support educators in the transition to online learning
3. Updated the ASBMB Education Award criteria
4. Held an online symposium in 2020, Teaching Remotely: Sharing Practice
5. Held an online symposium in 2021, Sharing Practice: A Focus on Assessment and Academic Integrity
6. Coordinated an Education Day at ComBio2022
7. Managed the Education Feature of the *Australian Biochemist*

1. To support and expand the Education SIG activities, a broader Education Committee was established, welcoming Dr Amber Willems-Jones (University of Melbourne), Dr Matthew Clemson (University of Sydney) and Associate Professor Maurizio Costabile (University of South Australia) to work alongside Associate Professor Nirma Samarawickrema (Monash University) and Associate Professor Tracey Kuit (University of Wollongong). The committee meets regularly to discuss changes in the education sector and plan SIG activities. All ASBMB members are welcome to contact the Education Committee regarding ideas or feedback.

2. At the start of the COVID-19 pandemic, the Education Committee curated resources to assist members in the transition to teaching online: www.asbmb.org.au/education. The webpage remains a place to share resources across the membership and suggested updates are welcome at any time.

3. In 2021, the ASBMB Education Award criteria were updated to clarify and expand the selection criteria and ways to evidence impact: www.asbmb.org.au/the-sdr-scientific-education-award.

4. With the pandemic impacting educators far and wide, the Education Committee decided to deliver an online Education Symposium in 2020 with the theme Teaching Remotely: Sharing Practice. This online event was well attended, with 131 participants from across Australia and a further 119 participants from overseas, many of whom were members of the FAOBMB. The symposium provided a platform to share insights and experiences to recognise good teaching practice. With the inclusion of a student panel for the first time, the symposium highlighted how educators nationwide were embracing online teaching during the pandemic and transforming the student learning experience.

The 2020 ASBMB Education Symposium Organising Committee.

5. Building on the success of the 2020 online symposium, a second online symposium took place in 2021, with the theme Sharing Practice: A Focus on Assessment and Academic Integrity. The online symposium showcased the quality and commitment of our educators, revealing how resilient and strong the biochemistry education community is. Over 160 educators, professional staff, researchers and students from Australasia and beyond connected virtually to share good practice, focusing on assessment and academic integrity.

Education: an ASBMB Special Interest Group

The 2021 ASBMB Education Symposium Organising Committee.

6. In 2022, educators joined ComBio2022 in person with great enthusiasm to showcase the lessons learned from the pandemic and how education practice was being advanced post-pandemic. The Education Day was studded with highlights demonstrating our educators' teaching excellence, innovation, talent and creativity. As always, our student panel discussion invoked much thought and deep reflection as our undergraduate students eloquently shared their experiences. A highlight was the inaugural Education Plenary lecture presented by Professor Merlin Crossley, Deputy Vice-Chancellor (Academic and Student Life), UNSW Sydney.

7. The Education SIG coordinates the Education Feature of the *Australian Biochemist*, published three times annually. In 2023, we updated the guidelines for authors and welcome submissions on contemporary topics. Notably, with the pandemic impacting education across the globe, a special issue was published in August 2020, with 13 stories of how biochemistry educators transformed their teaching during 2020. This feature included shared reflections from students and educators on how they adapted in response to the global emergency – one inspiring the other. Educators balanced asynchronous and synchronous online approaches to promote collaboration and teamwork, built virtual communities to provide peer feedback, simulated practicals and laboratory work and assessed presentations via Zoom to train the next generation of biochemists. Contributions to the Education Feature of the *Australian Biochemist* are welcomed at any time: www.asbmb.org.au/education.

What's happening in 2023?

In 2023, the Education SIG welcomed new leadership, with Associate Professor Tracey Kuit taking on the role of Chair and Education Representative on the ASBMB Council, and Dr Amber Willems-Jones taking on the Deputy Chair role. We thank Associate Professor Nirma Samarawickrema for her stellar leadership as the Education SIG Chair from 2019–2022.

In July, we hosted an online forum with *Biochemistry and Molecular Biology Education* Editor-in-Chief, Professor Phillip Ortiz, titled Publishing in *BAMBEd*.

ASBMB2023 will be held in Canberra in November and will include an Education session. We look forward to sharing ideas in the newly-built Kambri building at the Australian National University. Following on from the online forum held in July, we will hold a writing workshop with a member of the *BAMBEd* Editorial Board, Emeritus Professor Susan Howitt, ANU.

A working group – representing every state and territory – has recently been formed to develop Nationally Accepted Core Concepts for the Discipline of Biochemistry and Molecular Biology, with the aim of publishing the concepts as they pertain to an Australian context.

Biomolecular Horizons 2024 will be held in Melbourne in September next year. This event will include a strong education focus.

Tracey Kuit, Chair, Education SIG
asbmb.org.au/education-sig
tracey_kuit@uow.edu.au

The ComBio2022 Education Day Organising Committee, from left: Matthew Clemson, Amber Willem-Jones, Nirma Samarawickrema, Tracey Kuit and Maurizio Costabile.

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Competition: ASBMB2023 Word Search

Presenting the latest competition for members of the ASBMB. We are getting excited about the upcoming ASBMB2023 meeting, to be held at ANU, Canberra, from 15-17 November 2023. Locate the words associated with ASBMB2023 in the word search. One word is not found within the word search – this is the answer! Submit your entry to the Editorial Officer by 1 September 2023 to enter the draw to receive a gift voucher. With thanks to Joe Kaczmarski.

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ASBMB Awards 2024

SOCIETY MEDALS, AWARDS AND FELLOWSHIPS NOW OPEN

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NOMINATIONS FOR MEDALS AND AWARDS

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

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

ASBMB Awards 2024

APPLICATIONS FOR TRAVEL AWARDS AND FELLOWSHIPS

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

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

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

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

When Time is of the Essence – Timing Experimental Data Collection for Patent Applications

Dr Harriet Manley, Patent Scientist, and Dr Sarah Hennebry, Associate Principal, from FPA Patent Attorneys discuss the considerations regarding the timing of data collection for patent applicaions.

Harriet Manley (top) and Sarah Hennebry.

Introduction

In our previous article, we addressed some common misconceptions that arise when prospective inventors consider if they have enough experimental data for it to be worthwhile protecting their idea with a patent application.

But, once a decision has been made to proceed with a patent application, **when** exactly does the experimental data need to be obtained by? This article aims to clarify key deadlines for incorporating data into patent applications, and explores the option of utilising post-filing data to assist obtaining patent protection if these filing deadlines have passed.

