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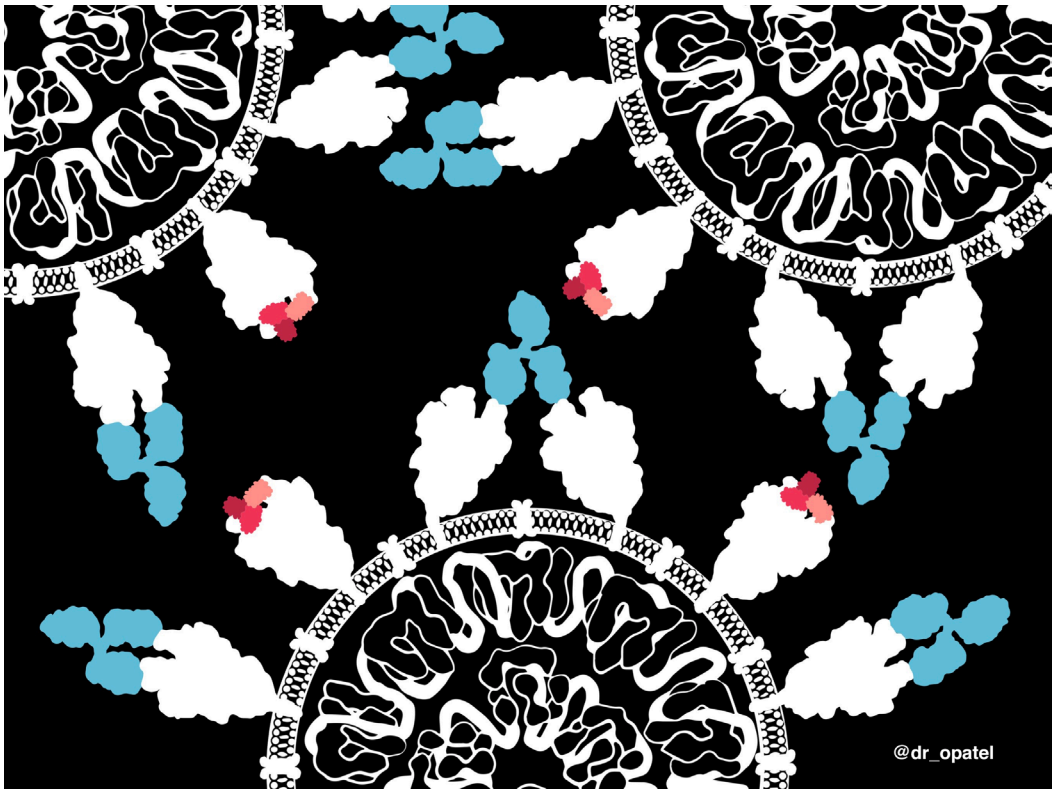

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The Australian Biochemist
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Front Cover

This artwork depicts the contrast between minibinders (small antiviral proteins in shades of red) and antibodies (blue) that bind to the spike proteins on the surface of the SARS-CoV-2 virus. Image credit: Onisha Patel.

