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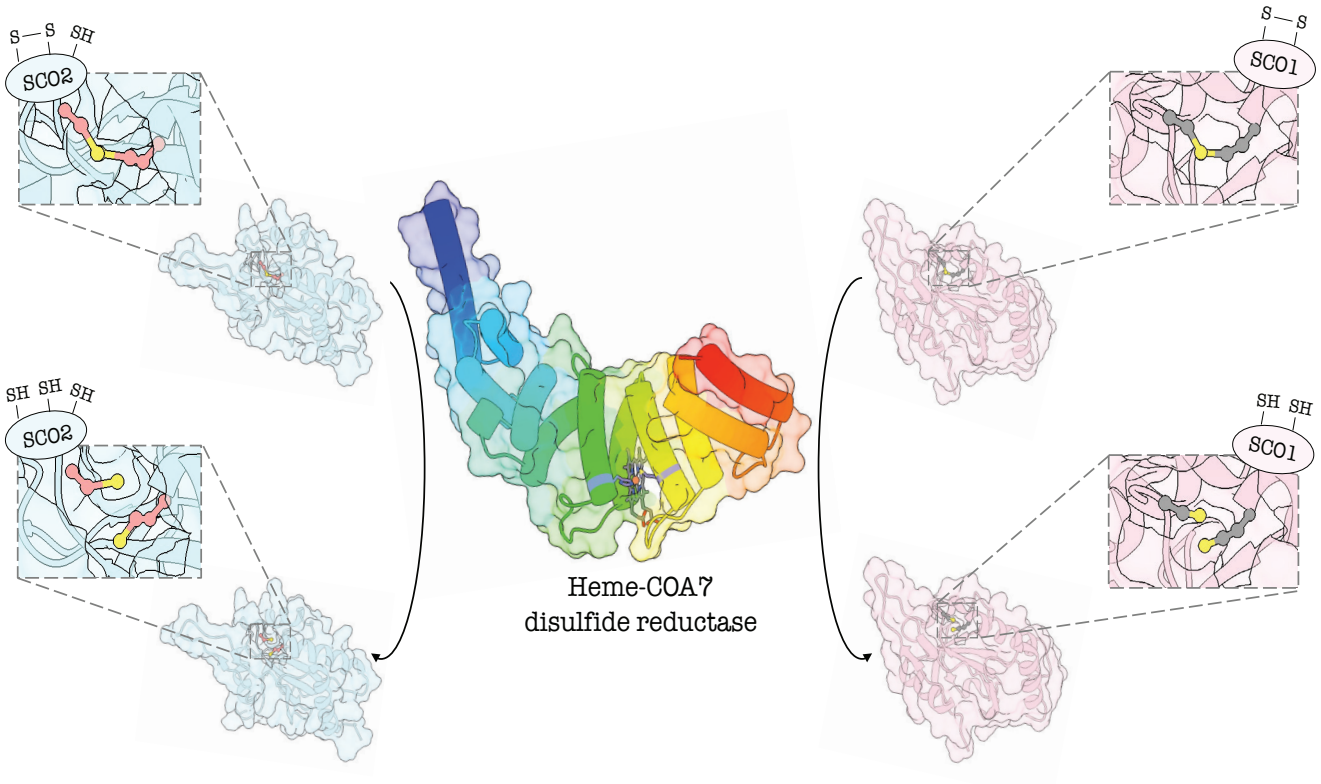

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Editor Tatiana Soares da Costa
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Front Cover

Heme bound COA7 functions as a disulfide reductase for copper metallochaperones SCO1 and SCO2. The heme-bound COA7 (rainbow) can redox cycle between oxidation states ferrous and ferric and shows disulfide reductase activity through reduction of disulfide bonds in copper metallochaperones SCO1 (pink) and SCO2 (cyan). Image credit: Dr Shadi Maghool, Bio21 Molecular Science and Biotechnology Institute, University of Melbourne.

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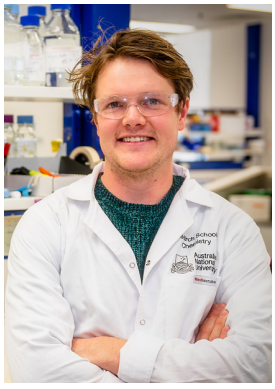

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ComBio2022 Provisional Programme Timetable

TUESDAY 27 September	09:25 - 16:45	**Career Development Forum: Held offsite - see: https://combio.org.au/combio2022/career.html**
	15:00 - 18:00	**Registration**
WEDNESDAY 28 September	07:30 onwards	**Registration**
	08:30 - 08:50	**Opening**
	08:50 - 09.30	**Plenary 1: Opening Keynote Lecture:** *Jennifer Doudna*
	09:35 - 11.05	Concurrent Symposia 1
	11:05 - 11:30	**Morning Tea**
	11:30 - 12:10	**Plenary 2:** *Jamie Cate*
	11:30 - 12:10	**Plenary 3:** *Siobhan Brady*
	11:30 - 12:10	**Plenary 4:** *Emma Teeling*
	12:15 - 12:55	**Plenary 5:** *Jodi Nunnari*
	12:15 - 12:55	**Plenary 6: Annals of Botany Lecture:** *Niko Geldner*
	12:55 - 14:00	**Lunch Break:** Lunches may be puchased at nearby cafés
	14:00 - 15:30	Concurrent Symposia 2
	15:30 - 15:55	**Afternoon Tea**
	15:55 - 16:35	**Plenary 7: ASBMB Education Plenary:** *Merlin Crossley*
	15:55 - 16:35	**Plenary 8: ASPS Jan Anderson Award & Lecture:** *Frances Sussmilch*
	15:55 - 16:40	**Plenary 9: ANZSCDB President's Medal Award & Lecture:** *TBA* **Includes the Presentation of the ANZSCDB Emerging Leader Award**
	16:40 - 18:10	Concurrent Symposia 3
	18:10 - 19:30	**Welcome Mixer**
THURSDAY 29 September	08.30 - 09:10	**Plenary 10:** *Roy Parker*
	08:30 - 09:10	**Plenary 11:** *Cristina Lo Celso*
	08:30 - 09:10	**Plenary 12:** *Lisette Waits*
	09:15 - 10:45	Concurrent Symposia 4
	10:45 - 11:30	**Morning Tea**
	11:30 - 13:00	Concurrent Symposia 5
	13:00 - 14:30	**Lunch/Exhibition/Posters**
	13:30 - 14:30	Poster Session A
	14:30 - 16:00	Concurrent Symposia 6
	16:00 - 16:25	**Afternoon Tea**
	16:25 - 17:05	**Plenary 13: ASBMB Lemberg Medal Award & Lecture:** *Leann Tilley*
	16:25 - 17:05	**Plenary 14: ASPS Peter Goldacre Award & Lecture:** *Maria Ermakova*
	16:25 - 17:05	**Plenary 15: GSA M.J.D. White Medal Award & Lecture:** *Marianne Frommer*
	17:05 - 17:45	**Plenary 16: ASBMB Shimadzu Medal Award & Lecture:** *Michael Lazarou*
	17:05 - 17:45	**Plenary 17: J.G. Wood Award & Lecture:** *Rudi Appels*
	17:05 - 17:45	**Plenary 18: GSA Ross Crozier Medal Award & Lecture:** *Clare Holleley*
	17:45 - 18:05	**ASBMB & NZSBMB Award Presentations:** ASBMB Eppendorf Edman Award, SDR Scientific Education Award, Fred Collins Award & Fellowships Awards, 50 Year Members Awards, NZSBMB Custom Science Award **ASPS Award Presentations:** ASPS-FPB Best Paper Award, Education and Outreach Award **GSA Award Presentations:** GSA Alan Wilton Talk and Presentation of Award, Presentation of GSA D.G. Catcheside Prize, GSA Excellence in Education Award
	18:10	Annual General Meetings
FRIDAY 30 September	08:30 - 09:10	**Plenary 19:** *Tony Hunter*
	08:30 - 09:10	**Plenary 20:** *Daniel St Johnston*
	08:30 - 09:10	**Plenary 21:** *Wolfgang Haak*
	09:15 - 10:45	Concurrent Symposia 7
	10:45 - 11:30	**Morning Tea**
	11:30 - 13:00	Concurrent Symposia 8
	13:00 - 14:30	**Lunch/Exhibition/Posters**
	13:30 - 14:30	Poster Session B
	14:30 - 14:45	Passport Draw
	14:45 - 16:15	Concurrent Symposia 9
	16:20 - 17:00	**Plenary 22: ASBMB Grimwade Keynote Lecture:** *Cynthia Kenyon*
	17:00 - 17:20	**Closing Ceremony and Award Presentations**
	17:20 - 18:30	**Closing drinks**

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 editor@asbmb.org.au.

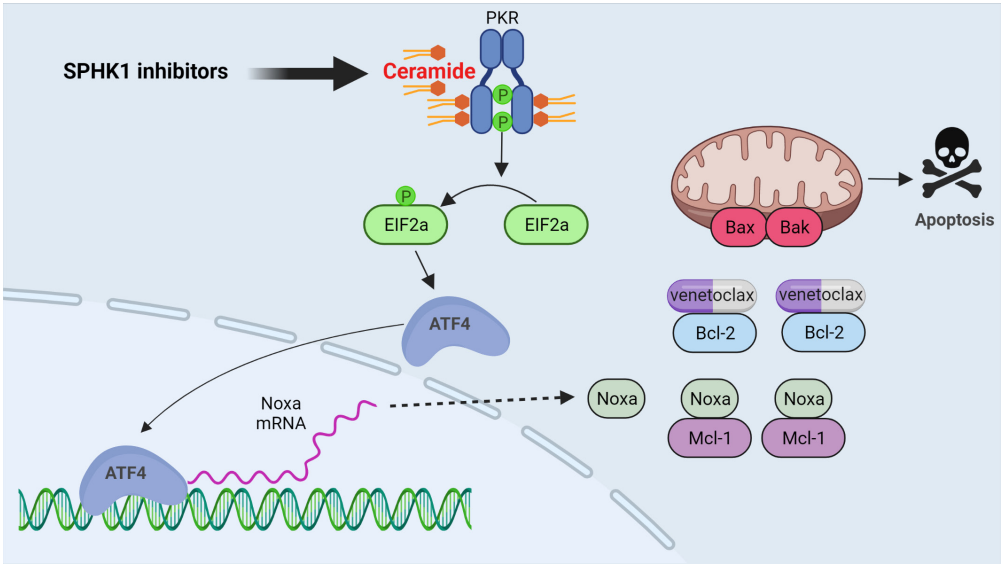
Ceramide-induced Activation of the Integrated Stress Response as an Approach to Target Acute Myeloid Leukemia

Lewis AC, Pope VS, Tea MN, Li M, Nwosu GO, Nguyen TM, Wallington-Beddoe CT, Moretti PAB, Anderson D, Creek DJ, Costabile M, Ali SR, Thompson-Peach CAL, Dredge BK, Bert AG, Goodall GJ, Ekert PG, Brown AL, D'Andrea R, Robinson N, Pitman MR, Thomas D, Ross DM, Gliddon BL, Powell JA*, Pitson SM*. Ceramide-induced integrated stress response as a mechanism to overcome Bcl-2 inhibitor resistance in acute myeloid leukemia. *Blood* 2022; In print.
***Corresponding authors: jason.powell@sa.gov.au, stuart.pitson@unisa.edu.au**

The Pitson laboratory has a strong interest in examining the role of sphingolipid metabolism in health and disease. Central to this is the so-called 'sphingolipid rheostat', whereby cell fate can be regulated by the balance between the pro-apoptotic sphingolipid ceramide and pro-survival sphingosine 1-phosphate (S1P). Sphingosine kinase 1 (SPHK1) is a critical player in this system, reducing ceramide and enhancing S1P, and thus, promoting resistance to cell death, one of the key hallmarks of cancer. SPHK1 is, therefore, an attractive therapeutic target in various cancers. Ceramide is a well-known inducer of apoptosis, but the mechanisms whereby this occurs have remained poorly defined. The Pitson laboratory and colleagues have uncovered a novel mechanism by which ceramide can induce apoptosis in acute myeloid leukemia (AML).

Our previous studies showed that targeting SPHK1 in AML with small molecule inhibitors reduced the expression of the pro-survival protein Mcl-1 and induced cell death in AML cells. Investigation into the mechanism of SPHK1 inhibitor-induced cell death uncovered TP53-independent transcriptional upregulation of the pro-apoptotic BH3-only protein Noxa, a pro-apoptotic protein that is known to selectively bind and induce degradation of Mcl-1. Transcriptomics revealed SPHK1 inhibition induced genes associated with the unfolded protein response (UPR), a cellular response that is triggered by the accumulation of misfolded proteins within the endoplasmic reticulum (ER). The PERK arm of the UPR was selectively activated by SPHK1 inhibition, typified by the activation/phosphorylation of eIF2α and induction of the master transcription factor ATF4. Ceramides and other saturated lipids have been shown to induce PERK activation independent of unfolded proteins via direct sensing of the lipid composition within the ER membrane.

As the ER is the main location of *de novo* sphingolipid



Sphingosine kinase 1 inhibition leads to accumulation of ceramide which activates PKR, inducing eIF2α phosphorylation to drive an apoptotic ISR mediated by master transcription factor ATF4. ATF4 promotes Bcl-2 dependency by the transcriptional upregulation of Noxa and the subsequent binding to and inactivation of Mcl-1, enhancing sensitivity of AML cells to venetoclax. Image created with BioRender.com

biosynthesis, we initially hypothesised that the accumulation of ceramides at this site in response to SPHK1 inhibition facilitated PERK activation. To test this hypothesis, we targeted PERK through various pharmacological and genetic approaches, and to our surprise, this had no effect on the cell signalling induced by SPHK1 inhibition, suggesting a different mechanism must lead to activation of eIF2α and ATF4. Alternative kinases, which are a part of the integrated stress response (ISR), can also phosphorylate eIF2α under varying stress conditions, and interrogation of these kinases revealed a clear role for protein kinase R (PKR) in ATF4 and Noxa induction. This novel finding was unexpected as PKR has classically been associated with innate immunity with activation through binding double-stranded (viral) RNA. As ceramide has been shown to modulate the function of numerous proteins, we speculated that ceramide might directly activate PKR to drive the ISR, Noxa upregulation and Mcl-1 degradation. Indeed, we found that ceramide bound to and activated PKR, proving the first report that endogenous ceramides can directly activate PKR and drive ISR signaling.

Mcl-1 is known to mediate resistance to Bcl-2 inhibition in AML, and its targeting could enhance the efficacy of these therapies. Thus, the effects of combining venetoclax with SPHK1 inhibition was interrogated. This combinational approach induced synergistic cell death in AML cell lines, primary patient samples and leukemic stem and progenitor cells. *In vivo*, this combinational therapy was well tolerated in mice with no pathologies detected and importantly, reduced leukemic burden in AML patient-derived xenografts. Patient samples harboring mutations that confer resistance to venetoclax were also sensitive to combinational therapies. In summary, our work advocates for the use of ceramide modulating agents as ISR activators to augment Bcl-2 inhibiting strategies for the treatment of AML and other cancers with high dependency on Mcl-1.

Jason Powell and Stuart Pitson
Centre for Cancer Biology
University of South Australia and SA Pathology

From left: Alexander Lewis, Jason Powell and Stuart Pitson.