Incorporating data into a patent specification

Provisional application filing

To file a provisional application, you must have enough information to explain the invention in enough detail for the skilled person to understand what the defined invention is (its entire scope), and be able to perform the invention (across its entire scope). These are referred to as support and sufficiency requirements. As described in our April 2023 article, the information included within the patent specification directly influences how narrow or broad the claims can be, impacting the scope of the monopoly that a granted patent would provide.

Because life sciences are often considered unpredictable, it is usually highly challenging to establish support and sufficiency requirements without any data. Data assists demonstrating the technical effect of the invention, and showing that the skilled person would reasonably expect the invention to work across the full scope of the claims. Data are also often important in helping establish that your invention is inventive (ie not routine or obvious to the skilled person in view of the prior art).

Filing an initial provisional application has no deadline as such, but it is the filing that initially *establishes the priority date*. The priority date is the date from which it is assessed whether or not your invention is novel and inventive, and the date from which the patent rights 'start' (t = 0) if the patent is granted (**Fig. 1**).

The inclusion of supporting data in the provisional application maximises the prospects of *retaining and securing* the earliest priority date.

If a provisional is filed without data, the chances of holding onto the priority date are reduced. This is because you risk not meeting support and sufficiency requirements during prosecution of the application. An examiner may deem that your application did not meet these requirements until data was incorporated into the specification – at which point the priority date becomes *the date sufficient data was incorporated*, not the initial date the provisional was filed.

Ideally, by the time that the decision to file a provisional application has been made, the inventors have some data to include that will support the concept of the invention (eg *in vitro* data showing an antibody binds to its intended target). When drafting, there will be considerations around the amount and type of data that is included (for example: wait for more data or file the provisional earlier; include *in vitro* data only, or both *in vitro* and *in vivo*; include positive data only or positive data with some negative data to help demonstrate a non-obvious/inventive result).

But of course, trying to establish a priority date can introduce time pressures! A provisional application may need filing in a short timeframe: for example, to prevent a competitor 'scooping' your idea; to protect an invention before it is publically disclosed in a scientific publication, announcement or presentation; or to meet investor expectations or funding requirements. The choices made regarding the amount and type of data included at the provisional stage are often affected by the need to file the provisional application as soon as possible.

The patent applicant may therefore plan to incorporate data (or more data) after the provisional is filed, and the immediate time crunch has passed.

Your patent attorney will be able to provide advice regarding balancing the risks of filing a provisional later with more data, or filing it earlier with less.

When Time is of the Essence – Timing Experimental Data Collection for Patent Applications

Complete/PCT application filed 12 months later

In a perfect world, the provisional application won't be filed until there is some quality data, and, if the invention is a pharmaceutical composition or method, there would be both *in vitro* and *in vivo* data in your provisional application. But data can still be of significant benefit if it's obtained during the 12 months after the provisional is filed.

Filing the provisional application can be thought of setting a patent application train in motion, ultimately travelling towards a granted patent (**Fig. 1**). Filing a provisional immediately sets a 12-month deadline to file a 'complete' application (in the life sciences space, this is commonly the international PCT application).

This complete application deadline is extremely important. It represents a hard deadline where no new data can be added to the specification after the complete application is filed.

The window between the provisional and the complete filing provides 12 months opportunity to gather additional data (**Fig. 1**). This may include more examples of the key concepts described in the provisional application (e.g. *in vivo* data showing an antibody binds to its intended target *and* exhibits a therapeutic function).

It is **crucial** to carefully evaluate your data position ahead of the 12-month deadline. The amount and type of data in the **final** complete specification is often **critical** to meet support and sufficiency requirements during prosecution, where the aim is to establish that the application can be granted with claims that have commercially valuable scope (i.e. are not so narrow in scope that they provide inadequate protection from competitor activities).

If a complete application is not filed by the 12-month deadline, and you don't 'get off the train' by withdrawing the provisional application before the deadline, the application will publish – becoming prior art that can significantly hinder your future filings, and also disclosing your inventive concept to your competitors without you having patent protection. If you do file a complete application, it establishes a number of follow-on deadlines, including deadlines to enter 'national phase' prosecution.

When approaching the your complete/PCT deadline, your patent attorney will be best placed to assess the data you've obtained in the period, and make appropriate updates to the application before filing the complete/PCT. Your patent attorney will also be able to assess whether there is enough data to progress the application, to ultimately meet your commercial goals.

What if I have no data, or not enough data, by the complete deadline?

Refiling

If there is not enough data by the complete/PCT deadline, it may be worth considering withdrawing the application and re-filing (**Fig. 1**). Re-filing effectively 'restarts the clock', providing additional time to perform experiments and analysis. But 'restarting the clock' gives up the priority date of the first filing – refiling a fresh provisional application establishes a new priority date. This presents a risk that new prior art could have been published in the meantime.