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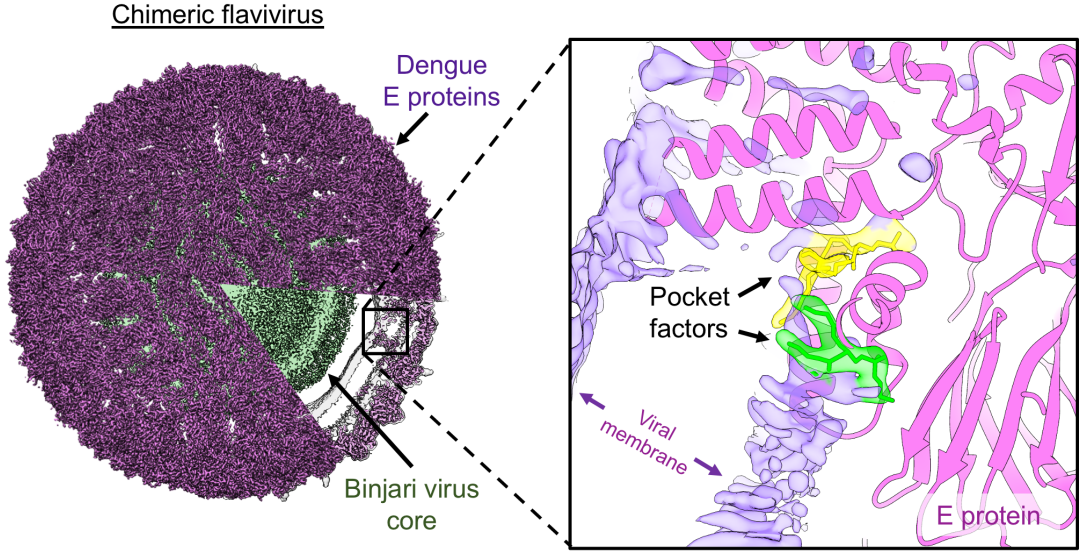
Chimeric Virus Structures Reveal New Therapeutic Targets for Pathogenic Flaviviruses

Hardy JM[#], Newton ND[#], Modhiran N, Scott CAP, Venugopal H, Vet LJ, Young PR, Hall RA, Hobson-Peters J, Coulibaly F*, Watterson D*. A unified route for flavivirus structures uncovers essential pocket factors conserved across pathogenic viruses. *Nat Commun* 2021;12:3266.
[#]Equal first authors
***Corresponding authors: fasseli.coulibaly@monash.edu, d.watterson@uq.edu.au**

Flaviviruses are notorious for their ability to cause seasonal and sporadic epidemics of unpredictable scale and severity. Isolating and culturing emerging flaviviruses is a time-limiting and hazardous step in their characterisation towards antiviral and vaccine development. We used an approach based on chimeric flaviviruses unable to infect humans to mimic medically-relevant strains, eliminating the need to culture the virulent pathogens. Using cryo-electron microscopy (cryo-EM), we determined the structures of several chimeric viruses at record resolution for flaviviruses. These structures proved that the chimeric particles were identical to their wildtype counterparts, validating their use as a research tool and vaccine platform. Unexpectedly, our structure of a chimeric dengue virus identified pocket factors bound to conserved sites in the envelope protein, which may represent new therapeutic targets.

Flaviviruses are transmitted to humans by mosquito or tick bite, with symptoms ranging from fever and myalgia to life-threatening neurological and congenital conditions. Flaviviruses such as dengue, yellow fever and Zika threaten almost a third of the world's population, and have a demonstrated potential to emerge from animal reservoirs with the potential to cause epidemics. There are currently no antiviral drugs for treating flavivirus infection and most flaviviruses lack a vaccine.

Flaviviruses are enveloped, positive-stranded RNA viruses. The envelope (E) protein forms a characteristic herringbone arrangement on the virion surface and is responsible for mediating cell recognition and entry. As such, most flavivirus vaccines target the E protein to prevent infection. While X-ray crystallography was instrumental in obtaining the first structures of the E protein in isolation, cryo-EM has revealed epitopes and functional sites that are only present on assembled viruses. However, cryo-EM structure determination of wildtype flaviviruses often is limited in resolution due to low particle numbers and heterogeneity. Moreover, highly pathogenic or emergent flaviviruses can only be imaged in very few laboratories where microscopes are contained in high biosecurity environments.



Cryo-EM reconstruction of chimeric dengue flavivirus. Structural analysis of these vaccine candidates reveals that they closely mimic native virus particles. Pocket factors (inset) were identified in a conserved region important for viral maturation and stability.