COA7 Keeps the Copper Flowing

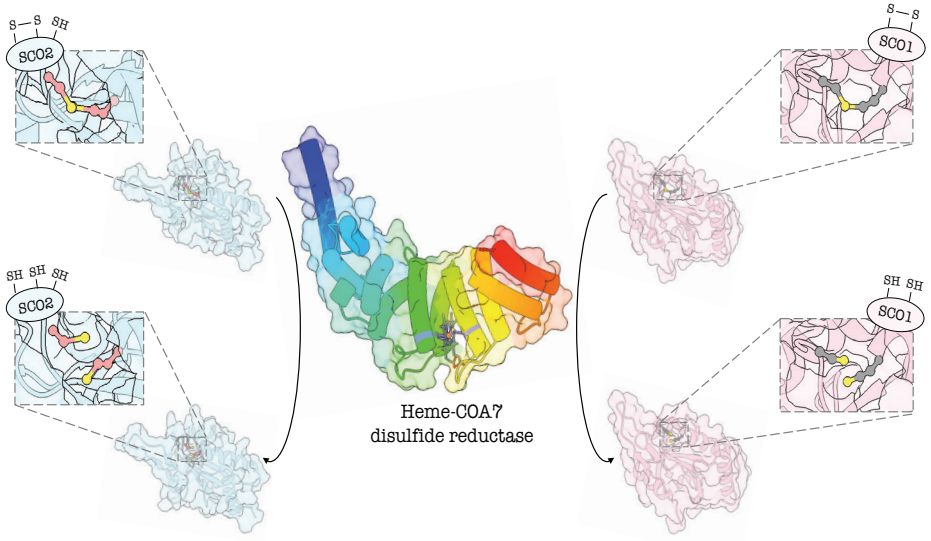
Formosa LE#, Maghool S#, Sharpe AJ, Reljic B, Muellner-Wong L, Stroud DA, Ryan MT*, Maher MJ*. Mitochondrial COA7 is a heme-binding protein with disulfide reductase activity, which acts in the early stages of complex IV assembly. *Proc Natl Acad Sci USA* 2022;119(9):e2110357119.
#Equal first authors
***Corresponding authors: michael.ryan@monash.edu, megan.maher@unimelb.edu.au**

Almost every cell in the human body contains miniature power plants to convert the energy needed to power life processes. These power plants, called mitochondria, do this by converting the food we eat into ATP for the cell to use in a process called oxidative phosphorylation (OXPHOS). A series of membrane complexes power OXPHOS, terminating with cytochrome *c* oxidase or complex IV, the last enzyme of the electron transport chain. Complex IV contains both copper and heme and catalyses the reduction of oxygen to water, completing the electron transport chain reactions. Complex IV has a complicated assembly process, as it is composed of 14 subunits encoded by both nuclear and mitochondrial (mt) DNA and requires more than 30 different assembly factors for its biogenesis. One such assembly factor, called COX assembly factor 7 (COA7), was suggested to play a role in the assembly of complex IV, as mutations in the COA7 gene led to mitochondrial disease with complex IV deficiency. The molecular function of COA7 however, was not known, so we set out to uncover how this protein contributes to complex IV assembly.

To uncover the role of COA7 in the assembly of complex IV, we combined genome editing, proteomics and structural biology approaches. We found that cells lacking COA7 had a total loss of complex IV and that the mtDNA encoded subunits COX2 and COX3 were rapidly degraded. To help pinpoint the stage at which COA7 functions, we also performed interaction studies using co-immunoprecipitation and proteomics and found that COA7 interacts transiently with complex IV assembly factors, many of which play a role in copper delivery to the mtDNA encoded subunit COX2 of complex IV. To understand the structural basis of COA7 function, we also solved the crystal structure of COA7 to 2.4 Å resolution, revealing five helix-turn-helix (α/α) repeats that are stabilised by five intramolecular disulfide bonds.

While we found a connection between COA7 and copper chaperones, COA7 itself did not bind copper *in*

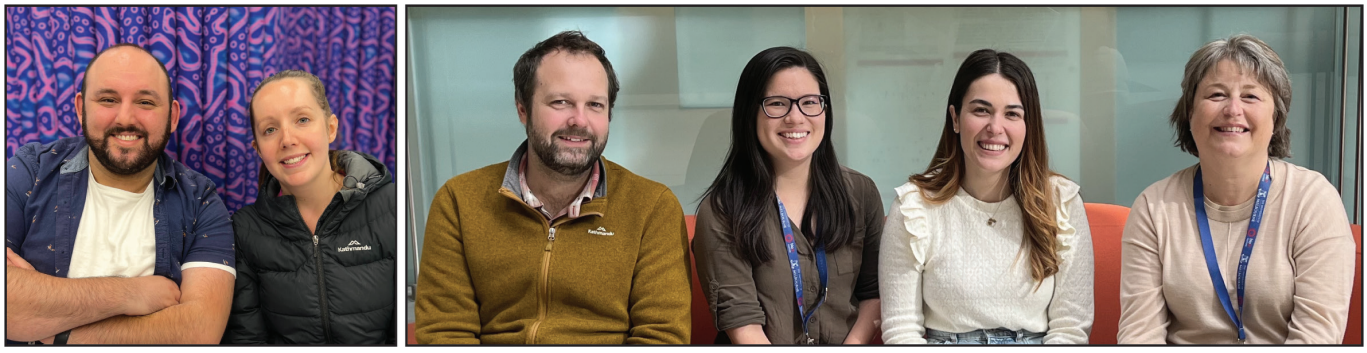
Publications with Impact



Heme bound COA7 functions as a disulfide reductase for copper metallochaperones SCO1 and SCO2. The heme-bound COA7 (rainbow) can redox cycle between oxidation states ferrous and ferric and shows disulfide reductase activity through reduction of disulfide bonds in copper metallochaperones SCO1 (pink) and SCO2 (cyan).

vitro, so we investigated if it could bind heme, the other co-factor required for complex IV activity. We found that heme iron is axially coordinated to histidine and methionine ligands. Mutations to these residues showed that heme binding was reduced *in vitro,* and resulted in a reduced capacity to rescue complex IV assembly in cells lacking COA7, suggesting these residues played an important role in the assembly process. Finally, we established that the COA7-heme complex does not play a role in chaperoning heme to complex IV, but rather has a newly discovered redox role. Given that we found that COA7 interacts transiently with copper chaperones, we tested if COA7 could reduce the copper chaperones SCO1 and SCO2, which undergo redox cycling while delivering copper to COX2. We found that heme-COA7 was able to reduce disulfide bonds in SCO1 and SCO2 *in vitro*, which coincided with the transition of the heme iron from the ferrous to the ferric oxidation states. We also determined that in cells lacking COA7, SCO1 and SCO2 were predominantly in their oxidised forms, suggesting that heme-COA7 plays an important role as a disulfide reductase, regenerating the copper relay system required for complex IV assembly.

Luke Formosa and Mike Ryan
Department of Biochemistry and Molecular Biology, Monash University
Shadi Maghool and Megan Maher
Bio21 Institute, University of Melbourne



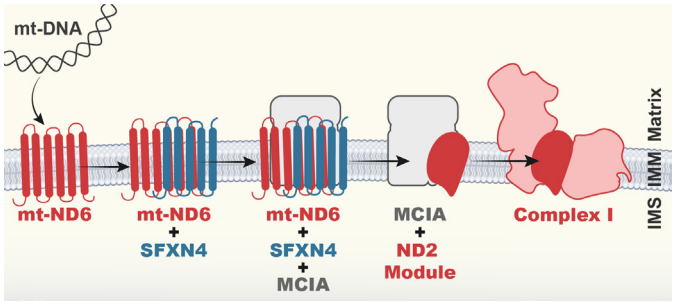
From left: Luke Formosa and Alice Sharpe (Monash University), David Stroud, Linden Muellner-Wong, Shadi Maghool and Megan Maher (Bio21 Institute).

Publications with Impact

A Complex Tale of Complex I Assembly – Identification of SFXN4 as a Novel Complex I Assembly Factor

Jackson TD, Crameri JJ, Muellner-Wong L, Frazier AE, Palmer CS, Formosa LE, Hock DH, Fujihara KM, Stait T, Sharpe AJ, Thorburn DR, Ryan MT, Stroud DA, Stojanovski D*.
Sideroflexin 4 is a complex I assembly factor that interacts with the MCIA complex and is required for the assembly of the ND2 module. *Proc Natl Acad Sci USA* 2022;119(13):e2115566119.
***Corresponding author: d.stojanovski@unimelb.edu.au**

The sideroflexin (SFXN) family comprises five paralogous proteins (SFXN1-5) of the mitochondrial inner membrane. SFXN1/2/3 have been shown to function as serine transporters required for efficient one-carbon metabolism. SFXN4, the most evolutionarily divergent member of this family has been linked to mitochondrial disease. We uncovered a role for SFXN4 in the assembly of complex I, unveiling why mutations in this gene cause mitochondrial disease.



Schematic representation of key findings. ND6 is a mitochondrial DNA-encoded subunit and associates with SFXN4 before interaction with the MCIA complex to give rise to the ND2 module and mature complex I. Credit: Jordan Crameri, PhD candidate, Stojanovski lab.

In 2021, we showed that the sideroflexins were a novel class of substrates of our favourite mitochondrial translocase, the TIM22 complex (1). Kory and colleagues showed that SFXN4, the most divergent member of the SFXN family, has no serine transport capacity unlike SFXN1-3 (2). Mutation in *SFXN4* causes a mitochondrial disease (MIM 615578) with features including macrocytic anaemia and complex I deficiency. This led us to ask, *does SFXN4 have a distinct function to the other SFXN proteins in mitochondrial function?*

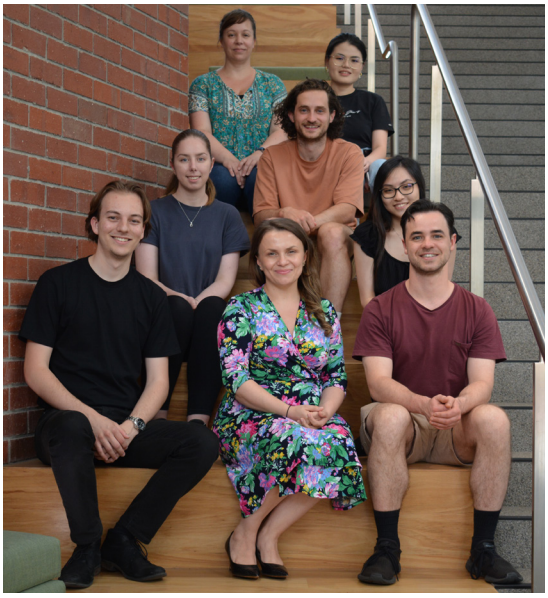
Genome editing of *SFXN4* coupled with quantitative proteomics gave us immediate insight into the function of SFXN4, revealing a striking depletion in numerous subunits of complex I. We confirmed that cells lacking *SFXN4* have an isolated complex I defect using BN-PAGE and assessing the enzymatic activity of the ETC. This hinted to a role of SFXN4 in complex I biology, but how, and why SFXN4? Affinity enrichment mass-spectrometry of SFXN4 revealed a profile of known, yet unexpected interacting proteins belonging to the MCIA complex (mitochondrial complex I intermediate assembly complex); a network of assembly factors required for the assembly the ND2 module of complex I. This complex was no stranger to us, as our colleague Professor Mike Ryan and his lab have been at the forefront of uncovering the molecular constituents of this complex. So, without intention, we entered the very complex world of complex I assembly!

Complex I, the first enzyme of the ETC, consists of 45 subunits and is assembled through an intricate pathway where 'modules' come together to build the mature complex. The inner membrane localised 'arm' contains seven mitochondrial DNA (mtDNA) encoded subunits, divided into distinct modules: ND1, ND2, ND4 and ND5. The ND2 module contains four mtDNA-encoded subunits: ND2, ND3, ND4L and ND6. The ND2 module and the MCIA complex appear to assemble initially, before ND3, ND4L and ND6 are added to this intermediate. Assembly factors had been described for ND2 and ND3, however, the existence of assembly factors that associate with ND4L or ND6, the two last subunits added to the module, remained unclear. Interestingly, ND6 was the most significantly enriched mtDNA encoded protein immunoprecipitated with ^{FLAG}SFXN4. *Could SFXN4 be serving as a platform for the integration of ND6 into the ND2 module?*

Steady-state levels of ND6 in cells lacking SFXN4 were drastically reduced, hinting to potential turnover or inhibition in protein synthesis in the absence of SFXN4. Reciprocal immunoprecipitation experiments using tagged-MCIA subunits showed endogenous SFXN4, confirming the SFXN4-MCIA interaction. *But does SFXN4 interact directly with ND6 and independent of the MCIA complex?* We expressed ^{FLAG}SFXN4 in a cell line lacking an MCIA subunit, where the MCIA complex is destabilised and could still capture the SFXN4-ND6 interaction. This suggests the SFXN4-ND6 interaction can occur independently, and likely upstream of the MCIA complex. In the final piece of the puzzle, we asked how the MCIA complex changes in the absence of SFXN4. We looked at the composition and abundance of the MCIA-complex I assembly intermediates following deletion of SFXN4, in cells expressing tagged-MCIA. Immunoprecipitation of the MCIA complex showed a striking depletion of ND6, meaning when there is no

SFXN4, ND6 is not found with the MCIA-complex I intermediate.

Our work has added another assembly factor to the growing list of complex I assembly factors, SFXN4. SFXN4 functions specifically the assembly of ND6 into the ND2 module. This work provides an explanation for the disease phenotype caused by mutations in *SFXN4*.



Stojanovski lab.

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2. Kory N, Wyant GA, Prakash G, Uit de Bos J, Bottanelli F, Pacold ME, Chan SH, Lewis CA, Wang T, Keys HR, Guo YE, Sabatini DM. *Science* 2018;362(6416):eaat9528.

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Rebooting Evolution

Raven SA, Payne B, Bruce M, Filipovska A, Rackham O. In silico evolution of nucleic acid-binding proteins from a nonfunctional scaffold. *Nat Chem Biol* 2022;18(4):403–411.