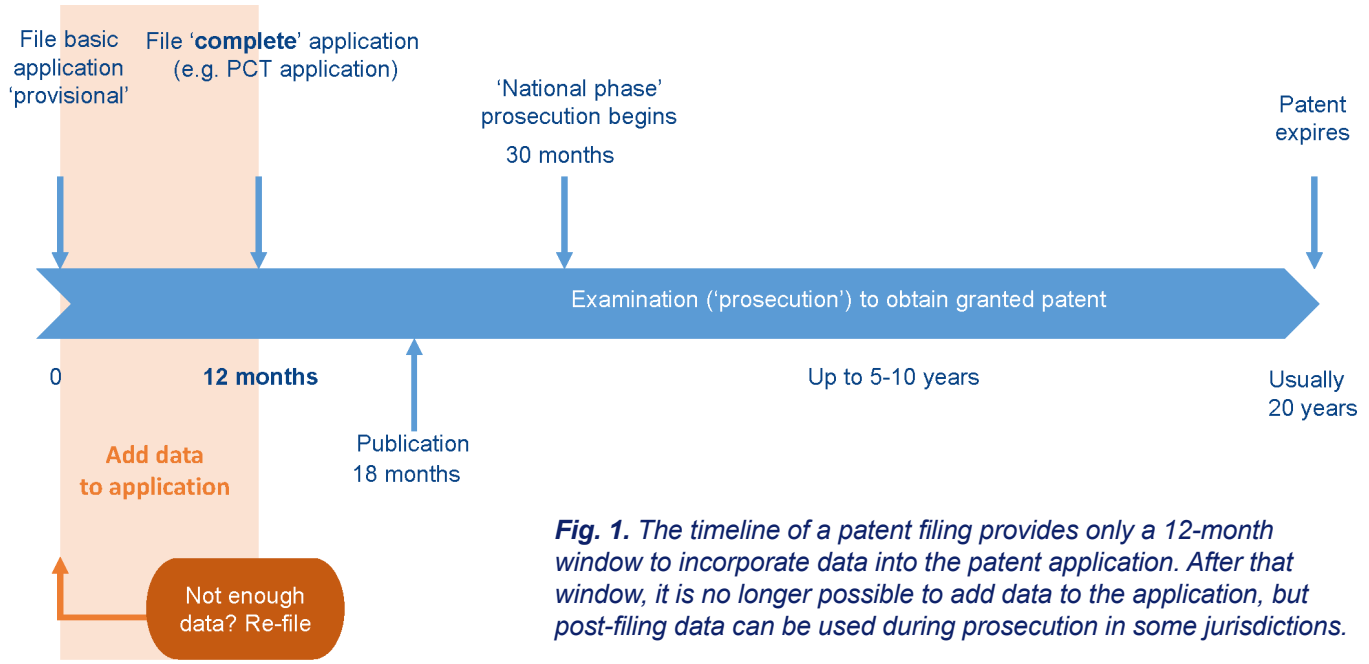

Fig. 1. *The timeline of a patent filing provides only a 12-month window to incorporate data into the patent application. After that window, it is no longer possible to add data to the application, but post-filing data can be used during prosecution in some jurisdictions.*

When Time is of the Essence – Timing Experimental Data Collection for Patent Applications

Prophetic examples

To meet the requirements of describing the invention in sufficient detail to support and enable the invention, in some jurisdictions (including the US and Europe) it is also possible to include prophetic examples. Prophetic examples do not require data showing that something works and is effective. They simply outline an expected experimental test and the expected outcome. For example, a prophetic example may be an outline of a proposed clinical trial, where the expected outcome is that treating patients with the invention X will improve treatment of a certain disease Y, as measured by Z.

There is no need to guarantee that a prophetic example actually works. But, they can support arguments for inventive step (showing a comparative advantage over the prior art), and/or provide basis for relying upon post-filing experimental data (see below) if you later have the data that aligns with results outlined in the prophetic example.

Importantly, there are significant limitations to what prophetic examples can achieve, and which jurisdictions will consider them. Including actual data is always preferable. Nevertheless, if the timing of filing is of essence, particularly at the provisional application stage, your patent attorney can assess if including prophetic examples would assist progressing your application.

What if you proceed with good data, but you obtain even better data after the 12-month deadline?

Post-filing data

Data obtained after the complete filing deadline cannot be incorporated into the patent specification. However, it can still be useful in progressing your application towards a granted patent.

In some jurisdictions, notably Europe and the US, data can be submitted 'post-filing' when prosecuting applications, to support arguments made for inventive step, support and/or enablement. For example, post-filing data may be data showing *in vivo* efficacy that wasn't collected in time for the complete application, or data showing a comparative benefit of your antibody against a prior art antibody that binds to the same target that the examiner has pointed to, but wasn't considered when filing your application. However, it should be kept in mind that some important jurisdictions, including China and South Korea, have stricter restrictions upon the type of post-filing data that can be used, and what it can be used for.

Inventors and applicants should consider carefully the use of post-filing data, and cannot always rely on post-filing data to correct for 'missing' data left out of the complete application. Your attorney can consider your prosecution strategy to identify if post-filing data may be able to assist obtaining granted patents in certain jurisdictions.

Another useful consideration for using post-filing data is that it does not necessarily have to be your own data – for instance, journal articles from other authors/groups can be submitted. This strategy requires caution to ensure that documents authored by others do not provide unhelpful contradictions or stray data points that weaken prosecution arguments. Your patent attorney can review documents you seek to rely upon to ensure they help, rather than hinder, your prosecution strategy.

File a new and different provisional application

If data obtained after the complete filing deadline is enough to support a new invention, it can form the basis for a new provisional application that is independent of the first filing.

Of course, this also depends on whether the previous filing discloses the new invention in any way. If your new data are a development from the earlier filing, the previous filing may be prior art for the new invention. In particular, your earlier filing could inadvertently disclose your new invention (making it lack novelty), or your new invention could be considered by an examiner to be obvious or non-inventive compared to the invention defined in your earlier filing.

To reduce the impact of earlier filings as prior art for later filings, your patent attorney will be able to advise upon the timing of filings and what subject matter (and data) to put in which application.

Take home messages

- There is not statutory requirement for a provisional application to contain experimental data, but in the life sciences, it is strongly recommended.
- The complete/PCT application deadline, 12 months after a provisional is filed, is the **final** opportunity to incorporate experimental data into a patent application.
- Prophetic examples (without data) can be useful in some jurisdictions, but should be used with consideration and caution.
- Re-filing a provisional may be an appropriate strategy if before the complete/PCT deadline, it appears there is insufficient data in the application to successfully prosecute and obtain the desired patents.
- Post-filing data can be a useful prosecution tool in some jurisdictions, to strengthen prosecution arguments where the data was not included in the complete application as filed.

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Australian Academy of Science Honours for ASBMB Members

On 14 March 2023, the Australian Academy of Science awarded twenty Australian researchers for their contributions to the advancement of science – two of the awardees are ASBMB members.

DAVID CRAIG MEDAL AND LECTURE
A Career Honorific
DAVID CRAIK
INSTITUTE FOR MOLECULAR BIOSCIENCE, UNIVERSITY OF QUEENSLAND

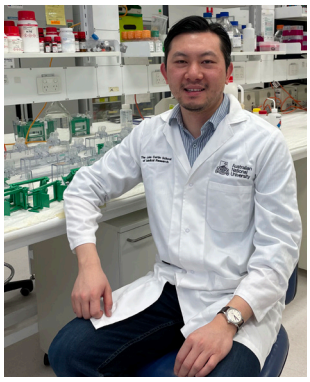
Professor David Craik is a Group Leader at the Institute for Molecular Bioscience at the University of Queensland. He obtained his PhD in Organic Chemistry from La Trobe University and undertook postdoctoral studies at Florida State and Syracuse Universities, USA, before returning to Australia and taking up a lectureship at the Victorian College of Pharmacy (VCP) in 1983. He was appointed Professor of Medicinal Chemistry and Head of School in 1988. VCP later merged with Monash University, becoming the Monash Institute of Pharmaceutical Science.

In 1995, he moved to the University of Queensland on an Australian Research Council Professorial Fellowship to set up a new biomolecular NMR laboratory in the Centre for Drug Design and Development, which later became the Institute for Molecular Bioscience (IMB), where he has been since. In his time at IMB, he has been an NHMRC Senior Principal Research Fellow, an ARC Laureate Fellow and currently holds an NHMRC Investigator Fellowship. He is also the Director of the Australian Research Council Centre of Excellence for Innovations in Peptide and Protein Science (CIPPS).