To overcome these barriers, we took advantage of a unique flavivirus first isolated from mosquitoes near the Binjari community in the Northern Territory. The virus has no known vertebrate host, making it easy to manipulate without risk of human infection. Our co-authors from the University of Queensland used Binjari virus as a platform to produce benign chimeric viruses with the E protein of medically-relevant viruses. At Monash University, we optimised the cryo-cooling of samples to obtain the extremely thin vitreous ice that is crucial for imaging with an electron beam. In partnership with microscopists at the Ramaciotti Centre for Cryo-EM, we collected high-quality datasets for 3D reconstruction on the MASSIVE supercomputer.

The first step was to validate our methodology and demonstrate that the chimeric viruses were structurally identical to their pathogenic counterparts. We determined the structure of a flavivirus with low pathogenicity, the Australian Kunjin virus, a low-virulence relative of the West Nile virus, and compared it to the structure of its chimera. The reconstructions reached resolutions of 3.1 Å and 2.9 Å, respectively. Importantly, agreement between the structure was very high not only at the level of individual proteins but as an intact particle.

In a second step, we wanted to apply the approach to a virus which would normally be too pathogenic to be easily imaged in a PC2 facility – the Murray Valley encephalitis virus (MVEV). We determined a structure of the MVEV chimeric virus at a resolution of 3.7 Å. Together, the Kunjin and MVEV structures provided improved models for flaviviruses from the Japanese encephalitis virus group and a basis for comparative analysis of neurotropic viruses. This allowed a more precise mapping of known antigenic sites and determinants of neurovirulence to follow the evolution of these viruses over decades of sporadic epidemics.

Finally, we turned to one of the most studied flaviviruses, dengue virus. Our chimeric viruses of dengue serotype 2, were highly homogenous and enabled us to achieve a record resolution for an enveloped virus – 2.5 Å. Reaching this level of detail allowed us to visualise water molecules as well as two lipid-like molecules bound to the envelope protein. Sequence analysis of the binding site indicated a high degree of conservation across medically-relevant flaviviruses and mutation of interacting residues abolished infectivity. We hypothesise that these pocket factors have a role in stabilising the virus particle in the late stages of viral maturation.

Together, these findings demonstrate the utility of the chimeric platform for rapid, high-resolution structure determination of flaviviruses and identify an attractive target for the development of broad-spectrum assembly inhibitors.

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Joshua Hardy (left) and Fasséli Coulibaly.

Catch Me If You Can: T Cell Cross-recognition of Seasonal Coronaviruses and SARS-CoV-2 Virus

Lineburg KE, Grant EJ Swaminathan S, Chatzileontiadou DSM, Szeto C, Sloane H, Panikkar A, Raju J, Crooks P, Rehan S, Nguyen AT, Lekieffre L, Neller MA, Tong ZWM, Jayasinghe D, Chew KY, Lobos CA, Halim H, Burrows JM, Riboldi-Tunnicliffe A, Chen W, D'Orsogna L, Khanna R, Short KR, Smith C, Gras S*. *Immunity* 2021;54:1055.
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Prior to the COVID-19 pandemic, exposure to coronaviruses would lead to the common cold. Four seasonal coronaviruses infect humans (OC43, NL63, HKU-1 and 229E), and share significant homology with SARS-CoV-2. Due to their similarities, it was proposed in early 2020 that previous infection by seasonal coronaviruses might provide some protection against COVID-19.

Publications with Impact

Illustration of T cells ability to cross-recognise SARS-CoV-2 and seasonal coronaviruses, by Vanette Tran.

We investigated the T cell response towards specific viral peptides that share high sequence homology between seasonal coronaviruses and the SARS-CoV-2 virus. We collected blood samples from COVID-19 recovered patients and donors unexposed to SARS-CoV-2. We discovered that a strong CD8+ T cell response (killer T cells) was observed towards peptides derived from the SARS-CoV-2 Nucleocapsid protein in COVID-19 recovered individuals and linked with the expression of a specific Human Leukocyte Antigen (HLA) molecule, HLA-B7. HLA molecules present peptides to the killer T cells that can in turn detect the presence of the virus and eliminate the infected cells.