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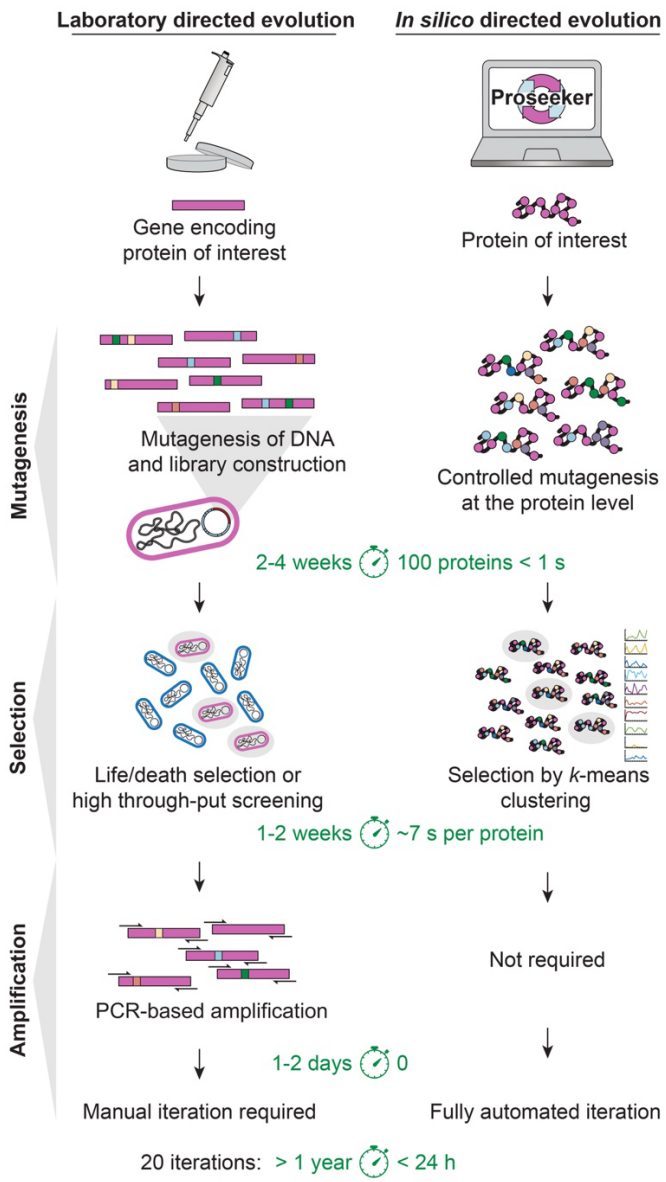
Laboratory evolution of proteins has revolutionised a surprising number of products that impact all of our lives – not just in life saving protein therapeutics and the chemicals produced by industrial biocatalysis but even in everyday laundry detergents. However, these proteins can only be obtained via the painstaking process of directed evolution. This method mimics natural evolution by making mutations in naturally-sourced, suboptimal proteins and selecting the best mutants, to be mutated and selected again in a time intensive and laborious process. The Rackham and Filipovska groups have used directed evolution over the years to produce programmable RNA-binding proteins and even ribosomes with altered functions. These approaches have proven to be very powerful but are technically challenging and particularly time and resource intensive – when someone is doing a directed evolution experiment the incubators are overflowing and benches are stacked high with petri dishes! To bypass these limitations, we wondered whether the whole process could be performed computationally.

Directed evolution seeks to alter protein function by mimicking natural evolution in three key steps: mutagenesis (where a library of variants of the chosen progenitor gene is constructed), selection (where the library is expressed and members with the desired function are enriched) and iterative amplification (where the genes encoding the selected variants are collected for sequencing or to generate templates for the next round of selection). Each of these steps often requires optimisation for each new protein of interest. We designed a computational method, that we call Proseeker, to emulate directed evolution *in silico*. The software package was developed in a Herculean effort over four years, with over five million lines of code constructed over the course of the project. Proseeker introduces random mutations into a protein sequence of interest and then assesses the physico-chemical characteristics of each mutant with reference to a library of proteins of interest, before choosing the best scoring proteins for additional rounds of mutagenesis and selection.

As a proof of principle for this approach, we evolved new nucleic acid-binding repeat proteins from a completely non-functional scaffold protein that could not bind nucleic acids. Only a few designs needed to be tested experimentally, using *in vitro* binding assays as well as protein fragment complementation assays in bacteria, to discover *de novo* RNA- and DNA-binding proteins. The ability to bind and manipulate DNA and RNA is key to understanding how genes orchestrate organismal function and will be critical to modify living systems for useful purposes. Therefore, the development of genome editing tools and other biotechnological approaches to manipulate nucleic acids would benefit from escaping the limited diversity of DNA- and RNA-binding proteins found in nature.

Phylogenic assessment of the protein sequences selected by Proseeker over time revealed highly ordered behaviour characteristic of organised systems arising

Publications with Impact



Computational evolution of proteins with new functions using Proseeker. A typical laboratory directed evolution experiment is compared to the Proseeker in silico *evolution approach.*

through evolution as opposed to random behaviour. We also found a preponderance of neutral mutations that eventually contributed to the development of new binding sites. These observations indicate that our approach mimics the natural processes of mutation and selection, providing new insights into the processes that guide protein evolution in nature. They also substantially improve the possibilities for protein engineering, because it eliminates the need for specialised skills associated with large scale directed evolution experiments and operates with a much lower cost in both time and resources.

Computational approaches, such as AlphaFold and Rosetta, have proven to be powerful tools to predict protein structure; we hope that Proseeker will usher in a new era in functionalisation of proteins. Future work will explore the potential applications and additional strengths and weaknesses of this approach. Although *in silico* directed evolution mimics the processes of natural evolution, it does not require a genetic template and therefore escapes all the limitations of natural genetic codes. For example, there are no limitations on transitions between different amino acids that are typically constrained by the codons that encode them and no codon biases. More importantly, this evolutionary system is no longer confined to nucleic acids or proteins and could in theory be applied to any chemical entity, for example lipids or small molecule compounds, such as drugs. Therefore, *in silico* evolution could be a powerful means to discover new drugs and bioactive molecules beyond proteins in the future.

Samuel Raven, Blake Payne,
Aleksandra Filipovska and Oliver Rackham
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ARC Centre of Excellence in Synthetic Biology
Curtin Medical School and Curtin Health
Innovation Research Institute
Curtin University
Telethon Kids Institute
School of Molecular Sciences
University of Western Australia

From left: Aleksandra Filipovska, Oliver Rackham and Blake Payne.

New Approach to Specifically Eradicate Disease Clones in Mutant CALR-driven MPNs

Tvorogov D, Thompson-Peach CAL, Foßelteder J, Dottore M, Stomski F, Onnesha SA, Lim K, Moretti PAB, Pitson SM, Ross DM, Reinisch A, Thomas D*, Lopez AF*.
Targeting human CALR-mutated MPN progenitors with a neoepitope-directed monoclonal antibody. *EMBO Rep* 2022;23(4):e52904.
***Corresponding authors: daniel.thomas@adelaide.edu.au, angel.lopez@sa.gov.au**

Blood cancers known as myeloproliferative neoplasms (MPNs) are a group of diseases in which the bone marrow produces too many red blood cells, white blood cells, or platelets. Our work focuses on mutations in calreticulin (CALR), which are the second leading cause of MPNs. CALR is a highly conserved chaperone protein that resides primarily in the endoplasmic reticulum and is involved in a variety of cellular processes. One of the genes is frequently mutated in a debilitating group of MNPs, which includes myelofibrosis and essential thrombocythemia. CALR mutations are the second most frequent mutation in MPNs after mutations in JAK2. These mutations were only recently identified (2013) and prior to this study, there were very few antibodies available for mutated forms of CALR – and they were expensive to purchase! We decided to develop our own antibodies to mutated CALR for biochemical studies. Little did we know that the antibodies we developed would have a great potential for the treatment of MPN patients.

Almost all CALR mutations in MPN are small insertions or deletions clustered in exon 9, resulting in a +1 frameshift and loss of the last four amino acids (KDEL) that form the endoplasmic reticulum retention signal, leading to altered distribution of CALR and the formation of a new sequence at the C-terminal tail of the protein (**Fig. 1**). Data from independent laboratories have shown that mutant CALR protein requires MPL for signalling, binds to the receptor and activates JAK–STAT signalling (**Fig. 2**, left side).

To study mutant CALR (mutCALR) transformation, Frank Stomski suggested developing a rat monoclonal antibody by injecting a 30-amino acid sequence in rat followed by sera test, fusion with myeloma cell

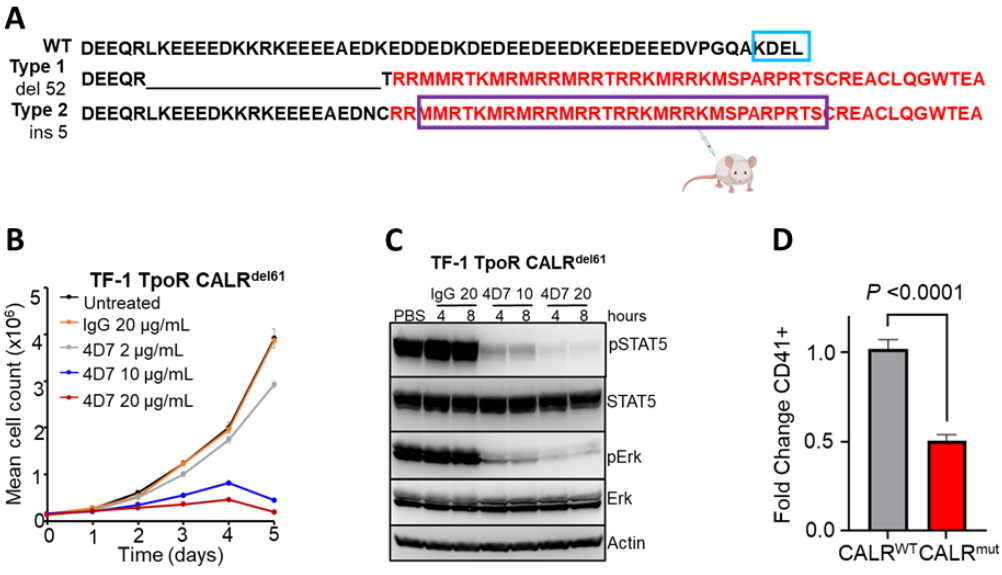

Fig. 1. *Anti-mutant calreticulin antibody inhibits mutant CALR-induced signalling.*

- ***A.*** *Schematic showing wild-type C-terminal calreticulin protein sequence and neoepitope sequences for 52 bp deletion or 5 bp insertion and peptide sequence used for immunisation in purple box.*
- ***B.*** *Proliferation curves of factor-independent TF-1 TpoR CALRdel61 cells cultured with 2, 10 or 20 µg/ml 4D7 or 20 µg/ml of control IgG antibody.*
- ***C.*** *Cell extracts blotted for phospho-STAT5, total STAT5, phospho-ERK, total ERK and actin from TF-1 TpoR/delCALR cells after incubation with 10 or 20 µg/ml 4D7 or IgG for 4 or 8 h.*
- ***D.*** *Summary of fold change reduction of CD41/CD61+ megakaryocytes by 4D7 in all tested CALR-mutated patient samples compared to CALR wildtype, normalised to IgG.*

Publications with Impact

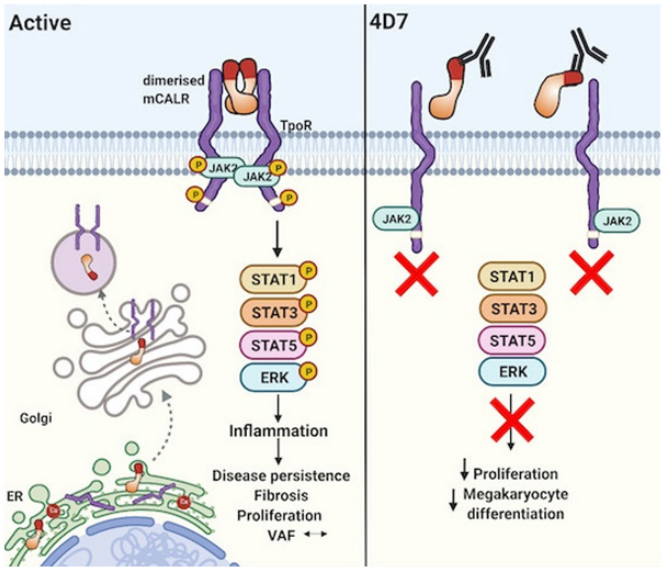

Fig. 2. *CALR is recurrently mutated in myelofibrosis, creating a surface-exposed neoepitope that activates the thrombopoietin receptor. A monoclonal antibody (4D7) with mutation-specific efficacy in CALR mutant progenitors disrupts the receptor-CALR complex and inhibits proliferation.*

line, cloning and clone screening. The monoclonal antibody, 4D7, was generated in the Antibody Facility at the WEHI Biotechnology Centre. It was effective in immunoprecipitation and western blotting, thus representing a valuable tool for biochemical studies. To our surprise, when Mara Dottore applied 4D7 to TF1 cells, which were expressing Tpo receptor and were converted to cytokine-independence via mutCALR expression, this antibody showed very strong inhibitory activity in proliferation assays (**Fig. 1**). After several rounds of repetition and controls, we were finally convinced that this is true and had a look at at the effects of the antibody application. We observed significant inhibition of JAK–STAT pathways and realised that this antibody may be developed as a treatment. Chloe Thompson-Peach and the Daniel Thomas group, with which Angel Lopez has a long-established collaboration, revealed that 4D7 does have inhibitory effects on MPN samples derived from mutCALR patients (**Fig. 1**). What was especially exciting is that this antibody strategy, if clinically developed, will only target mutant cells, leaving normal haematopoiesis intact. This would represent a significant shift from the currently used MPN treatment of ruxolitinib, a JAK inhibitor that suppresses both mutation-driven and normal haematopoiesis. We had a brief look at the mechanism of 4D7 action and we revealed that 4D7 treatment prevents Tpo receptor activation and JAK–STAT signalling initiated by mutated CALR (but not by normal receptor stimulation with Tpo) (**Fig. 2**). Thus, combined efforts of biochemists, antibody facility scientists and clinicians have allowed this discovery to be made. The antibody is now in clinical trials, and we hope it will represent a novel therapy avenue for the treatment of CALR-driven myeloproliferative neoplasms.

Denis Tvorogov
Centre for Cancer Biology
SA Pathology and University of South Australia

From left. Front: Denis Tvorogov, Mara Dottore, Chloe Thompson-Peach, David Ross. Middle: Paul Moretti, Angel Lopez, Kelly Lim. Back: Stuart Pitson, Frank Stomski, Daniel Thomas.

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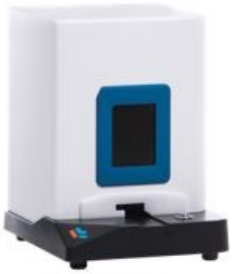

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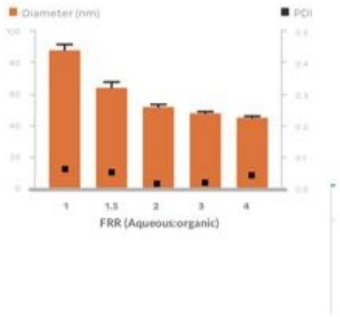

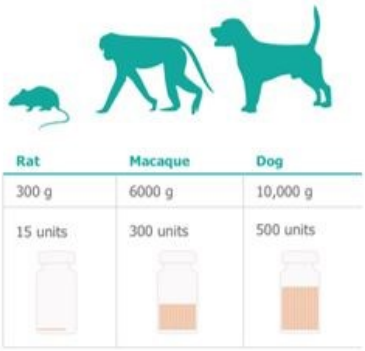

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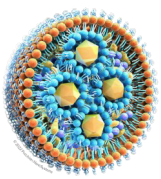
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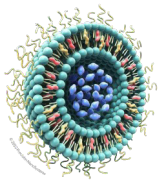
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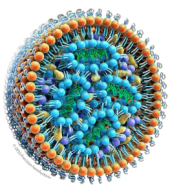
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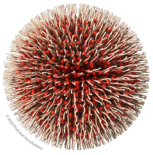
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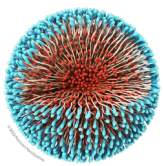
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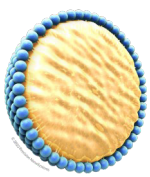
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Tutorial Presentation Redesign to Improve Engagement and Development of Core Skills

Jody Gorman, School of Chemistry and Molecular Bioscience, University of Wollongong

Presentation skills are key to communicating the sciences and a core skill for a wide range of graduate destinations. Teamwork is also a core skill valued by industry and applicable across disciplines. Group presentations of a research paper in a weekly tutorial had been the traditional method of developing these skills in a second-year introductory genetics subject with approximately 250 students. Students attended weekly tutorials with half their cohort, presenting a current research paper as a group in a designated week. The presentations aligned to and supported lecture content with current research examples but engagement by the audience majority was observably minimal despite 'bonus marks' being awarded to those asking questions. A redesign of this task has not only improved engagement but encourages critical thinking and active participation in discussion to additionally develop these skills in our young scientists.