His research focuses on applications of cyclic peptides, peptide toxins and NMR in drug design and is best known for his discovery of cyclotides, a large family of ultrastable proteins from plants that have applications in medicine and agriculture. Cyclotides have a head-to-tail cyclised backbone and knotted arrangement of disulfide bonds that contribute to their exceptional stability. His group pioneered methods for the synthesis of cyclotides, their structural characterisation and their applications as scaffolds for peptide-based drug design.

Professor Craik is a Fellow of the Royal Society and a Fellow of the Australian Academy of Science, is author of more than 800 scientific articles and has trained 70 PhD students.

GOTTSCHALK MEDAL
An Early-career AAS Award
SI MING MAN
JOHN CURTIN SCHOOL OF MEDICAL RESEARCH, AUSTRALIAN NATIONAL UNIVERSITY



Professor Si Ming Man completed a Bachelor of Medical Science (Hons I, University Medal) at UNSW Sydney. During his Honours, Si Ming investigated the role of mucosa-associated bacteria in children with inflammatory bowel diseases. His interests in host–pathogen interaction inspired his move to the UK, where he completed his PhD at the University of Cambridge in 2013 under the supervision of Professor Clare Bryant. During his PhD, he studied macrophage responses to the foodborne pathogen *Salmonella*, generating two first-author publications in *PNAS* and a first-author publication in the *Journal of Immunology*.

With the support of an NHMRC RG Menzies Early Career Fellowship, Si Ming moved to the US, where completed his postdoctoral training at St. Jude Children's Research Hospital under the mentorship of Dr Thirumala-Devi Kanneganti. During this time, Si Ming and his colleagues identified a role for disease-fighting proteins in liberating microbial ligands to drive activation of innate immunity and the activation mechanisms of immune receptors in cancer.

Si Ming returned to Australia to establish his lab at the Australian National University in 2017. He is now Professor and CSL Centenary Fellow. His laboratory focuses on understanding the role of innate immunity in the host defence against infectious diseases and the development of cancer. His recent work showed that toxins with different mechanisms of action produced by pathogens such as *Bacillus* and *Clostridium* species are sensed by the same cytosolic innate immune sensor. This host strategy offers a single pathogen sensor the flexibility to recognise and defend against different types of pathogens at different stages of infection.

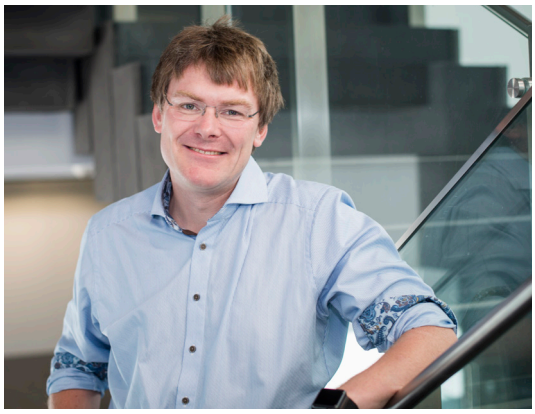
Si Ming was awarded the 2022 Frank Fenner Prize for Life Scientist of the Year at the Prime Minister's Prizes for Science, the 2020 ASBMB Eppendorf Edman ECR Award and the 2019 Commonwealth Health Minister's Medal for Excellence in Health and Medical Research. He was named a Clarivate Highly Cited Researcher in 2020 and 2022.

ASBMB Member Elected Fellow of the Australian Academy of Science

On 25 May 2023, the Australian Academy of Science announced the election of 20 new Fellows for their outstanding contributions to science, including ASBMB member, Professor David Komander.

David Komander was born in Germany in 1976. After undergraduate studies in Germany and Scotland, he received his PhD for work on protein kinase structure and biochemistry, from the MRC Protein Phosphorylation Unit in Dundee, Scotland, under supervision of Professor Dario Alessi and Professor Daan van Aalten. During his postdoctoral studies (2005–2008) at the Institute of Cancer Research (ICR, London) with Professor David Barford, he started to work on the ubiquitin system with a focus on cancer-associated deubiquitinases (DUBs) CYLD and A20. His lab at the MRC Laboratory of Molecular Biology (Cambridge, 2008–2018, tenured 2013) aimed to understand specificity in ubiquitin signaling. In 2018, he joined the Walter and Eliza Hall Institute (WEHI) to establish the first ubiquitin research division in Australia, which now comprises five labs and more than 50 staff. Komander also lead establishment of the WEHI Parkinson's Disease Research Centre, the Australian Centre for Targeted Therapies and is founder of Entact Bio, a spin-out company operating in Boston and Melbourne.

Professor Komander is a key opinion leader in understanding the 'ubiquitin code'. His work unveiled unexpected specificity in the ubiquitin system, and delineated conceptual frameworks for chain linkage specificity in E3 ligases and ubiquitin binding domains, and especially, in DUBs. Komander provided many widely used tools and protocols to study chain specificity; discovered the human DUB OTULIN, its role in inflammation, and named OTULIN related autoinflammatory syndrome; characterised DUBs in bacteria and viruses; and reported first specific small molecule DUB inhibitors, showing that DUBs are a viable target class in human disease. A further focus of his



David Komander.

work centers on PINK1/Parkin mediated mitochondrial turnover (mitophagy). Komander has characterised this process biochemically and structurally, providing detailed molecular insights into this essential cellular process, informing cell biology and drug discovery alike. An ultimate aim of this work is to provide disease-modifying drugs to halt Parkinson's disease and related neurodegenerative conditions.

Komander has authored over 120 papers (h-index 67). He has contributed the highest cited reviews in ubiquitin biology and DUB research to date. Komander has received numerous awards, including the Karl Lohmann Prize (German Society for Biochemistry and Molecular Biology) and the Early Career Research Award (Biochemical Society, UK). He is an EMBO Young Investigator (2011), Lister Institute Research Prize Fellow (2012) and EMBO Member (2014). He was named a Research Field Leader in Biochemistry in *The Australian's* Research magazine (2020).

Cryptic Crossword Result

The winner of the April competition is Yu Chinn Joshua Chey, School of Biomedicine, University of Adelaide. Congratulations to Joshua, who will receive a gift voucher.

King's Birthday Honours for ASBMB Members

Professor David Craik was awarded an Officer of the Order of Australia (AO) for distinguished service to science in the field of biological and medicinal chemistry, to tertiary education, and as a mentor.