We discovered that the strong CD8+ T cell response, observed in approximately 80% of HLA-B7+ COVID-19 recovered patients, was due to a single peptide called SPR derived from the SARS-CoV-2 nucleocapsid protein. Importantly, there is no known mutation in this nine-residue long peptide, which could be of advantage to develop a universal vaccine against all variants of SARS-CoV-2. Sequence alignment of the SARS-CoV-2 nucleocapsid protein with other seasonal coronaviruses showed that there are homologous peptides (SPR like) in these viruses sharing high sequence similarity with the SPR peptide.

T cells from both COVID-19 and unexposed donors were able to not only recognise the SPR peptide but also its seasonal coronaviruses' homologues derived from the OC43 and HKU-1 viruses, but not from the 229E or NL63 viruses. This means that T cells could recognise the SARS-CoV-2 peptide prior to viral infection, providing pre-existing immunity to unexposed HLA-B7+ donors. While the NL63 SPR-like peptide did not activate T cells, the 229E SPR-like peptide activated T cells that were only able to recognise this specific peptide, but not the SARS-CoV-2 or OC43/HKU-1 homologous peptides.

To further understand the basis of the T cell cross-recognition, we used X-ray crystallography to reveal the structure of the peptides presented by the HLA-B7 molecule. The crystal structures showed that the 229E SPR-like and the SARS-CoV-2 SPR peptide, that only differ by three residues, were adopting different conformations when bound to HLA-B7. These differences explained why the same T cell can't 'see' both peptides, as well as why the T cell cross-recognition is specific only for some coronaviruses, and not for all.

Altogether, the study gave us initial insights on the molecular and functional basis of antigen specific T cell response in COVID-19.

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Gras Lab, from left: Christopher Szeto, Dhilshan Jayasinghe, Demetra Chatzileontiadou, Stephanie Gras, Brianna Hans, Emma Grant, Christian Lobos and Andrea Nguyen.

Publications with Impact

The Integration of Kinase and Phosphatase Activity Offer RNA Polymerase II a Moment of Pause; a Delicate Balance Between the Integrator–PP2A Complex and CDK9

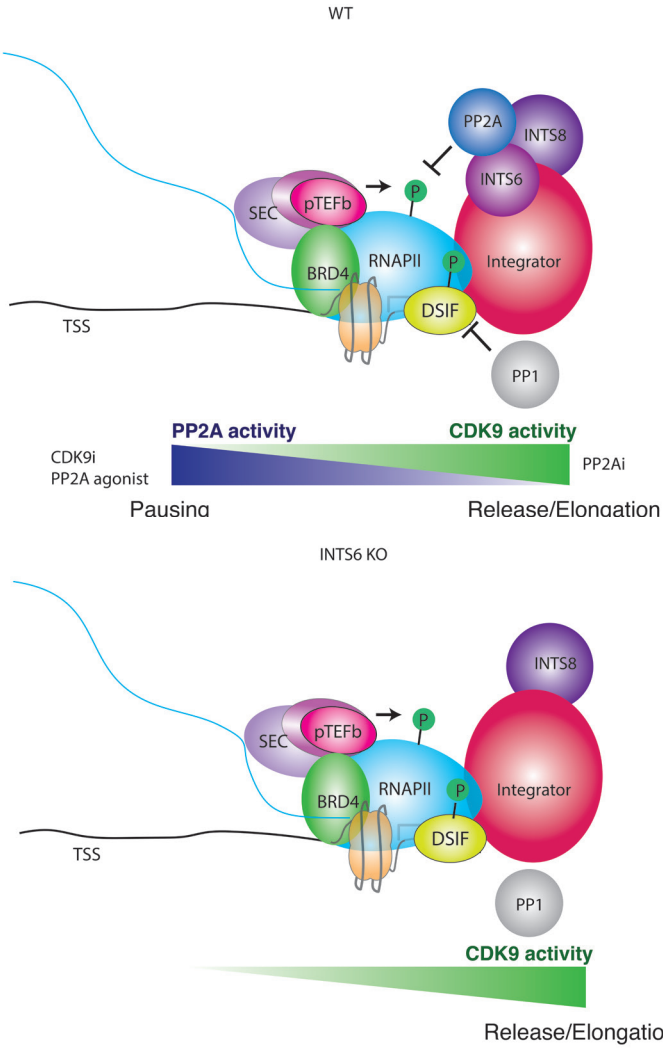
Vervoort SJ*, Welsh SA, Devlin JR, Barbieri E, Knight DA, Offley S, Bjelosevic S, Costacurta M, Todorovski I, Kearney CJ, Sandow JJ, Fan Z, Blyth B, McLeod V, Vissers JHA, Pavic K, Martin BP, Gregory G, Demosthenous E, Zethoven M, Kong IY, Hawkins ED, Hogg SJ, Kelly MJ, Newbold A, Simpson KJ, Kauko O, Harvey KF, Ohlmeyer M, Westermarck J, Gray N, Gardini A*, Johnstone RW*. The PP2A-Integrator-CDK9 axis fine-tunes transcription and can be targeted therapeutically in cancer. *Cell* 2021;184(12):3143–3162.e32.
***Corresponding authors: stephin.vervoort@petermac.org, agardini@wistar.org, ricky.johnstone@petermac.org**