Redesign came in the form of condensed and intense participation in one elected small group tutorial. The new task required students to do more than just present someone else's research (**Fig. 1**). In addition to the presentation component, students were also required to peer-review other presentations using a rubric in the Workshop tool on Moodle, giving them the opportunity to assess strong and weak points and learn from other students' work; complete a group and self-assessment using the Team Evaluation tool in Moodle to improve accountability, and participate in a small group tutorial where they would each ask and answer questions which encouraged discussion and even debate. All components contributed to their assessment mark and the assessment weighting for the task was increased accordingly.

Changes to presentation structure meant student groups still had to identify a current research paper to base their presentation on but were limited to four key topic areas. Rather than presenting in traditional paper format (intro, methods, results and discussion), students were required to present in four sections that saw them focusing on the genetic technology of the research paper, other applications of that technology, and consideration of the safety/ethical concerns associated with the technology, see **Fig. 2**. This meant students had to go beyond the scope of their chosen paper and conduct additional research. This improved their knowledge of the technology and its potential applications. It also meant they had to apply some critical thought to the technology they were describing and its potential health and/or moral

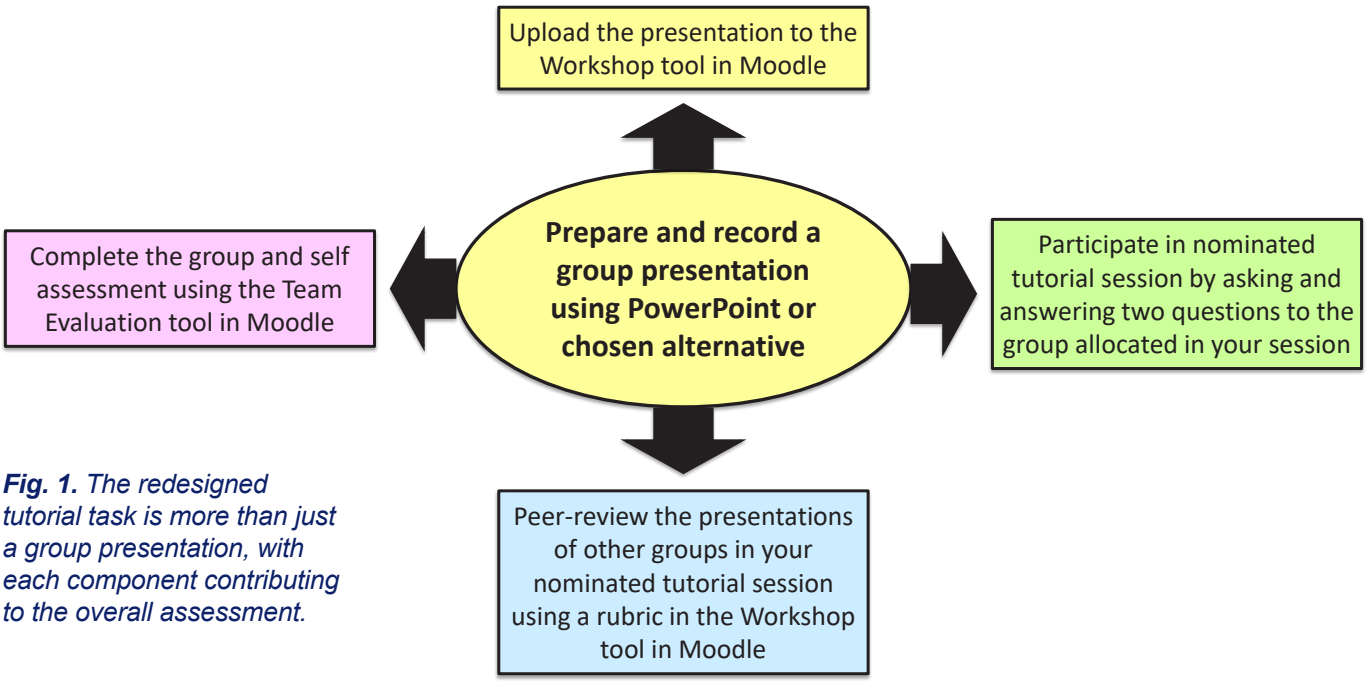

Fig. 1. *The redesigned tutorial task is more than just a group presentation, with each component contributing to the overall assessment.*

Presentation Topics	Presentation Sections
Gene editing to fight disease	Background and motivation
Agricultural biotechnology	Outline of the genetic technology
Commercial human genome sequencing	Other applications of the focus technology
Human cloning for stem cell therapeutics	Safety/ethical concerns of the technology

Fig. 2. *Presentations were focused on four sections that required students to research beyond the scope of their chosen research paper.*

impact. This resulted in all students of the cohort being exposed to research examples and genetic technologies in four current and controversial topic areas.

Feedback from the tutors facilitating the tutorials was very positive. One of the tutors, who had managed and marked presentations in the traditional format, commented that "The tutorials were organised in a way that encouraged the students to take the lead and autonomy with their own learning. In many instances, they required little facilitation. The vast majority of students were genuinely engaged, demonstrated sound understanding of the research discussed and were able to think critically when prompted on bigger questions." Informal conversations with students also indicated a positive experience by the majority which was supported by feedback in the subject survey. One student commented, "it was engaging and I got to learn from marking and discussion", another wrote "small group was good to engage better with the content," and a third, "I really enjoyed the research group task. It was nice to have a task that really reflected the effort you put in."

Despite student numbers in excess of 200, a migration back on campus post-COVID, and the level of back-end management required to run tutorials in this format, the redesign seemed to achieve its aim of improved engagement and core skill development and will be a fixture in Introductory Genetics at UOW into the future.

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Shifts in Student Behaviours During COVID-19: Impacts of Social Interaction on Academic Integrity

Ann Rogerson, Faculty of Business and Law, University of Wollongong

Institutional data management of academic integrity cases and types can reveal patterns of both reporting and student academic integrity related behaviour. Previous institutional reporting from 2017–2019 demonstrated that cases of poor academic practice identified in the early years of higher education can be remedied by targetted and structured intervention programs (1).

Results from cases logged during 2020 and 2021 which were impacted by the switch to remote delivery teaching and local lockdowns revealed some differences in student behaviour when compared to academic misconduct cases from previous years. Of particular note is the reduction observed in cases from first year undergraduate students, and a marked increase in instances of collusion by students in other years. Collusion cases primarily fell into two categories – those influenced by technology and others that were the consequence of students gathering, studying and taking exams in the same location as lockdown restrictions eased.

In trying to determine the reasons for the reduction, initial investigations indicate that it was a consequence of first year students having little opportunity to form and build the new social connections that can influence cheating behaviours. There could also be the influence of shifting teaching to remote formats and changes to traditional assessments which has impacted not only first year students, but students in later years of study. We have to remember that we are now coping with more than one cohort of students who have only studied remotely rather than on campus – this has changed social dynamics and consequently some of the ways students are behaving. What was recognised is that for large cohorts it is difficult to manage large groups of students with varying degrees of poor academic practice in a process that is designed to manage a smaller number of individual cases. As a result of this recognition, our institution is introducing newer and simpler reporting for cases of poor academic practice as a way of addressing behaviour through interventions that

have been demonstrated to work.

With students beyond the first year of study there was a marked shift from purchased materials to instances of collusion. This involved the effects of sharing site use such as Chegg (2) in addition to the use of gaming networks to communicate with other students during online assessment tasks. Further collusion cases became evident as lockdown restrictions eased in the Spring session (July–November 2020, and the first half of 2021) where students gathered in small numbers permitted under the COVID restrictions to undertake study or assessment tasks. This resulted in higher levels of similarity of content and errors identified using text matching available through services such as Turnitin®.

In trying to address some of the possibilities of collusion in online exams has seen online proctoring/invigilation tools adopted by some institutions to provide one alternative to monitoring in-person/on-campus examinations. There are a range of tools or software solutions available such as Proctorio® and ProctorU, which cover a range of services including identity validation, browser lockdown, IP address comparisons, recorded monitoring or synchronous live monitoring, but have limited interface points to existing learning management systems or require an additional platform setup. It is apparent that these technological methods of monitoring students may be a useful alternative for on campus text-based examinations, but are not necessarily as user friendly or practical for content that requires assessment of calculations, formulae, numeric or chemical calculations.

The COVID-19 pandemic has resulted in changes to teaching that requires us to continue refining the way we teach, assess work and manage cases of academic misconduct (2). As educators, we also need to reconsider how we are explaining academic integrity and, in particular, the influence of social connections on collusion and sharing behaviours in light of the evidence now available on cheating behaviours that have arisen via the global pandemic.

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2. Lancaster T, Cotarlan C. *Int J Educ Integr* 2021;17(3): 1–16.

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Using Digital Technologies to Create an Engaging Small Group Learning Experience in Large Cohorts

Michelle Rank

Department of Anatomy and Physiology, University of Melbourne

Students have been impacted by a high degree of social isolation over the past two years of emergency remote learning. Many students early in their undergraduate learning journey have been disproportionately affected by the lack of on-campus interaction and have not yet had the opportunity to foster new social connections and participate in their education as part of a community of learners. This is important in the context of learning because effective learning is an inherently social activity. For students to gain new understandings, they need to be able to learn from and with one another (1). One way to support social learning is to incorporate activities that foster collaboration. In this article, I report our efforts efforts to create small group collaborative learning opportunities in timetabled sessions within a large second-year undergraduate biomedical science core subject. A blended synchronous learning (BLS) approach was used to deliver team-based learning activities, in online and face-to-face modes concurrently, to over 550 students. Using a combination of digital technologies (Campuswire, Padlet and Zoom) and abundant enthusiasm, the large group lecture experience was transformed into a workshop format with collaborative small group activities.

Small group learning experiences were deployed in a traditional 'lecture' timeslot scheduled in a large capacity theatre. On-campus students were accommodated in the lecture theatre, while remote learning students accessed the live session via Zoom. Students were presented with a series of four to six Challenge Questions, similar to short answer style exam questions, that challenged students to integrate subject content across disparate topics. Students were then instructed to self-organise into groups of up to ten participants and select two to three Challenge Questions to discuss as a team; team names were encouraged. On-campus student groups worked together within the lecture theatre, whereas remote learning students were instructed to self-organise into online groups accessed via chatrooms within the subject's Campuswire discussion board. After

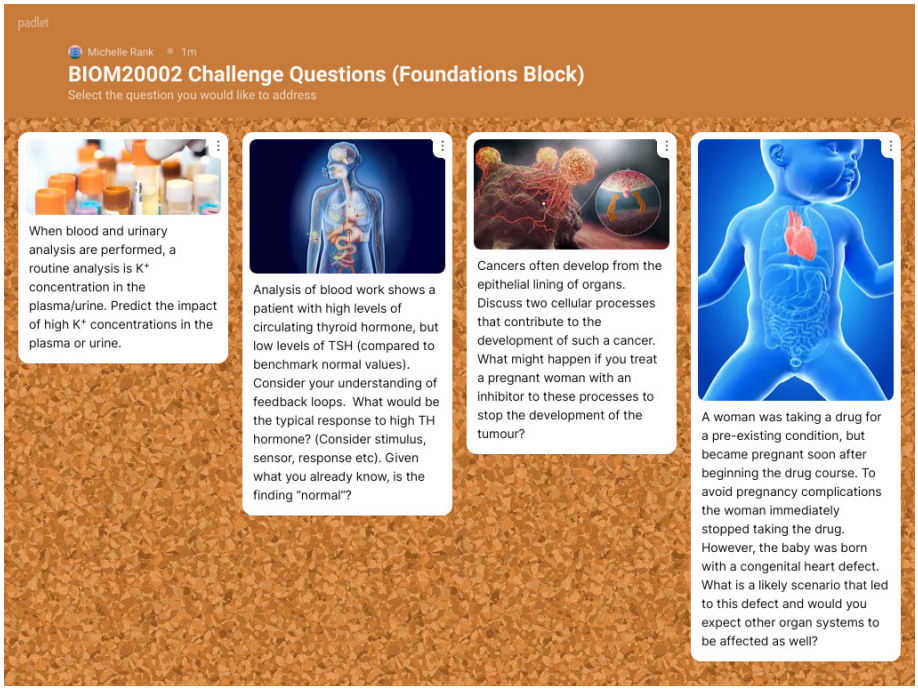

Fig. 1. *A sample Padlet wall showing integrated Challenge Questions posed to students during a large cohort workshop session in a second-year undergraduate core biomedicine subject. Students organise into small groups of up to ten students during a 'lecture session' to collaboratively discuss and propose answers to the Challenge Questions on the Padlet wall. Students can then engage in real-time review and peer feedback of all posted responses.*

20–25 minutes of discussion, students were asked to post their groups' responses to Padlet, a real-time collaborative notice board platform. Utilising Padlet allowed both on-campus and remote-learning students to interact seamlessly in real time. For the remainder of the session, student groups were encouraged to read and discuss the Padlet posts made by other groups and provide feedback, comments and upvotes. Students who were unable to attend the live session, either on-campus or remotely, could access Padlet and add their independent input (i.e. Challenge Question responses or feedback to other posts) at any time of their choosing. After the session, subject coordinators would provide informal feedback to the Padlet wall. The previous week's responses to the Challenge Questions were discussed by the subject coordinators at the beginning of the next timetabled session.

These collaborative small group learning workshops, delivered using a BSL approach to a large cohort, provided students with the opportunity to experience connected social learning as part of a community of learners. Students were able to collaborate with peers, communicate scientific thought, give and receive feedback and engage in formative learning based on exam-style short answer questions. Student feedback on the sessions was enormously positive, with a majority of respondents agreeing that the sessions had a positive impact on their learning experience:

"The Challenge Questions were really useful to go over what we had learnt in a different way, just to cement our learning with our groups. It was good to be able to interact with our lecturers and peers!"

An unexpected benefit of using the Campuswire chatrooms to facilitate discussion among remote learning students was that on-campus students who preferred to interact online had the opportunity to do so. Thus, each student could maintain their learning autonomy and engage with the activity in a personalised way that best suited their learning preferences. From the perspective of an academic, the small group learning workshops were initially quite challenging to execute, given the use of multiple technologies simultaneously, but this was quickly overcome with practice. The sessions were best staffed by two academics, or with the assistance of at least one tutor, to ensure both the on-campus and remote learning students were able to interact with content experts; this was particularly true for the remote learning students who thrived with a dedicated tutor:

"It was really exciting to see students engaged with one another in the lecture theatre in this way, and fantastic that students were inclusive of their online peers too. As a teacher it's seeing this kind of excited engagement from your students that is one of the most rewarding parts of the job"

This approach is certainly not for the faint of heart, but the core principles can be variably applied, in part or in whole, to yield a positive socially connected student experience even in very large cohorts.