Professor Craik is a Group Leader at the Institute for Molecular Bioscience at the University of Queensland. He obtained his PhD in Organic Chemistry from La Trobe University and undertook postdoctoral studies at Florida State and Syracuse Universities, USA, before returning to Australia and taking up a lectureship at the Victorian College of Pharmacy (VCP) in 1983. He was appointed Professor of Medicinal Chemistry and Head of School in 1988. VCP subsequently merged with Monash University, becoming the Monash Institute of Pharmaceutical Science.

In 1995, he moved to the University of Queensland on an Australian Research Council Professorial Fellowship to set up a new biomolecular NMR laboratory in the Centre for Drug Design and Development, which later became the Institute for Molecular Bioscience (IMB), where he has been since. In his time at IMB, he has been an NHMRC Senior Principal Research Fellow, an ARC Laureate Fellow and currently holds an NHMRC Investigator Fellowship. He is also the Director of the Australian Research Council Centre of Excellence for Innovations in Peptide and Protein Science (CIPPS).

His research focuses on applications of cyclic peptides, peptide toxins and NMR in drug design and is best known for his discovery of cyclotides, a large family of ultrastable proteins from plants that have applications in medicine and agriculture. Cyclotides have a head-to-tail cyclised backbone and knotted arrangement of disulfide bonds that contribute to their exceptional stability. His group pioneered methods for the synthesis of cyclotides, their structural characterisation and their applications as scaffolds for peptide-based drug design.

Professor Craik is recipient of a number of prizes in the peptide field, including the American Chemical Society Ralph Hirschmann Award, the American Peptide Society du Vigneaud Award as well as major awards from the European Peptide Society and Chinese Peptide Society. Australian awards include the Royal Australian Chemical InstituteHG Smith Medal, the Ramaciotti Medal for Excellence in Biomedical Research, the GlaxoSmithKline award for Research Excellence and the Australian Academy of Science David Craig Memorial Award. Professor Craik is a Fellow of the Royal Society and a Fellow of the Australian Academy of Science, is author of more than 800 scientific articles and has trained 70 PhD students.

Professor Melanie Bahlo was awarded a Member of the Order of Australia (AM) for significant service to genetic and infectious disease research, and to public health.

Professor Bahlo is a Laboratory Head and Leader of the Healthy Development and Ageing Theme at WEHI (Walter and Eliza Hall Institute), where she oversees the scientific strategy for three divisions – including the Population Health and Immunity division, which she co-established in 2015.

As a bioinformatician and statistical geneticist with over 20 years of experience, Professor Bahlo's research aims to understand the genetic basis of human diseases, with a focus on neurological and retinal disorders including epilepsy, ataxia, macular telangiectasia type 2 (MacTel) and age-related macular degeneration.

Having led a statistical genetics laboratory at WEHI since 2007, Professor Bahlo's research lab has developed innovative methods to gain insights into complex genetics. This research has led to major genetic discoveries in neuroscience, including the critical identification of around 20 novel genes and genetic pathways implicated in epilepsy and the development of world-first bioinformatic methods to detect repeat expansions – a type of mutation that leads to over 50

King's Birthday Honours for ASBMB Members

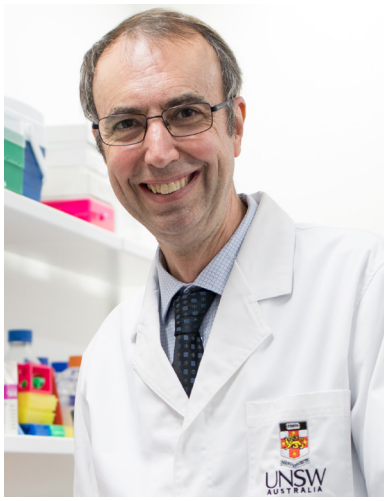
genetic disorders, including Huntington's disease.

Professor Bahlo's landmark research on MacTel identified five distinct genetic causes of the disease, as well as a key metabolic pathway involved in the disorder. These findings redirected worldwide research efforts to develop the first effective treatment for MacTel. This body of work has led to the genetic diagnosis of hundreds of patients, delivered the first genetic insights into the architecture of several complex diseases and has produced algorithms, analytical insights and software that are now used worldwide.

Professor Bahlo's reputation as an esteemed leader in her field is built not only on her outstanding research discoveries, but also through her collaborative spirit and commitment to nurturing the next generation of research leaders. She is committed to providing a positive environment to foster diversity in science and has mentored scientists locally and abroad to secure fellowships and grants.

Professor Bahlo is a member of the Viertel Medical Advisory board and is the external member of the steering committee of Gen V, Australia's largest population cohort. She is also a member of the editorial board of *Communications Biology*.

Professor Bahlo's previous honours include the Australian Academy of Science Moran Medal (2009) and the Genetics Society of Australasia Ross Crozier Medal (2015). Professor Bahlo was named a Fellow of the Australian Academy of Health and Medical Sciences in 2020.



Professor (Paul) Merlin Crossley was awarded an Member of the Order of Australia (AM) for significant service to education, and to molecular biology.

A devoted fan of the ASBMB, Merlin began as a science student at the University of Melbourne. He remembers the first year biology practicals that were held from 7–10pm (known as pyjama pracs), and he loved the inspiring lectures of Jim Pittard and Mike Hynes.

He went to Oxford for his doctorate, supported by a Rhodes Scholarship, and studied some unusual cases of haemophilia that resolved after puberty. Mutations in the regulatory region of the clotting factor IX gene impaired the normal developmental expression of the gene. He moved to Harvard to study gene expression in red blood cells with Stu Orkin, and was involved in identifying and cloning some of the first transcription factors, and their cofactors.

He was appointed to a lectureship at the University of Sydney in 1995, where he benefited from the mentorship of Gerry Wake, and enjoyed both research and teaching. His lab in Sydney had many wonderful students, including Archa Fox, Hannah Nicholson and Kate Quinlan. He collaborated with the protein experts, Joel Mackay and Jacqui Matthews, and together they analysed many partners of new zinc finger transcription factors.

Ian Macreadie invited Merlin to give a seminar on the yeast two hybrid system at an ASBMB event and Merlin later applied to be the NSW State Representative. He learnt a lot on the Council, from successive Presidents Nick Hoogenraad, Tony Burgess, John de Jersey, John Wallace and Phillip Nagley. He later became the Honorary ASBMB Secretary, and then the Acting Dean of Science, and Acting Deputy Vice-Chancellor Research at the University of Sydney. During this time he enjoyed working with David Day, who took over as Dean of Science at the University of Sydney.

In 2010, he moved to the University of New South Wales as Dean of Science, where he benefitted from the Ramaciotti Centre for Genomics and the wisdom of Ian Dawes.