As in life, at the molecular level it is all about finding the right balance, and when this delicate equilibrium is disrupted, it inevitably causes things to go awry. We discovered that this is very much true for the process of RNA polymerase II (RNAPII)-mediated transcription.

Gene-expression networks are tightly regulated and respond to a variety of environmental and cellular cues throughout life. To attain spatio-temporal control of this process, a multilayered regulatory system has evolved, which regulates RNAPII mediated RNA synthesis, ranging from chromatin architecture, structure to the epigenome. Additionally, RNAPII mediated transcription itself is highly regulated along its journey from start to finish. Similar to the cell cycle, RNAPII driven transcription is largely unidirectional and composed of distinct checkpoints, each of which is regulated by a dedicated set of cyclin-dependent kinases (CDKs) and their cognate cyclin pairs, a process coined the transcription cycle. After RNAPII has initiated, it quickly comes to a halt at transcription start site (TSS) proximal regions. At this pause–release checkpoint, RNAPII awaits further cellular cues that arrive through CDK9/Cyclin-T1 mediated CTD phosphorylation, resulting in release of pausing factors, conformational changes and CDK12/13 controlled productive elongation (Fan *et al. Science Advances* 2020).

Transcription cycle dysregulation frequently occurs in cancer through for example, MYC amplifications or MLL rearrangements. The idea that transcriptional dysregulation is fundamental to oncogenesis has prompted the development of small molecules targeting core transcriptional components to correct the imbalance and improve therapeutic outcomes (Vervoort *et al. Nature Reviews Cancer* 2021).

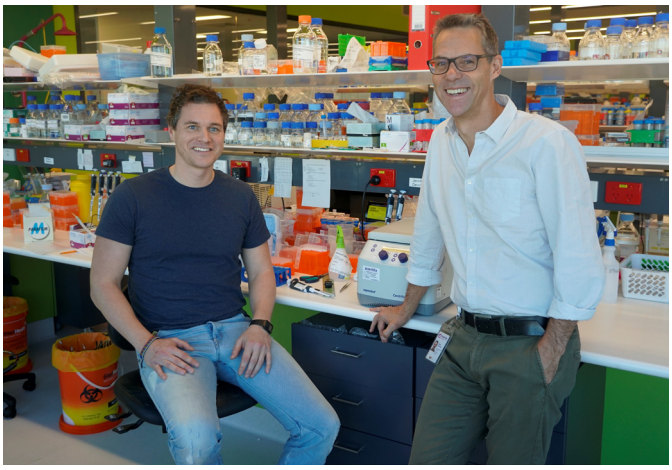
Although CDK-mediated transcription cycle regulation is relatively well characterised, how this process is fine-tuned remained poorly understood. To determine whether cellular CDK9 activity at the RNAPII pause–