References

1. Bandura A (1986) *Social Foundations of Thought and Action: a Social Cognitive Theory.* Prentice-Hall.

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ASBMB EDUCATION SYMPOSIUM AT COMBIO2022

Lessons Learned from the Pandemic and Advancing our Teaching Beyond…

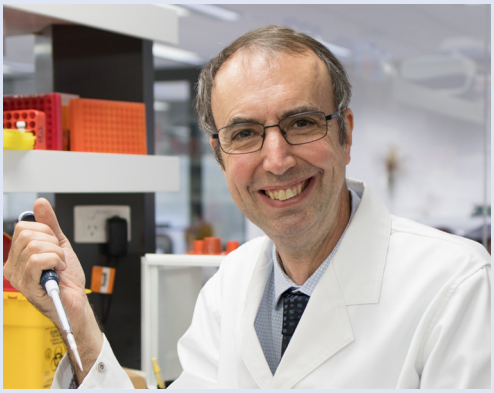
Wednesday 28 September 2022

The keynote presentation, Supporting Academic Careers as Student Numbers and Technology Change, will be given by Professor Merlin Crossley, Deputy Vice-Chancellor Academic and Student Life, UNSW Sydney.

The symposium will include invited presentations from Professor Susan Rowland (University of Queensland) and Dr Robyn Yucel (Deakin University).

We will hear from the 2022 education award prizewinners from the Australian Society for Biochemistry and Molecular Biology, Genetics Society of Australia and Australian Society of Plant Scientists. We will gain important insights from our Student Panel.

This is a great opportunity to network with fellow educators, share practice and advance our teaching.



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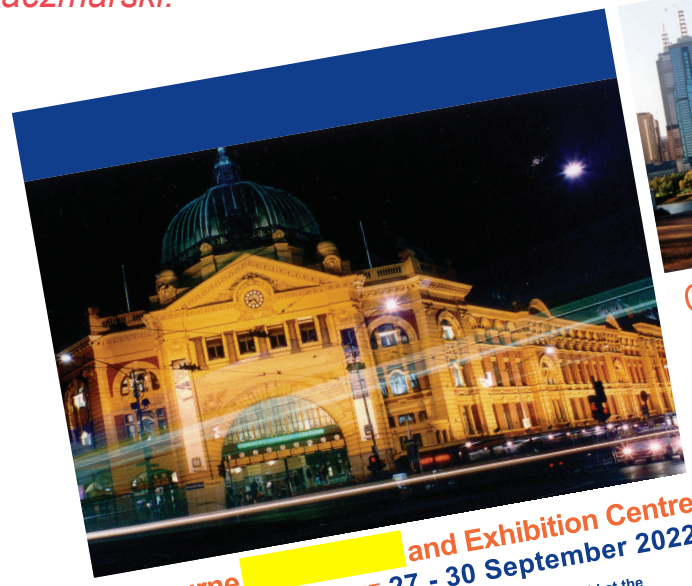
Competition: Word Search

Presenting the latest competition for the members of ASBMB. All correct entries received by the Editor (editor@asbmb.org.au) by 5 September 2022 will enter the draw to receive a voucher. With thanks to Joe Kaczmarski.

Oh no! There's been a printer malfunction and the ComBio2022 advertisement is missing some key names and words (highlighted in yellow) – help find the missing names and words amongst the word search on the next page. Once you have found all the words, the red highlighted letters that are NOT included in any of the words can be unjumbled to spell the secret word!



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We extend a warm invitation to you to be part of ComBio2022 to be held at the Melbourne Convention and Exhibition Centre (MCEC). After a long pause in our plans, we anticipate that this will be a vibrant return to face-to-face scientific exchange with our colleagues.* ComBio2022 will be held in a spectacular arm of MCEC that is adjacent to the Yarra River and walking distance from numerous restaurants and cafes serving the widest imaginable variety of food. Melbourne is home to many sporting and cultural events and world class museums and galleries plus an aquarium are in the immediate vicinity. There is also an abundance of budget priced accommodation within walking distance of MCEC. ComBio in Melbourne in the Spring of 2022 should be a 'must' for all. (*Covid-safe protocols will be in place as advised closer to the date)

We are pleased to announce that the Opening Keynote Plenary Lecturer is Nobel Laureate Jennifer and the ASBMB Grimwade Keynote Plenary Lecturer is Cynthia

Jennifer is an internationally renowned Professor of Chemistry and Molecular and Cell Biology at U.C. Berkeley. She and her colleagues rocked the research world in 2012 by describing a simple way of editing the DNA of any organism using an RNA-guided protein found in bacteria. This technology, called CRISPR-Cas9, has opened the floodgates of possibility for human and non-human applications of gene editing and was the basis for her co-award of the Nobel Prize in 2020. Jennifer is a Howard Hughes Medical Investigator, a member of the National Academy of Sciences, the National Academy of Medicine, the National Academy of Inventors and the American Academy of Arts and Sciences.

Cynthia is Vice President, Aging Research, at Calico and expert on the genetics of aging. In 1993, Cynthia's discovery that a single-gene mutation could double the lifespan of the roundworm *C. elegans* has led to a new understanding of the genetics of aging. She has received many honors and awards for her findings. Cynthia is a member of the US National Academy of Sciences, the American Academy of Arts and Sciences, and the Institute of Medicine and she is a past president of the Genetics Society of America.

Plenary Speakers:

- **Siobhan** University of California, Davis, CA, USA
- **Jamie** University of California, Berkeley, CA, USA
- **Jennifer** University of California, Berkeley, CA, USA
- **Geldner,** Université de Lausanne, Switzerland
- **Wolfgang** Max Planck Institute, Germany
- **Tony** Salk Institute, CA, USA
- **Cynthia** Calico LLC, South San Francisco, CA, USA
- **Lo Celso,** Imperial College London, London, UK
- **Jodi** University of California, Davis, USA
- **Parker,** University of Colorado, Boulder, USA
- **St Johnston,** Gurdon Institute, Cambridge, UK
- **Emma** University College Dublin, Ireland
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ASBMB Education Plenary

- **Merlin** Deputy Vice-Chancellor Academic and Student Life University of New South Wales

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Registration/Exhibition
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KEY DATES:

Late Poster Submission Deadline: Monday, 8 August 2022

Onsite Poster Submission Deadline: Wednesday, 21 September 2022

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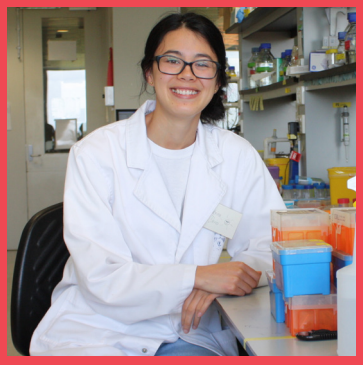
Q Q C F R D J C F S I C C L T E S F P S
S S T E U O C W S E B A I W E A A E Y D
K Z P O K E N Y O N T S X L A Y C Z Z A
B O D Q C J T A V E M J I X A Y G U M N
N U N N A R I S C I E N T I S T S W D I
L N O E Y T N R M H G W V O Q C J C B E
L A T N E M P O L E V E D K J I H R L L

Once you have found all the missing words and names, the red highlighted letters that are NOT included in any of the words can be unjumbled to spell the secret word.
Hint: words may be backwards and diagonal.

'Cryptic Crossword' Result

The winner of the April competition is Sabrina Davies, School of Molecular Sciences, University of Western Australia. Congratulations to Sabrina, who will receive a gift voucher.



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Category Winner

Prism Awards 2022
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* (Ultra-quiet scan)

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SDS Page:
Short Discussions for Students Page

How to Prepare a Poster for a Scientific Conference

Christopher Szeto[1,2] and Andrea Nguyen[1,2]

[1]Department of Biochemistry and Chemistry, La Trobe Institute for Molecular Science, La Trobe University

[2]Department of Biochemistry and Molecular Biology, Biomedicine Discovery Institute, Monash University

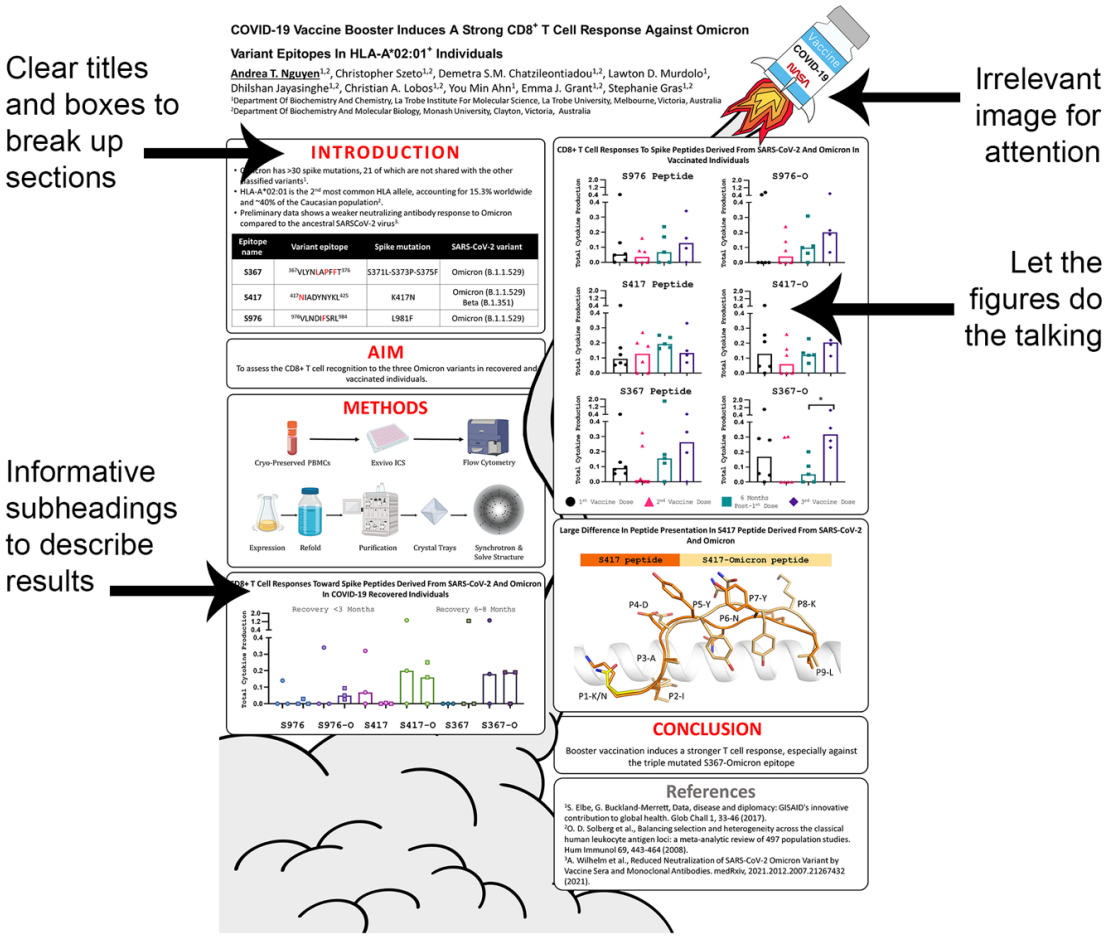
A poster presentation is a great way to practice honing our science communication skills. Presenting a poster can be quite daunting, but it should be viewed as an opportunity within a safe and casual setting to receive feedback, practice answering questions, and foster conversations with other scientists, which is so important for networking. If made well, the poster should be a perfectly crafted balance between clarity and storytelling, where the transmission of information should be made as simple and clear as possible, whilst still sparking engagement, curiosity, significance and interest by guiding our audience through our research story. We've summarised below what we believe to be the five most important tips to help craft a clear and engaging poster.

1. Visual clarity

People like clean and clear posters, they are visually appealing and more approachable. It signals to the audience that we have a clear direction and mindset, and that it won't take up too much of their time investment to appreciate the research we are working on. Posters with over-crowded sections and slabs of text are at best intimidating, and could convey that the author has poor organisation and storytelling skills.

2. Keep it simple, stupid

An important aspect to any presentation is knowing our audience. Even at a biochemistry conference, try to keep the content understandable at the graduate level. There



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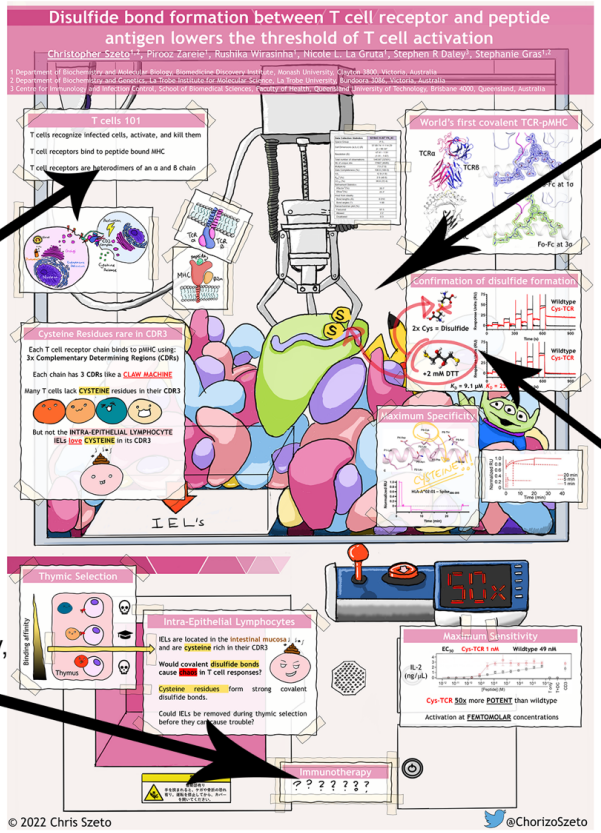
As an ECR, I am to draw attention to myself & spark conversation about my research. Visual clarity is very poor, but wow factor is high.



Very simple immunology introduction

Analogy that TCR binding is like a claw machine reduces use of technical jargon

Results as figures only; presented as a stepped logical progression of experiments

Close with significance in immunotherapy, left empty to generate discussion

might be non-specialist, multidisciplinary scientists, or new research students wanting to know more. Try to avoid using jargon, but if it can't be helped, make sure to simplify scientific terms and concepts if they are vital in understanding the research. If there's a multidisciplinary aspect to the project (bioinformatics, immunology, cell biology, etc.), it might be worth toning down the technical language in your introduction so that the audience can follow along.

3. Show and not tell

Assuming we all go back to in-person conferences, an important thing to note is that WE are the PRESENTATION, and our POSTER is a visual aid. Our poster shouldn't have to be a stand-alone presentation. During the poster session, we should be alongside our poster to answer questions, explain our methods, interpret our results, and engage with the audience. This allows us to replace slabs of text with what we're going to say, and instead, show off those important diagrams and figures in their place. Use eye-catching titles that are informative and appropriately summarise a section of information. These also double as verbal cue prompts during the presentation.

4. Present a story

We are evolutionarily hard-wired to pay attention to stories. Tying our aims, methods and results into a story will keep the audience engaged. We understand that students are told this over and over, and sick of hearing this advice. The harsh reality is that you might think your project is awesome, but others probably do not. Thus, you need to make certain that the research is relatable. Start by providing context and significance as to why the research is being done. Follow up with a logical progression explaining why a particular method was used, or why the results led you to the next step of your research. Finally, always relate your findings back to your original aims and significance. This will allow your research to have a beginning, middle and end, providing closure or a well-anticipated sequel.