In 2016, desiring to support excellence in teaching, he became Deputy Vice-Chancellor Education, and has been variously DVC Academic, Academic and Student Life, and Academic Quality ever since. During this time, his lab characterised mutations associated with Hereditary Persistence of Fetal Haemoglobin and is exploring CRISPR-gene editing to treat sickle cell disease, and this year, he taught into the large first year biology course, BABS1201.

Merlin is committed to science communication. He has done many interviews on Robyn Williams' ABC Science Show and has written articles for *Times Higher Education, Sydney Morning Herald, The Age, The Australian* and *The Conversation*. He serves as Chair of the Editorial Board of *The Conversation* and is also Deputy Chair of the Australian Science Media Centre. He was also a member of the governing body of the Australian Museum. In recognition of his work, a new species of iridescent butterfly bobtail squid was named after him – *Iridoteuthis merlini*.

Eppendorf Edman ECR Award Report

MAITs in Gothenburg

It was an honour to receive the Eppendorf Edman Award in 2022, which made it possible for me to go to the most recent 12th International CD1-MR1 meeting, which took place in Gothenburg, Sweden, from 22–26 May 2022. The Gothenburg Old Town region is just a short walk from where the meeting took place, which is at the Elite Park Avenue Hotel. I was able to spend some time getting acquainted with the city when I first arrived, taking the opportunity to see the lovely Kungsportsavenyn canal and the botanical garden, all of which are only ten minutes walk away from the hotel.

The Gothenburg Old Town region canal.

The biennial conference's main topic was the biology of T lymphocytes, namely natural killer T (NKT) cells and mucosal associated invariant T (MAIT) cells, that are constrained by the non-conventional MHC class-I like molecules CD1 and MR1. Following a COVID-related pause, the 2022 European Molecular Biology Organisation (EMBO) CD1-MR1 workshop gave a timely update, and a wealth of new and exciting research was presented, discussed, and friendships and collaborations were rekindled. The symposium covered the most recent findings in research, including the fundamental biology of T cells and the antigens they detect, their development, activation, and many roles in health and disease, as well as an exploration of therapeutic strategies that target these cells.

At the conference, I was fortunate to give an oral presentation on some of my latest research on molecular mechanisms underlying MAIT cells' functions, and how they receive activation signals from the immune system to fight bacteria. Without the right signals and guidance, MAITs can contribute to cancer and autoimmune diseases. Following my talk, the audience provided me some valuable feedback.

After this meeting, I took a train to Lund in the province of Scania, southern Sweden, where I visited the Department of Biochemistry and Structural Biology in the Centre of Molecular Protein Science (CMPS) at Lund University, where I pursued my PhD in 2015. At the institute, I had conversations with a number of PIs, postdocs and PhD candidates. It was wonderful to see my former lab and reconnect with PhD mentors and friends. I had the opportunity to tour the MAX IV synchrotron radiation facility. MAX IV offers access to 16 beamlines that provide modern X-ray spectroscopy, scattering/diffraction and imaging techniques to contribute to solving scientific questions in a wide range of areas.

This trip was an excellent chance for me to develop new networks in the field of structural biology and strengthen my networks within the MAIT biology field. The feedback I received on multiple projects was constructive and has inspired me to try some new ideas in the lab! I would like to sincerely thank the ASBMB and Eppendorf for the funding to support this journey.

Wael Awad is a Group Leader in the Department of Biochemistry and Molecular Biology, Monash University.

Australian Society for Biochemistry and Molecular Biology Inc
PUBLICATION SCHEDULE FOR *AUSTRALIAN BIOCHEMIST*, volume 54, 2023

Issue	ASBMB Content	Copy Deadline	Issue Date
April 2023 54(1)	Profiles of medal, award and fellowship winners Nominations for Executive/Council	Monday 6 February	Monday 3 April
August 2023 54(2)	Nominations for medals, awards and fellowships Notice of AGM/proposed constitutional changes	Monday 5 June	Monday 31 July
December 2023 54(3)	Annual reports ASBMB meeting report	Monday 2 October	Monday 4 December

Election of Council 2024

Nominations are called for the following positions on the Council of the Australian Society for Biochemistry and Molecular Biology Inc for 2024: President Elect, Secretary, Treasurer, Editor, Education Representative, FAOBMB Representative, Secretary for Sustaining Members and State Representatives.

Eligible for re-election
§ Position open

The ASBMB Council for the period 1 January 2023 to 31 December 2023 is composed of the following members:	President	R Hannan
	Past President	J Matthews
	Secretary	D Ng #
	Treasurer	K Quinlan #
	Editor	T Soares da Costa #
	Education Representative	T Kuit #
	FAOBMB Representative	N Samarawickrema #
	Secretary for Sustaining Members	S Parsons
Representatives for:	ACT	C Spry §
	NSW	L Sharpe §
	VIC	L Osellame §
	QLD	M Landsberg §
	SA	M Roach #
	TAS	Vacant §
	WA	A Van Dreumel #

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

NOMINATIONS MUST REACH THE SECRETARY BY 5PM 20 OCTOBER 2023
(PRIOR TO THE ANNUAL GENERAL MEETING TO BE HELD ON 16 NOVEMBER 2023).

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

The 67th Annual General Meeting of the Australian Society for Biochemistry and Molecular Biology Inc. will be held on Thursday 16 September 2023 at 1710 hours Australian Eastern Standard Time.
The meeting will be conducted at Australian National University (room to be determined).

AGENDA

1. Apologies
2. Confirmation of the Minutes of Annual General Meeting No. 66
3. President's Report
4. Treasurer's Report
5. Fees for 2024
6. Elections to Council
7. ASBMB Awards 2024
8. Amendments to Constitution and By-laws
9. Any Other Business

Dominic Ng
Secretary, ASBMB

ASBMB Welcomes New Members

A warm welcome is extended to the following new members who joined ASBMB from 1 July 2022 to 30 June 2023

NSW
DR EMMY FLEUREN
MS HAYLEY GOODSON
DR YAN JIANG
MISS TAHNEE MCEWAN
DR KATE MICHIE
Dr STEFAN MUELLER
MR MICHAEL O'DEA

QLD
MR CHRISTOPHER BATHO
DR KAI-EN CHEN
MR HENRY LAMB
PROF DES RICHARDSON
DR JING ZHI ANSON TAN
DR RAINE THOMSON
A/PROF STEVEN ZURYN

SA
A/PROF PIRJO APAJA
DR CHER-RIN CHONG
MISS EMILY MACKIE
DR MICHAEL ROACH
DR JULIAN VIVIAN

TAS
MR AHMED MAKLAD
MR MOHAMMED SEDEEQ

VIC
PROF MELANIE BAHLO
DR PETER BOAG
MR SAI VARA PRASAD CHITTI
MISS LISA CIACCHI
MISS LAURA CIACCHI
DR SIMON COBBOLD
MS AYLWEN COTTER
DR GRANT DEWSON
DR SIYANG DING
DR FIONA DURAND
MR BENJAMIN ESPINOZA
DR ERIC KUSNADI
DR TIING JEN LOH
DR HARRIET MANLEY
DR EVE MAUNDERS
DR HAMISH MCWILLIAM
MS TIEN NGUYEN
DR JASON PAXMAN
A/PROF TRACY PUTOCZKI
DR SAMUEL RODGERS
DR ADAM SHAHINE
A/PROF KAYLENE SIMPSON
DR CHATHURA SURAWEERA
DR RACHEL UREN
MR CARL WANG

WA
MS MABEL GILL-HILLE
MS CLARA WOODCRAFT

WEST JAVA
DR SAFRI ISHMAYANA

Our Sustaining Members

mexec is an Executive Search Recruitment firm that also provides support to individuals seeking to transition to a new role.