5. Keep practicing

Practice presenting the poster. The entire presentation should be kept under three minutes. Communicating key concepts of the research and a cohesive story is far more important at this level of science communication. If the audience are interested in our three-minute 'elevator pitch', they will ask questions.

SDS Page: Short Discussions for Students Page

Students at different stages of their postgraduate research will have varying proportions of content. For those who are starting out, it's okay to have more background. Set the scene for your story, describe why the research is exciting, identify the gap of knowledge you want to fill and explain how you want to do it. For those halfway through their research, focus on relating your results to your aims, noting what is still missing and what you will do to address this. For those who are almost done, your focus should be networking, building interest in your skills and getting your name out there. Really try to wrap up your research with a good story and try to explain how your work has advanced science within your field.

The poster assessors or examiners will look for presentation quality, but also look to see how well you understand your own research. They may try to differentiate students who have independent thoughts and ideas in driving their own project versus those who are just following orders from their supervisor. You simply need to know your project well and show that you understand it. Being able to answer questions and explain it as simple as possible will be greatly advantageous.

My PhD student, Andrea Nguyen (AKA five-time poster prize champ), and I have annotated recent poster presentations to highlight the techniques we have used. Hopefully, you'll find these trade secrets useful!

Dr Christopher Szeto is a postdoctoral researcher in the Department of Biochemistry and Chemistry, La Trobe Institute for Molecular Science, La Trobe University.

Andrea Nguyen is a PhD student in the Department of Biochemistry and Molecular Biology, Infection and Immunity Program, Biomedicine Discovery Institute, Monash University.

Tips and Tricks for Writing a Review Article

Ridam Kapoor

Department of Anatomy and Physiology, University of Melbourne

Writing a review article is a great way to gain a deep understanding of the work that has been published in your chosen research topic. This will allow you to learn about approaches used in the area, identify gaps in the literature and come up with ideas about what to do next. A well-written review can also form the basis for the introduction chapter of a thesis. The following is a list of points to keep in mind while writing a review article.

1. Choosing the topic

Choose a topic depending upon the length of the review article you want to write. If you want to write a short review, pick a narrower topic. But if you are going to write a long review article, choose a topic which is broad enough so that you will be able to find enough articles to discuss. Pick something you are interested in and that you have experience researching.

2. Check for the aims and scope of the journal

Before writing a review article, it is important to check the aims and scope of the journal. There are some journals that don't accept review articles, while some only accept invited reviews.

3. Don't write too long an article at first

Generally, journals have a specified word limit for review articles; therefore, make sure to check the word limit according to the journal to prevent frustration later.

4. Write an effective introduction

Writing a powerful and catchy introduction is something which will draw more readers. Start with some basic information regarding the topic and mention why writing a review article on this topic is valuable. Make it clear how your review is distinct from previously published reviews in that area and highlight the novelty of your review within the introduction.

5. Writing your title, abstract and keywords

Give thought in writing a strong title, abstract and keywords. This will definitely be helpful in increasing the visibility of your article online and making your article available to the right readers. Your title and abstract should be clear, concise, accurate and informative.

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6. Choosing and managing the citations

Most journals prefer to have the latest citations in a review article. You can include older references to describe general terms or methodologies, but they should not be kept to a minimum. I am aware of a journal which proposed to have less than 50% of the cited references to be older than five years. The best way to find this out is by going through the latest review articles of the journal you are interested in publishing. Managing so many references is also a huge task. Therefore, it is advisable to make use of reference manager software such as Endnote, Mendeley, Zotero and Paperpile, which can make this task easy.

7. Make sure to address a research gap

This is something that will contribute towards the novelty of your review article. One of the reasons review articles are written is to draw new conclusions from the existing data and help to extract prospective ideas for future studies.

8. Include a critical discussion

Make sure that your review article is not just a descriptive summary of the topic, instead it should demonstrate critical discussion. I personally had this experience where my article was rejected by the journal because it mainly was a compendium of the facts rather than a critical review of the literature. Apart from this, you can also mention contradictory studies in your area of research, which includes an element of debate and presents both sides of the argument.

9. Think about figure inclusion

Another important inclusion for a review article are figures – “a picture is worth a thousand words”! It will not only increase the chance of your article being accepted but will also help the readers to understand the topic and give them clear perspective of your ideas. You can use graphic software such as BioRender, Adobe Photoshop and Adobe Illustrator to make clear and detailed figures.

10. Writing a conclusion

Write a brief conclusion including possible future research on the topic. Your focus should be on communicating what has been discovered in the research topic, what still remains unknown and why the research needs to be continued.

11. Checking for errors

Feedback is vital to writing a good review. It should be sought from not only your supervisor and authors in the paper, but also lab mates, colleagues and friends (even outside of science).

Ridam Kapoor is a PhD student at the Department of Anatomy and Physiology, University of Melbourne.

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Off the Beaten Track

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

From Measuring Specificity to Examining Biodiversity

Rachael Impey, Lab Manager, EnviroDNA

My university pathway could be considered linear, in that I graduated with a Bachelor of Biomedicine at La Trobe University immediately before completing my Honours degree and PhD with Dr Tatiana Soares da Costa at the La Trobe Institute for Molecular Science. During my PhD, I worked on the characterisation of several essential proteins in antibiotic-resistant bacteria, an area I was incredibly passionate about. The focus of my research meant I was awarded two competitive travel grants to the UK. These allowed me to work with our collaborators at Public Health England. These trips were instrumental in allowing me to create a genetic knockout of the genes encoding the proteins of the DAP pathway, the focus of my thesis. Our research was successful and I published four first-author publications during this period. However, nearing the end of my PhD, I concluded that academia was not my end-goal. Moreover, while I loved lab work, I had no driving desire to seek funding and have the pressure of my career rely on successful grant outcomes.

Fast-forward to May 2020, amid a pandemic and writing up my thesis, a close friend asked if I was interested in casual work at EnviroDNA processing several large projects. EnviroDNA is a small biotech company that evaluates biodiversity using environmental DNA (eDNA). In any given week, I can process over 1,000 samples looking for a specific species, such as platypus, or as a general biodiversity assessment utilising next-generation sequencing. Our work can trigger habitat regeneration efforts or halt multicorporation developments that threaten the environment. One of our biggest accomplishments was getting platypus listed on the threatened species list in Victoria in January 2021. This led to the creation of the Great Australian Platypus search which aims to map platypus distribution across Australia, while also measuring the vertebrate biodiversity of our waterways. This study will be the first eDNA project of this scale and will provide incredible ecological data on Australian wildlife.

The last two years with EnviroDNA have allowed significant professional growth as my casual role became a full-time maternity leave cover, which in turn as the company grew, allowed me to progress to my current role as molecular biology lab manager. What started as a position where I was the only wet lab-based employee has now turned into a managerial role, where I lead a team of three permanent and several casual staff. I manage the day-to-day operations of the lab, including organising and structuring project experiments, researching and developing our protocols and reporting outcomes to our project managers.

Rachael Impey

During my PhD, I was proficient in protein chemistry, microbiology and genetic recombination of bacteria. At EnviroDNA, my role involves a different genetics-based skill set centred around eDNA purification, qPCR, PCR and metabarcoding sequencing library preparation. While these techniques don't appear directly transferable, it wasn't the specific experiments that I performed during my PhD that helped me progress in this field but learning how to study science in general. Utilising and implementing information and methods from publications, strict organisation and sterile handling of samples in a lab setting and finally, the understanding of proper experimental controls, are what have helped me most in my current role. Furthermore, data analysis, learning to sort and easily navigate large datasets as well as succinctly present outcomes are invaluable skills no matter the area of work.

One difference I have found between academia and industry is the style of work and the structure of deadlines. When I moved to industry, the presence and importance of client deadlines were novel to me. In the beginning, I had the mindset that every project had to be completed the moment it arrived, though as our company grew, I

had to learn to structure, plan and implement project schedules whilst giving realistic expectations to clients for delivery. This was in stark contrast to my PhD in which my work was my own, and if something fell behind, I was the only one impacted. To overcome this change, I began using project management software within our team and relied on the experience of the senior staff members, but this is still a work in progress.

My advice for anyone who desires to change fields is that the importance of a network within science and industry cannot be understated. In our company, many staff members have been recruited through personal or professional connections with existing staff members, which is what happened to me. I attended conference networking events and connected with vendors and industry representatives, whilst also taking advantage of any programs offered by my university to link with industry professionals. One such program was IMNIS (Industry Mentoring Network In STEM), where PhD students are matched with a successful industry mentor. My mentor was biotech CEO, Kathy Harrison, who herself had gone through multiple career changes. She spoke of the importance of soft skills but also taught me how to sell myself to each role specifically. She was able to introduce me to some of her industry connections, which further expanded my network. In the end, while it was a personal connection that led me to my current role, this network has still increased collaboration and increased the opportunities I have been offered while working here.

In the last quarter of 2022, and just in time for the next round of funding applications, the Canberra Protein Group will organise a series of Australian Biochemistry lunch seminars under the banner 'Making Futures' to promote YOU, our outstanding field of early- and mid-career fellowship applicants in biochemistry and molecular biology. The seminar series aims to spotlight you, act as an amplifier to promote your work and make you known more widely in the Australian biochemistry community. With the help of our supportive biochemistry community, we are determined to set up our next generation biochemists for success.

We invite self-nominations to participate in the program, and encourage nominations from a diverse group of scientists. To self-nominate, please send a title and short abstract (under 500 words) to t.huber@anu.edu.au before Wednesday 31 August 2022.

Canberra Protein Group: an ASBMB Special Interest Group

The Canberra Protein Group (CPG) was established in June 2017 and has since been recognised as a Special Interest Group (SIG) of the ASBMB. The goal of the CPG is to promote research in all areas of protein science across the ACT, and to provide a platform for discussion between researchers and facilitate the establishment of new collaborations and networking opportunities. In particular, the CPG has a focus on providing opportunities for early- to mid-career researchers (EMCRs) and graduate students to communicate their research.

Since 2017, the CPG was holding regular monthly meetings with attendances of over 50 researchers, and saw three short talks from researchers, an announcements section and an open discussion session at the end. Unfortunately, COVID and shutdown periods (both at the university and state level) saw a reduction in our capacity to function. One highlight from this time was the competition for designing the CPG logo, and we would like to congratulate Joe Kaczmarski, who had the winning design! After a short hiatus, we are back to running a dual-format (online and in-person) monthly meeting with a total of approximately 180 members on our mailing list, and after the establishment of our new CPG Executive Committee for 2022, we are looking to see our community return to its previous form.

One of the major changes for 2022 has been Simon Williams (co-founder of the CPG along with Matt Johnson) stepping down as the Chairperson, and we thank him for his contributions to the protein community in ACT. Megan Outram has been elected as Chairperson, and Sacha Pulsford and Stephen Fairweather have been welcomed onto the Committee. Rebecca Frkic, Matt Mortimer and Xiaoxiao Zhang have continued their contribution to the Committee. We started off the year strong with great talks from a new ANU group leader, Kai Chan, and Honours student Nick East. We have an exciting line up for the next few months, including speakers from the ANU Mass Spectrophotometry facility and Centre for Advanced Microscopy.

Carl McCombe.

We recently held the annual CPG Symposium. Three PhD students, Sacha Pulsford, Cassidy Whitefield and Carl McCombe, were selected to present their research, with the best talk awardee having the opportunity to represent the CPG with a SIG talk at ComBio2022. An independent panel of six judges had the difficult task of selecting the awardee. Carl, whose work focuses on fungal nudix hydrolases, was judged to be the winner and was also the People's Choice Winner.

We would love to have more Canberra-based protein researchers join us. For more information, visit our website: canberraproteingroup.wordpress.com and join our mailing list. Follow us on Twitter: @CanberraProteinGroup.

Megan Outram
Chairperson
Canberra Protein Group
Email megan.outram@csiro.au

CPG Symposium participants.

Back to Basics – Revisiting Fundamental Patent Concepts

In this issue, Sheila Barbero from FPA Patent Attorneys discusses patent fundamentals, including the structure of patent specifications, the typical patent timeline, the rights conferred by a granted patent, and the effect of self-disclosures on obtaining future patent protection.

Sheila Barbero

IP and patents are niche topics. Before becoming a patent attorney, I didn't truly know what a patent attorney really did, or even what a patent really was! Soon after joining the profession, I quickly became aware of many key patent concepts that would have helped me better understand patents when I was a researcher.

In this article, I am taking a step back and revisiting some patent fundamentals. For readers less familiar with IP and patents, this article may give you insights into key patent concepts and make patents more accessible. For regular readers of this series, this article may be a useful refresher and help you get more out of your dealings with patents.

We discuss below the various parts of a patent specification, the typical process for obtaining a granted patent, and the rights conferred by a granted patent. I also discuss how self-disclosures can affect your ability to obtain patent protection.

How to navigate a patent specification

As a researcher, you may have had experiences where you were exposed to patent documents (patent specifications). For example, you might have come across patent specifications that are referenced in scientific articles or cited as 'prior art' for a patent application. Or you might have worked together with a patent attorney to draft a patent specification for a new invention relating to your research.

Patent specifications relating to life science technologies can be long and complex – if you have not had much experience with them, they can appear somewhat daunting. Understanding the structure of patent specifications can help make them easier to navigate, which is discussed below.

Broadly speaking, patent specifications should fully describe an invention such that a worker of ordinary technical skill can reproduce the invention. It should also clearly define the invention in the claims. A typical patent specification can be broken down into the following parts, appearing in order:

Field: A general statement setting out the field the invention relates to.

Background: Akin to the introduction of a scientific article, the background sets the scene for the invention. The background usually describes the current state of the field and the problems in the field that the invention aims to address. A discussion of the invention is not included here – that's dealt with in the sections below.

Summary: The summary usually includes statements of invention that generally correspond to the claims. The summary can also include statements of technical advantages and/or benefits that can be provided by the invention.

Brief description of the drawings (optional): Similar to figure legends in scientific papers, this section lists any drawings (figures) that are included in the patent specification and an explanation of what is shown in each.

Detailed description: The detailed description usually includes details about specific embodiments of the invention. This section is often the longest part of patent specifications relating to life science technologies. The embodiments discussed in this section should fall within the scope set out in the summary and claims.

This section can be a particularly useful part of the patent specification to go to when you are seeking to understand the invention or extract information that is in a published patent specification. It may include a definition section, which can be helpful for understanding what certain phrases mean in the context of that patent specification. The detailed description will also typically include an examples section, which can be similar to the experimental, results and discussion sections of scientific articles.

Claims: This is the legal part of the patent specification. The claims define the scope of what the patent applicant is claiming as their patent monopoly. Before grant, it defines the monopoly being sought, whereas after grant, it defines the actual monopoly conferred to the patentee. During examination, the claims may be amended to overcome objections that arise, so it is not unusual for the claims of a granted patent to be of different scope – they are usually less broad.

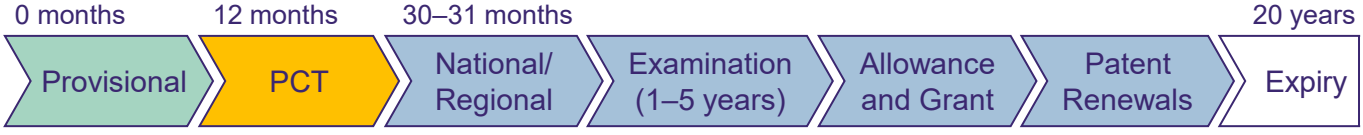

Fig. 1. *A typical patent timeline from the filing of a first provisional application to expiry of a granted patent.*

Back to Basics – Revisiting Fundamental Patent Concepts

Drawings (optional): Drawings (figures) can be included to support what is described in the patent specification. In patent specifications relating to life science technologies, the drawings usually include the types of figures you might see in a scientific article, such as graphs and images relating to experimental results and also schematics and diagrams that can help explain the invention.