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Conjugate your antibody in three simple steps without the risk of antibody loss from a traditional, post-conjugation purification step. Simply pipette your antibody or biomolecule of choice into the vial of a lyophilized mixture containing the label of interest and incubate for just 15 minutes (Lightning-Link® Fast range) or 3 hours (Lightning-Link® range). Our conjugation kits only require 30 seconds of hands-on time. Access the largest range of labels including fluorescent dyes, enzymes, biotin/streptavidin, metals, latex, oligos to complete your experiment for 10µg–100mg of antibody.

Find out more at:
www.abcam.com/ConjugationKits

Our Sustaining Members

GenScript
Make Research Easy

One-stop Solution for IVT mRNA Service

mRNA provides new therapeutic opportunities for a range of diseases. *In vitro* transcribed (IVT) mRNA's versatility lies in several key features: simplified cell-free manufacturing, cell cycle independent performance, and insertional-mutagenesis risk-free.

The simple and expedited mRNA manufacturing workflow offers more opportunities for personalised medicines, such as patient-specific cancer vaccines or protein replacement for rare diseases.

GenScript's solution to mRNA production streamlines your workflow starting from gene synthesis to IVT mRNA production. mRNAs produced at GenScript are optimised with our proprietary production platform, ensuring the quality and expression efficiency of your mRNA.

Workflow

1. Codon Optimisation – Ready-to-use UTR designs
2. Gene Synthesis – with PolyA-built in vectors
3. Cloning/Plasmid Preparation – Stable Poly(A) tracts with variance of only +/- 5-10 nt
4. Enzyme Production – T7 polymerase, RNase inhibitors, DNase I, Proteinase K
5. mRNA Synthesis – RUO to preclinical, with advanced purification and QC

Highlights

- Poly A tails length more than 100 base pairs
- Engineered UTR that enhances the expression efficiency
- Catalogue mRNA available: EGFP, F-Luc, mCherry, eSpCas9, SB-100, etc

To learn more about GenScript IVT mRNA complete solution, please visit: www.genscript.com/ivt-mrna-production.html or contact:

Claire claire.sui@genscript.com or
Tzehlong tzehlong.fu@genscript.com

CapellaScience

Termaks is a leading manufacturer of laboratory drying ovens, incubators, cooling incubators and environmental chambers. Founded in Sweden in 1952, Termaks became a leading supplier of drying ovens, incubators, cooling incubators and environmental chambers to the Scandinavian market. Termaks products are distributed exclusively across Australia by Capella Science. Their highlights include: forced air variable fan speed circulation, OLED display, keypad and PIN, stainless steel interior, precise temperature control, decontamination function in incubators and cooling incubators.

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

SAPPHIRE BIOSCIENCE

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Every year, there are about four million new cases of cancer diagnosed in the world, with over eight million cancer-related deaths. There are over 100 different types of cancer, with often significant genotypic and phenotypic heterogeneity even among tumours of the same kind. Research is one of the best weapons to oppose this scourge, and great progress has been made in cancer diagnosis, treatment and prevention. In addition, scientists have made enormous strides dissecting the mechanisms and pathways that drive carcinogenesis and metastasis, and in offering approaches as to how these processes can be potentially targeted for therapeutic purposes.

GeneTex offers over 15,000 antibodies for cancer research, for investigating oncoproteins, tumour suppressor proteins, epithelial-mesenchymal transition, cancer immune checkpoints, hypoxia, angiogenesis, cancer stem cells and cancer metabolism. GeneTex are committed to providing the most stringent standards of product performance and are dedicated to the goal of accelerating discoveries in cancer research.

GeneTex's products are distributed in Australia and New Zealand by Sapphire Bioscience.

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What is the problem we are solving?

Live cell fluorescence microscopy enables an in-depth understanding of dynamic cellular processes, but has disadvantages, such as photobleaching, phototoxicity and probes that may interfere with cell survival.

How does Livecyte solve this?

Livecyte's novel ptychographic acquisition produces high contrast images rivalling fluorescence, without the need for toxic fluorescent illumination or dyes. Users can monitor cell growth in culture continuously for weeks at a time without influencing or damaging the cells. Livecyte quantifies and performs single-cell to population analysis automatically, with kinetic, morphological and behavioural characteristics, generating a significant amount of unique statistical data in a limited time – ideal for a core imaging facility.

Dr Constantinos Mikelis and Dr Ulrich Bickel from Texas Tech University have been using the Livecyte in cancer and vascular research. They noted, *"Livecyte is the only instrument that has these qualifications so it was the natural choice. I have not seen another system that is able to do the same things, in the same manner."*

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Expanded Range of Baculovirus Protein Expression Systems

Oxford Expression Technologies' flashBAC™ baculovirus expression kits provide superior recombinant protein yields in a shorter time when compared to other expression systems. The flashBAC™ product range has been expanded with the addition of flashBAC PRIME, bacPAK6 and bacPAK6 sec+.

flashBAC PRIME, combines the simplicity of the flashBAC™ one step baculovirus expression system with increased recovery and yield of virus like particles (VLPs) and protein complexes. It is based on the original Autographa californica nucleopolyhedrovirus (AcMNPV) genome without any of the gene deletions characteristic of the other flashBAC™ vectors. Thus the infected cells induce cell lysis in the late stages of infection which facilitates release and subsequent purification of VLPs (or other proteins) that form in the cytoplasm or nucleus of infected cells.