Sequence listings (optional): List of amino acid and nucleotide sequences of peptides/proteins and genetic material referred to in the patent specification.

By understanding their structure, you can more easily navigate patent specifications and focus on the details you are interested in.

Getting a granted patent might take longer than you think

Obtaining grant of a patent application is an important milestone, not least because it provides official recognition that the claimed invention is patentable, but also because patent applications are only enforceable once they are granted.

An example of a typical patent timeline is shown in the figure. In brief, the path to grant usually involves the following steps:

- *At 0 months: Filing a provisional application.*
- *Within 12 months: Filing a Patent Cooperation Treaty (PCT) application at the World Intellectual Patent Office (WIPO).*
- *Within 30–31 months: Filing national and regional phase applications in each jurisdiction you wish to obtain patent protection.*
- *Examination of patent applications: Each patent application will be examined by the patent office in the jurisdiction it is filed. Timing depends on jurisdiction and complexity of examination and usually takes between one to five years.*

Once a patent application has successfully progressed through examination, it will be allowed and, in most cases, subsequently granted. The granted patent can then be maintained (kept in force) by paying regular patent renewal fees. Patents usually expire after twenty years from the filing date of the PCT application, though this can be longer for certain pharmaceutical inventions.

The path to obtaining grant involves several steps – as can be seen from the figure, it is not unusual for the process to take more than five years from the date the initial provisional application was filed! Of course, there are also alternative approaches, including options to streamline patent filings and accelerate examination. Ideally, the approach taken should align with the patent applicant's commercial goals.

A granted patent does not automatically give you 'freedom to operate'

What rights does a granted patent provide to the patent holder?

Having a granted patent gives patent holders the 'right to exclude' others from practicing (e.g. making, using or selling) the invention claimed in the patent without their permission. These rights are restricted to the jurisdiction in which the patent has been granted and for the duration of the patent term.

However, a granted patent does not give patent holders automatic right to practice their claimed invention.

If the invention is covered by a granted patent held by another party (who have the same exclusive rights for their invention), then practicing the invention may infringe the other party's granted patent. In other words, the patent holder may not have freedom to operate.

As an example, you might have developed and obtained patent protection for a new medical device, but that medical device incorporates technology that is covered by another party's granted patents. Therefore, there is a risk that the other party's granted patents could block you from manufacturing, distributing or selling your product in countries where the other party has patent protection.

In view of these risks, freedom to operate is an important consideration when seeking to commercialise a new product. If a potential issue is identified, that does not necessarily mean the end of the road – there are options available which may help resolve the issue. For a deeper dive into freedom to operate considerations, see the August 2021 article.

Beware of (accidentally) self-disclosing your invention

Academic research involves not only knowledge generation, but also knowledge sharing. This can be in the form of publishing articles, presenting research at conferences, and working collaboratively with other research groups.

When conducting research which may lead to an invention, and where patent protection for that invention is desirable, be aware that knowledge sharing can result in disclosures that may block you from obtaining future patent protection. This is because in order to obtain a granted patent, the invention claimed in a patent application must be novel (new) and inventive over the 'prior art', which broadly speaking includes any information that has been publicly disclosed anywhere in the world before a patent application is filed. Any non-confidential disclosure can become prior art, even disclosures by the inventors themselves (self-disclosures).

In a knowledge-sharing environment, self-disclosures

Back to Basics – Revisiting Fundamental Patent Concepts

can be made unintentionally or without knowing the consequences. Therefore, it is important to be aware of what information you are sharing, to avoid precluding a later opportunity to obtain patent protection.

Ideally, a patent application should be filed before the invention is publicly disclosed. If a self-disclosure has been made, and is found to be problematic, it may possible to get around the disclosure by filing a patent application within the 'grace period' (usually six to twelve months) from the disclosure in certain jurisdictions. However, it should be kept in mind that some important jurisdictions, notably Europe, do not provide a grace period.

For some examples of less obvious self-disclosures and tips for avoiding these, see our the April 2022 article.

Take home messages

- Understanding the structure of patent specifications can make them easier to navigate.
- Obtaining a granted patent involves several steps and can take more than four to five years.
- Having a granted patent provides a 'right to exclude', and does not provide automatic freedom to operate.
- Be aware of self-disclosures that can potentially block you from obtaining patent protection for your invention.

sheila.barbero@fpapatents.com

ASBMB Member Elected Fellow of the Australian Academy of Science

On 26 May 2022, the Australian Academy of Science announced the election of 22 new Fellows for their outstanding contributions to science, including ASBMB member, Professor Michelle Haber.

Michelle Haber AM FAA FAHMS

Professor Michelle Haber AM FAA FAHMS is a world-renowned authority in the field of childhood cancer research. She tackles research translation with verve, with therapeutics that have directly arisen from her research entering the clinic. With her building of the Children's Cancer Institute, Sydney, into the premier childhood cancer research institution in the country, and her leadership of the national Zero Childhood Cancer Personalised Medicine Program, Haber is recognised as a key leader of health and medical research in Australia.

Despite improved treatment outcomes, cancer kills three Australian children every week – more than any other disease – and most survivors have extensive later health problems. Professor Haber's research has led to major advances in basic cell and molecular biology, in defining clinically relevant molecular targets and prognostic indicators for neuroblastoma – the most common cancer diagnosed in children under one year old – and to insights into disease pathogenesis, new clinical approaches and development of potential therapeutics. She is regarded as an international leader in neuroblastoma biology and therapy, with over 13,300 citations in peer-reviewed scientific journals, as exemplified by her invited *Nature Reviews Cancer* (2010) article on the role of ABC transporters in drug resistance and tumour cell biology (with over 1,000 citations). Moreover, Haber's research with colleagues Norris and Marshall, using molecular genetic techniques to improve the diagnosis and treatment of children with cancer – including acute lymphoblastic leukaemia, the commonest childhood malignancy – has had a major impact on healthcare practice.

ASBMB Member Elected Fellow of the Royal Society

On 10 May 2022, the Royal Society announced the election of 62 new Fellows for their outstanding contributions to science, including ASBMB member, Professor Jamie Rossjohn.

Professor Jamie Rossjohn from the Biomedicine Discovery Institute, Faculty of Medicine, Monash University, is principally known for his contributions to the understanding of disease and the vertebrate host response, both from the aspect of protective and deleterious immunity. Namely, he has used structural biology to understand how T cell receptors recognise peptides, lipids and metabolites. Specifically, he has unearthed structural mechanisms of major histocompatibility complex (MHC) polymorphism impacting on viral immunity, drug and food hypersensitivities and T cell mediated autoimmunity. Rossjohn has pioneered our molecular understanding of how T cells bind lipid-based antigens presented by the CD1 family. He has elucidated the structural basis of how vitamin B metabolites are presented by the MHC class I related protein, MR1; this revealed an entirely new class of antigen for T cells. Rossjohn has published over 460 papers and mentored numerous researchers towards obtaining higher degrees and nationally competitive fellowships.

Since 2018, Rossjohn has developed scientific outreach activities that embrace those in the community that are disadvantaged and has initiated the Monash Sensory Science program (with the assistance of legally blind artist-in-residence, Dr Tandori). This program includes holding multisensory/multimodal scientific exhibitions for the blind and low vision community and a disability internship program in his lab.

Rossjohn has held a number of full-time research-only appointments, including Australian Research Council (ARC) and National Health and Medical Research Council (NHMRC) Fellowships, an NHMRC Investigator Award (2022), ARC Laureate Fellowship (2016), NHMRC Australia Fellowship (2011) and ARC Federation Fellowship (2006). He is a Fellow of the Australian Academy of Science (2014), Academy of Medical Sciences (UK and Australia, 2017), Learned Society of Wales (2015) and the Royal Society (2022).

Jamie Rossjohn
FAA FAHMS FLSW FMedSci FRS

His research leadership has been recognised by the 2003 ASBMB Roche Medal, 2004 Science Minister's Prize for Life Scientist of the Year, 2007 Australian Academy of Science Gottschalk Medal, 2007 Commonwealth Health Ministers Award for Excellence in Health and Medical Research, 2013 Eureka Prize for Scientific Research (jointly with Dr Kjer-Nielsen and Professor McCluskey), 2017 Federation of Asian and Oceanian Biochemists and Molecular Biologists (FAOBMB) Award for Research Excellence, 2018 ASBMB Lemberg Medal and 2018 Royal Society of Victoria Research Excellence in Biomedical and Health Sciences (joint winner with Professor Burkitt). He is a Highly Cited Researcher (Clarivates/Web of Science, 2018–2021).

Australian Society for Biochemistry and Molecular Biology Inc
PUBLICATION SCHEDULE FOR *AUSTRALIAN BIOCHEMIST*, volume 53, 2022

Issue	ASBMB Content	Copy Deadline	Issue Date
April 2022 53(1)	Profiles of medal, award and fellowship winners Nominations for Executive/Council	Monday 7 February	Monday 4 April
August 2022 53(2)	Nominations for medals, awards and fellowships Notice of AGM/proposed constitutional changes	Monday 6 June	Monday 1 August
December 2022 53(3)	Annual reports ComBio2022 report	Monday 3 October	Monday 5 December

FAOBMB Education Award 2022

The ASBMB congratulates Associate Professor Nirma Samarawickrema on being named the winner of the FAOBMB Education Award 2022. She will present at the 29th FAOBMB and 2022 CSBMB Conference to be held in China in October.

Nirma is a member of academic staff at Monash University. She completed her Bachelor of Science and Master of Science at the Australian National University and her PhD in Molecular Parasitology and Biochemistry at the University of Queensland.

She has extensive experience teaching Biochemistry to undergraduates both in Sri Lanka and Australia. Her students have varied capabilities, expectations and come from diverse backgrounds all transitioning to university. She is a skilful educator whose practice has focussed on diversity and large classes. She astutely applies transition pedagogy in her teaching and supports and mediates the learning experience of her students through a curriculum that ensures engagement. She leads curriculum design teams to ensure that teaching approaches, assessments, and learning pathways are strongly student-centred.

At Monash University, Nirma teaches Biochemistry to students enrolled in a range of courses, including Bachelor of Medical Science and Doctor of Medicine, Bachelor of Biomedical Science, Bachelor of Science, and Bachelor of Nutritional Science. She has successfully adapted her teaching to accommodate large classes of over 600 students. Her curriculum designs and teaching practices focus on building partnerships among students transitioning to university. She purposefully involves students in co-teaching, peer-assessing, peer-reviewing and co-creating learning resources; in all this she deliberately fosters learner agency. Nirma has also implemented efficient and innovative assessment approaches, such as peer partnerships in assessments. Her learning activities and assessments are designed to encourage critical thinking, teamwork and collaboration, and metacognitive and evaluative judgement. Through building these skills and helping students to make career connections early in their first year, she supports her students to succeed as they continue their university studies. In addition, Nirma teaches and assesses students using case studies, making conceptually difficult information contextualised and, therefore, more accessible and engaging. Nirma also actively mentors early-career academics and fosters their teaching practice.

Nirma Samarawickrema

Nirma's teaching-intensive role drives her research and scholarship, which is focussed on pedagogical investigations to improve student learning. She has skilfully used her disciplinary research on human papillomavirus and cervical cancer to enrich her classroom curricula and to inspire her students. She has thereby demonstrated the strong nexus between her teaching and her research. Her recent research has been on peer assessment and the benefits of peer partnerships in assessments. This research identified the need to design assessment tasks that build graduate attributes – the critical skills students must develop while at university. Her research in case-based learning has demonstrated that the approach promotes deep learning and engagement. Since Nirma's research is focused on her practice, the findings have always fed back into improving her teaching.

Nirma is Co-Director of Education in Biochemistry and Molecular Biology, Monash University, and Chair of the ASBMB Education Special Interest Group. Nirma is also a member of the Editorial Committee of the *Australian Biochemist*. In recognition of her extensive contribution to teaching, learning and scholarship, she was made a Fellow of the Monash Education Academy in 2017. Her contributions to learning and teaching were further acknowledged when she was made a Fellow of the Higher Education Research and Development Society of Australasia in 2019, and awarded the 2020 ASBMB Education Award.

BioMolecular Horizons 2024:

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26th IUBMB Congress

19th ComBio Conference

17th FAOBMB Congress

22-26 September 2024

Melbourne
Australia

For information please email

iubmb2024@wsm.com.au

ASBMB Awards 2023

SOCIETY MEDALS, AWARDS AND FELLOWSHIPS NOW OPEN

Nomination or application forms for all 2023 Medals, Awards and Fellowships can be obtained from the ASBMB website: https://www.asbmb.org.au/awards/nominations/

Nominations or applications must be submitted no later than **31 October 2022**. Nominations or applications must be emailed to the Secretary of the Society: secretary@asbmb.org.au Please note that hard copies are not required.

There are membership requirements for all nominations/applications. These are outlined on the nomination forms available from the ASBMB website. Contact the ASBMB Secretary with any queries.

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 2023

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.*

Election of Council 2023

Nominations are called for the following positions on the Council of the Australian Society for Biochemistry and Molecular Biology Inc for 2023: Secretary, Treasurer, Editor, Education Representative, FAOBMB Representative, Secretary for Sustaining Members and State Representatives.

The ASBMB Council for the period 1 January 2022 to 31 December 2022 is composed of the following members:	President	J Matthews
	President Elect	R Hannan
	Secretary	D Ng #
	Treasurer	M Kvansakul §
	Editor	T Soares da Costa #
	Education Representative	N Samarawickrema §
	FAOBMB Representative	T Piva §
	Secretary for Sustaining Members	S Jay §
Representatives for:	ACT	C Spry #
	NSW	L Sharpe #
	Vic	L Osellame #
	Qld	M Landsberg #
	SA	M Pitman §
	Tas	I Azimi #
	WA	A Van Dreumel #

Eligible for re-election
§ Position open

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

NOMINATIONS MUST REACH THE SECRETARY BY 5PM 15 SEPTEMBER 2022
(14 DAYS BEFORE THE ANNUAL GENERAL MEETING TO BE HELD ON 29 SEPTEMBER 2022).

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

The 66th Annual General Meeting of the Australian Society for Biochemistry and Molecular Biology Inc. will be held will be held on Thursday 29 September 2022 at 1810 hours Australian Eastern Standard Time. The meeting will be conducted within the Melbourne Convention Centre (room to be determined).

AGENDA

1. Apologies
2. Confirmation of the Minutes of Annual General Meeting No. 65
3. President's Report
4. Treasurer's Report
5. Fees for 2023
6. Elections to Council
7. ASBMB Awards 2023
8. Amendments to Constitution and By-laws
9. Any Other Business

Dominic Ng
Secretary, ASBMB

Our Sustaining Members

ASBMB welcomes the following new Sustaining Members:

Bio Molecular Systems
Biora by MineARC
Bio-Rad Laboratories
Bioneer Pacific
Corning Life Sciences, China
Integrated DNA Technologies
Interpath Services
Klein Scientific
Labwit Scientific
Leica Microsystems
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Mimotopes
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Rowe Scientific
Sapphire Bioscience
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United BioResearch Products

Diagnostic TECHNOLOGY

The iCatcher 12 is an automated nucleic acid purification system using a novel membrane column extraction method which allows for optimised kits targeting rare nucleic acids normally not purified in detectable quantities on automated platforms like circulating free DNA (cfDNA).

Key benefits this platform allows:

- Input volumes of up to 4000µl to eluate out only 30ul of your purified sample.
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This automated platform can lyse, bind, wash dry and elute using a broad range of kits targeting different sample types.

If you have any questions regarding the technology, please contact us at info@diagnostictechnology.com.au for more information.

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Hamilton Robotics offers a wide range of liquid handling workstations and laboratory automation solutions and is now regarded as one of the world's leaders in manufacture and supply of Automated Liquid Handling Solutions.

Key to the products is their air displacement pipetting and monitoring technology as well as the software controlling their systems. With a belief that every laboratory automation project is unique, their workstations and software serve as a high precision and flexible base upon which to provide automated solutions.

Sample traceability is enabled by barcode scanning options, combined with the ability to verify sample transfers with a traceable, digital-audit trail, providing sample tracking and chain-of-custody processing for your assays.

The automated Liquid handler workstations provide consistent results for assays, ranging from low-throughput pipetting protocols to high-throughput systems with integrated sample storage. A wide range of systems are available based on functionality, capacity and budgets such as the the ML Prep, Nimbus range and STARline instruments respectively, as well as the Vantage for maximum integration and walk away times.

For more information, please contact **Bio-Strategy**
T: 1800 008 453
E: info@bio-strategy.com
www.bio-strategy.com

Disclaimer

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AXT

Apricot S1/S3 Automated Pipettors

Are you looking to make the move to automated pipetting or simply fed up with the tedium and time required for manual pipetting? Great news, the apricot S1 and S3 are the perfect solution for anyone looking to take their first step towards automation, offering flexibility, versatility and affordability.

These systems offer high-performance pipetting and cater for high and low throughput applications and will also increase your output, compared to manual pipettes. The simple and intuitive interface allows you to fully program all aspects of the system offering repeatability and traceability.

To ensure optimal liquid delivery, the apricot series liquid handlers have easily interchangeable pipette cores. With volumes up 1000µL and accuracies down to 0.1µL there is sure to be a core to suit your application.

Both systems are also very compact and will easily fit on a bench in even the smallest lab. They also only require a standard power outlet.

Why waste time filling 96 and 384 well plates by hand? Free yourself up for more important tasks like designing new experiments or analysing data while at the same time eliminating the possibility of human error.

For more details visit axt.com.au/apricot or email info@axt.com.au.

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Evolution or Revolution? Introducing the Award-winning ORCA®-Quest qCMOS Camera

Since the 1980s, Hamamatsu Photonics developed high-sensitivity, low-noise cameras using its unique camera design technology… strongly contributing to the development of cutting-edge scientific and technological research.

From Hamamatsu Photonics and SDR Scientific, we are proud to release the ORCA-Quest: the world's first camera to incorporate the qCMOS image sensor and to be able to resolve the number of photoelectrons using newly-developed, dedicated technology.

The ORCA-Quest offers you the following:

- Low readout Noise: 0.27 electrons rms (Ultra-quiet scan)
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- Impressive Pixel Size: 4.6 x 4.6um
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This camera achieves the ultimate in quantitative imaging, and has been awarded accordingly:

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- ORCA-Quest Camera wins the Innovation Award 2022, Biophotonics & Medical Engineering Category

Evolution or revolution... we'll let you decide!

SDR Scientific is proud to represent Hamamatsu in Australia/New Zealand. Discover the ORCA-Quest or other members of the Hamamatsu imaging family by reaching out to your friendly SDR Scientific Technical Sales and Support Specialist on 02 9882 2882 or by clicking Here.

MP Biomedicals™

MP Biomedicals is dedicated to giving scientists and researchers innovative, quality tools and superior service to aid them in their quest for ground-breaking discovery.

MP Biomedicals offers a comprehensive line of life science, fine chemical, and diagnostic products. Some of our product offerings include FastPrep-24™ 5G bead beating grinder and lysis system, MPure-32 automated magnetic bead-based nucleic acid extraction system and a wide range of high-performance purification kits.

MP Biomedicals has recently introduced a fully automated magnetic bead-based nucleic acid extraction system – MPure-32™ aNAP System. MPure-32™ aNAP System can be used to support sample preparation for scientific research.

MPure-32™ aNAP System can process up to 32 samples simultaneously within a short period of time (around 40 to 60 minutes). Besides its capability to extract nucleic acid with high purity and yield, MPure-32™ aNAP System is easy to use; this eliminates the risk of human error and cross-contamination.

MPure-32™Automated Nucleic Acid Extraction Platform gives you:

- Superior Purity and Yield
- High Flexibility (Open to Customization)
- Simple Workflow
- Fast and Consistent Results

MP Biomedicals also offers a range of reagent kits for various types of biological samples. MPure-32™aNAP System is intended to be used in combination with MP Biomedicals' DNA/RNA extraction kits to extract the DNA/RNA from clinical/non-clinical specimens. Users have the flexibility to self-assemble the reagents with the relevant consumables for maximum cost-effectiveness or purchase the pre-assembled reagent kits for greater convenience.

Contact us to discuss your research requirements and learn more about our newest products.

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NanoAssemblr Accelerates Nanomedicine Production

Genomic nanomedicines represent the next era in drug innovation with improved performance, reduced side effects and personalised medicine for otherwise “undruggable” targets. Consisting of small molecules or nucleic acids packaged into lipids and polymers designed to protect the cargo, they enhance solubility and control distribution for targeted release. The success the Moderna and BioNTech/Pfizer COVID-19 mRNA vaccines has driven the acceleration of this disease-agnostic platform to be adapted to produce a wide range of RNA-based treatments beyond infectious diseases to include gene and cell therapy.

Traditional methods used to develop genomic medicines can present several challenges. Ingredients can be costly or in limited supply while the final product can lack consistency, have low throughput, be a slow and laborious process and difficult to scale. **The NanoAssemblr platform from Precision Nanosystems** is enabling drug innovators to overcome these and many other challenges by making highly scalable instrument platforms and LNP reagents to support all stages from concept (Spark: 25–250μL) to clinic (Ignite: 1–20mL, Blaze:10mL–10L) through to commercial manufacture (GMP:>20L/h).

The proprietary NxGen microfluidic mixer at the heart of NanoAssemblr systems is the only technology that can scale from mL/min to L/h with the same mixer design. It uses precisely controlled mixing to generate highly reproducible polymer nanoparticles, liposomes and nucleic acid lipid nanoparticles (LNPs) particles – every time.

For more information or to arrange a demo, contact us:

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We know that in recent years, academic workloads have increased and time is scarce. When surveying our community, 86% of respondents identified staff workload as a current challenge.

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The Flexdrop iQ Non-contact Dispenser provides rapid, precise, and flexible dispensing from up to 96-source wells into 96, 384 or 1536 well plates with a dead volume of 1 µL. Generating individual droplets between 8 to 50 nanoliters (nL) in size at 100 droplets per minute, researchers can quickly automate their low volume dispensing workflows with ease. The FlexDrop iQ uses positive pressure and droplet verification to achieve highly reliable and accurate liquid transfers.

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BioNovus LIFE SCIENCES

Human Coronavirus Antigens

The Native Antigen Company develops and manufactures premium quality recombinant antigens and antibodies as well as offering a range of services for the diagnostic and biopharmaceutical industries.

Native Antigen's proprietary VirtuE™ mammalian expression system has been developed for the purpose of producing native-like proteins, which are being widely adopted by leading in vitro diagnostic, vaccine and academic groups in cutting-edge R&D, where correct folding and glycosylation are vital. Our contract services range from antibody generation, to scale production of recombinant and native antigens, bespoke assay development and QC.

Human Coronavirus

There are six different coronaviruses which can infect humans and cause illness. These comprise the four common coronaviruses; 229E and NL63 (alpha coronaviruses), OC43 and HKU1 (beta coronaviruses), and two other coronaviruses, MERS-CoV and SARS-CoV, both of which can cause severe illness and remain a significant public health concern.

Following the declaration of SARS-CoV-2 pandemic by the WHO in March 2020, Native Antigen has rapidly expanded the range of SARS-CoV-2 recombinant antigens and antibodies. To support the investigation of SARS-CoV-2 variants, The Native Antigen Company offers a growing range of mutant Spike antigens. Expressed proprietary the VirtuE™ mammalian expression system, these antigens display full glycosylation and proper folding for use in the development of high-performance assays and other applications.

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Now, anyone can produce high-quality, reproducible NGS libraries with >99% mean success rate* at just a touch of a button.

The MagicPrep™ NGS system combines robust technology with cartridge-based reagents and consumables for unprecedented ease of use. Anyone can start a run in less than 10 minutes after approximately 30 minutes of training. Eliminating the need for mixing or aliquoting numerous reagents, MagicPrep™ NGS offers consistent, reproducible results minimising the possibility of user errors. With no other user interactions required, start a run whenever you are ready and continue with your day.

Tecan's MagicPrep™ NGS system offers many benefits and features:

- >99% mean success rate*. Confidently generate NGS libraries with push button ease. The pre-aliquoted reagents, pre-optimised scripts, and robust automation provide a reliable solution for library preparation with minimal errors.
- Set up a run in 10 minutes. Spending hours or days on manual pipetting is over.
- No installation. No scripting. No master mixes. Eliminate costly mistakes during library preparation with optimized reagents, consumables and simple setup for error-proof operation and consistent data. Anyone can do it!

Learn more at tecan.com/magicprep-ngs or book a remote demo at tecan.com/magic

* *Success rate is based on mean internal data. Sample quality and variability may have an impact on the success rate.*

CapellaScience

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The Elite features a touchscreen user interface which allows users to easily monitor and control homogenisation preferences and is customisable with programmable protocol settings for speed, power, time, number of runs, and dwell time. The Elite's 8-gigabyte memory allows users to store over 100 protocol settings and includes a 'quick-run' feature and tutorial.

Specifically designed for laboratories that require high throughput sample disruption, the Elite's optimised tube motion, with speeds up to 8 meters/second, results in rapid and efficient sample disruption. Unrivaled in versatility, the Elite is compatible with the widest range of accessories, including an array of interchangeable tube carriages capable of processing sample volumes from 250µL to 50mL. Up to 24 x 2mL samples can be processed simultaneously.

The BR Elite is equipped with a sealed processing chamber, lid safety interlock, and a convenient front-loading design. An optional Cryo cooling unit is available for processing heat-sensitive samples.

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

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Our Diagnostics & Scientific Group is backed by Paragon Care's commitment to deliver optimal outcomes, now and into the future. Three leading innovators in this space, LabGear Australia, Immuno and Immulab have joined forces to deliver an integrated solution for your diagnostic and scientific laboratory requirements. Our hands-on Australian based team are with you all the way.

LabGear Australia represent names that you know and quality brands that you trust. Providing access to a range of quality laboratory essential equipment and consumables, we are far more than a reseller. We are your distribution partner, dedicated to the supply and technical support of reliable solutions locally.

Able to offer a range of Ultra-Low Temperature storage options, large laboratory equipment for centrifugation, sterilisation, vacuum concentration and more, we also have your smaller benchtop equipment and consumable needs covered.

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Visit www.bmglabtech.com to view detailed specifications.

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A warm welcome is extended to the following new members who joined ASBMB from 1 July 2021 to 30 June 2022

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ComBio 2022 MELBOURNE

Melbourne Convention and Exhibition Centre

South Wharf, MELBOURNE 27 - 30 September 2022

We extend a warm invitation to you to be part of ComBio2022 to be held at the Melbourne Convention and Exhibition Centre (MCEC). After a long pause in our plans, we anticipate that this will be a vibrant return to face-to-face scientific exchange with our colleagues.* ComBio2022 will be held in a spectacular arm of MCEC that is adjacent to the Yarra River and walking distance from numerous restaurants and cafes serving the widest imaginable variety of food. Melbourne is home to many sporting and cultural events and world class museums and galleries plus an aquarium are in the immediate vicinity. There is also an abundance of budget priced accommodation within walking distance of MCEC. ComBio in Melbourne in the Spring of 2022 should be a 'must' for all. (*Covid-safe protocols will be in place as advised closer to the date)

We are pleased to announce that the Opening Keynote Plenary Lecturer is Nobel Laureate Jennifer Doudna and the ASBMB Grimwade Keynote Plenary Lecturer is Cynthia Kenyon.

Jennifer Doudna is an internationally renowned Professor of Chemistry and Molecular and Cell Biology at U.C. Berkeley. She and her colleagues rocked the research world in 2012 by describing a simple way of editing the DNA of any organism using an RNA-guided protein found in bacteria. This technology, called CRISPR-Cas9, has opened the floodgates of possibility for human and non-human applications of gene editing and was the basis for her co-award of the Nobel Prize in 2020. Jennifer is a Howard Hughes Medical Investigator, a member of the National Academy of Sciences, the National Academy of Medicine, the National Academy of Inventors and the American Academy of Arts and Sciences.

Cynthia Kenyon is Vice President, Aging Research, at Calico and expert on the genetics of aging. In 1993, Cynthia's discovery that a single-gene mutation could double the lifespan of the roundworm *C. elegans* has led to a new understanding of the genetics of aging. She has received many honors and awards for her findings. Cynthia is a member of the US National Academy of Sciences, the American Academy of Arts and Sciences, and the Institute of Medicine and she is a past president of the Genetics Society of America.

Plenary Speakers:

- **Siobhan Brady,** *University of California, Davis, CA, USA*
- **Jamie Cate,** *University of California, Berkeley, CA, USA*
- **Jennifer Doudna,** *University of California, Berkeley, CA, USA*
- **Niko Geldner,** *Université de Lausanne, Switzerland*
- **Wolfgang Haak,** *Max Planck Institute, Germany*
- **Tony Hunter,** *Salk Institute, CA, USA*
- **Cynthia Kenyon,** *Calico LLC, South San Francisco, CA, USA*
- **Cristina Lo Celso,** *Imperial College London, London, UK*
- **Jodi Nunnari,** *University of California, Davis, USA*
- **Roy Parker,** *University of Colorado, Boulder, USA*
- **Daniel St Johnston,** *Gurdon Institute, Cambridge, UK*
- **Emma Teeling,** *University College Dublin, Ireland*
- **Lisette Waits,** *University of Idaho, USA*

ASBMB Education Plenary

- **Merlin Crossley,** Deputy Vice-Chancellor Academic and Student Life *University of New South Wales*

Conference Streams:

- Proteins, Peptides and Structural Biology
- Plant Biology
- Development, Stem Cell and Regenerative Medicine
- Evolutionary and Ecological Genetics
- Mechanisms of Disease
- Genomics, Genome Editing and Systems Biology
- Biochemistry and Metabolism
- Cell Biology and Signalling
- Education

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KEY DATES:

Late Poster Submission Deadline:
Monday, 8 August 2022

Onsite Poster Submission Deadline:
Wednesday, 21 September 2022

ComBio2022 incorporates the annual meetings of:

- Australian Society for Biochemistry and Molecular Biology
- Australian Society of Plant Scientists
- Australia and New Zealand Society for Cell and Developmental Biology
- Genetics Society of AustralAsia
- New Zealand Society for Biochemistry and Molecular Biology

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Photos courtesy of MCVB

Siglo Bar on Spring Street by Ben King