BacPAK6 linear DNA is the original convenient, highly efficient reagent for generating recombinant viruses. It comprises a modified AcMNPV genome with lacZ inserted in place of the native polyhedrin gene coding region. The lacZ and part of ORF 1629 have been removed which are essential for AcMNPV gene to function. Co-transfection of insect cells with linear BacPAK6 DNA and a compatible transfer vector containing the complete ORF 1629 and a foreign gene of interest, results in recombination and restoration of the circular, infectious virus genome. A single plaque assay titration is used to identify recombinant plaques. Once isolated they are amplified in a few days to create working stocks of purified recombinant virus.

BacPAK6 Sec+ is able to increase the yield of recombinant protein and the ease of harvesting. The deletion of the chitinase gene (chiA) from the original BacPAK6 viral backbone, prevents the chitinase protein from inhibiting the function and efficacy of the secretory pathway. This results in an increased secretion of target proteins into the cytoplasm and thus greatly enhances the yield of harvestable recombinant protein.

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SHIMADZU
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Multi-omics Analysis Package

The Shimadzu Multi-omics Analysis Package, is released on the GARUDA™ open research platform.

It was developed for metabolic engineering applications for LC/MS and GC/MS, providing the ability to automatically generate metabolic maps and perform a variety of data analyses in metabolomics, proteomics and flux analysis. It offers a powerful platform to support drug discovery, bioengineering and other life science research applications.

- The package dramatically reduces the amount of work required for bottleneck processes of analysing and visualising data, such as displaying data on a metabolic map and analysing correlations.
- In combination with various other gadgets connected on the GARUDA™ platform, it offers optimal workflows for multi-dimensional analyses.
- It includes various data processing gadgets which connect with other gadgets, providing a seamless, connected experience of a single software program.
- It is also designed to work in combination with various Shimadzu databases prepared with 'Ready-to-Use Methods' for everything from sample pre-treatment to analytical conditions, ensuring a smooth workflow, from obtaining mass spectrometer measurements to data analysis.

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ChemiSOLO – High-quality, Quantitative Chemiluminescent Imager

The chemiSOLO from Azure Biosystems is a new, personal chemiluminescent imager by that delivers high-quality, quantitative imaging suited to applications such as Chemiluminescent Western Blotting, Densitometry and Visible Gel Imaging.

The chemiSOLO detects low-expressing proteins with femtogram sensitivity and captures marker images at the push of a button. The chemiSOLO's wide dynamic range can be further enhanced by using Extended Dynamic Range function (EDR). This feature allows for linear, quantitative data, while avoiding saturation.

A unique web browser interface allows the chemiSOLO to be controlled by phone, tablet, or PC, without the need to install any additional software and it's compact design will fit neatly into any busy lab space.

In addition to Western blots, the chemiSOLO captures Coomassie stained protein gels, silver stained protein gels, colorimetric stained blots, densitometry and plant bioluminescence.

The imager measures 29.2 x 43.2 x 22.2cm and weighs only 9kg. It is equipped with a 6.29MP 16-bit back illuminated, peltier cooled CMOS camera, ethernet port for direct connection, two USB ports for internet connection or direct data transfer, embedded LEDs for capturing marker and colorimetric gel images and an image stage with a field of view 10 x 15cm.

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Etaluma Launch 800 Series Microscopes for Live Cell Imaging Inside Incubators

Etaluma have launched the new 800 series microscopes that offer the latest advances in optics, cameras, throughput and user flexibility. They also offer improved image quality, motion speed, illumination and software flexibility over the previous model LS720 making them an ideal automated, walk-away solution with the highest quality wide field microscopy images for your research.

Building on the success of the LS720, the new LS850 and LS820 series microscopes use a new Basler USB3 12 bit camera married to low profile multi-mode transmitted illumination, Z-stacking with 100nm resolution and the latest Python-based application compiled for Windows, Mac and Linux with scripting. Both models are more compact compared to the LS720, making them easier to fit in your incubator.

The flagship LS850 also offers a motorised turret and high-speed automated stage. The LS850 and LS820 also offers three colour fluorescence, autofocus and are compatible with a host of commercial objective lenses. With gentle LED illumination, they offer minimal photo toxicity and the ability to be operated automatically or remotely inside an incubator, providing the most stable environment for conducting long-term live cell imaging studies.

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

During the past years, science has focused on identifying and tracking viral pathogens. To test for viruses, samples are subjected to DNA extraction and qPCR to analyse gene expression. In addition, 2X concentrated master mix formulations deplete faster, which can be problematic when there are supply chain issues. To support the growing need for an inhibitor resistant, high-performance, 4X concentrated master mix that allows for direct amplification of crude samples, Integrated DNA Technologies has developed the PrimeTime™ 1-Step 4X Broad-Range qPCR Master Mix.

PrimeTime One-Step 4X Broad-Range qPCR Master Mix exhibits many attributes that will ease the workflow issues experienced by scientists researching viruses or other gene expression applications. The new Master Mix has shown high endpoint fluorescence in crude samples, which increases researchers' confidence in their data interpretation. In addition, the Master Mix is resistant to inhibitors (heparin, hematin, and humic acid) often found in challenging samples, and therefore, reduces time and cost associated with crude sample purification steps. With its 4X concentration and ability to support both extracted samples and crude samples with a single, inhibitor-resistant formula, IDT's PrimeTime One-Step 4X Broad-Range qPCR Master Mix can help accelerate the road to discovery.

For research use only. Not for use in diagnostic procedures. Unless otherwise agreed to in writing, IDT does not intend these products to be used in clinical applications and does not warrant their fitness or suitability for any clinical diagnostic use. Purchaser is solely responsible for all decisions regarding the use of these products and any associated regulatory or legal obligations.

ASBMB Council 2023

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BIOMOLECULAR HORIZONS 2024:

DISCOVER CREATE INNOVATE

22-26 SEPTEMBER 2024 MELBOURNE AUSTRALIA

IUBMB FAOBMB ComBio 2024 MELBOURNE

Join us at "Biomolecular Horizons 2024: Discover, Create, Innovate" to be held in Melbourne, Australia 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 together to discuss and examine the latest developments and research. This truly global forum will bring together renowned scientists from across the world, from Nobel Laureates to early career scientists.

Over the five days, the Congress will offer a series of plenary and keynote sessions, symposia, workshops, technical talks and poster presentations. Connect with colleagues from across the world exchanging ideas and research, and building valuable professional networks.

You will also be able to experience a showcase of the latest products and services in the exhibition, an integral element of the Congress.

Scientific Themes:

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- Biotechnology & Synthetic Biology
- The Microbial World
- Cell Signalling & Metabolism
- Genomics, Gene Regulation & Epigenetics
- Bioinformatics, Computational Biology & 'Omics
- Structural Biology & Biophysics
- Molecular Basis of Disease
- Molecular Physiology
- RNA Technology
- Gene Editing
- Climate Change
- Education

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