The Integrator submodule composed of INTS6/8/PP2A functionally antagonises CDK9 at the RNA polymerase II pause–release checkpoint. When this module is perturbed, CDK9 activity is unopposed, which may drive tumorigenesis and confer resistance to targeted therapy.

release checkpoint was functionally antagonised, we performed a series of genome-wide CRISPR/Cas9 KO screens to identify genes of which deletion enabled survival and transcription in the presence of CDK9 inhibition. We observed that the loss of the integrator complex genes INTS6 rendered cells resistant to selective CDK9 inhibition. Immunoprecipitation – mass-spectrometry, phospho-proteomics and size-exclusion chromatography experiments – revealed that the Integrator complex comprised a novel submodule composed of INTS6, INTS8 and PP2A (INT–PP2A/INTAC), which actively dephosphorylated CDK9 substrates. When INTAC is perturbed, this results in sustained phosphorylation and allows for normal transcription when CDK9 activity is limited. We found that this INT–PP2A mediated antagonism of CDK9 likely exists to prevent excessive transcriptional activation in response to stimuli and rapidly suppress transcription post removal. This process may play an important role in cancer, where perturbation of PP2A and/or INTS6 may drive a transcriptionally dysregulated state. Finally, we were able to shift the balance from a transcriptionally hyperactive state, driven by for example MLL-AF9 mediated aberrant recruitment of CDK9, back to a more normal state by concurrently inhibiting CDK9 and activating PP2A using small molecule inhibitors and agonists, respectively. This combination therapy resulted in synergy *in vivo* and *in vitro* in both solid and hematopoietic malignancies. Taken together, our work discovered a novel fundamental regulatory complex operating at the pause–release checkpoint, that is dysregulated in cancer but can be therapeutically exploited to improve therapeutic outcomes.

Stephin Vervoort and Ricky Johnstone
Walter and Eliza Hall Institute of Medical Research



Stephin Vervoort (left) and Ricky Johnstone.

Is Milk Just Nutrition or Also a Cross-species Communication Source?

Samuel M, Fonseka P, Sanwlani R, Gangoda L, Chee SH, Keerthikumar S, Spurling A, Chitti SV, Zanker D, Ang CS, Atukorala I, Kang T, Shahi S, Marzan AL, Nedeva C, Vennin C, Lucas MC, Cheng L, Herrmann D, Pathan M, Chisanga D, Warren SC, Zhao K, Abraham N, Anand S, Boukouris S, Adda CG, Jiang L, Shekhar TM, Baschuk N, Hawkins CJ, Johnston AJ, Orian JM, Hoogenraad NJ, Poon IK, Hill AF, Jois M, Timpson P, Parker BS, Mathivanan S*.
Oral administration of bovine milk-derived extracellular vesicles induces senescence in the primary tumor but accelerates cancer metastasis. *Nat Commun* 2021;12(1):3950.
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The idea that ingested dietary biomolecules including RNA may be bioavailable in host organism, and their purported ability to regulate gene expression in tissues and the phenotype of an organism, has ignited unprecedented interest in cross-kingdom and cross-species communication. Whilst few studies challenged existing paradigms and highlighted that dietary RNAs could be absorbed via food intake, circulate in the blood, reach various organs and modulate gene expression, it also kindled additional debate among the regulatory boards of genetically modified organisms. Furthermore, the concept was challenged by few well-controlled studies emphasising the instability of nucleic acids which ultimately succumb to the membrane barriers and nucleases of the mammalian gastrointestinal tract. Hence, the observations were often criticised as diet-responsive endogenous RNAs or artefacts due to non-adherence of rigorous procedures. While lipid bilayered extracellular vesicles (EVs) are proposed to be protectors of the rich cargo of proteins and RNA, concrete *in vivo* evidence to support cross-species/kingdom communication via EVs are limited and hence the concept remained controversial.

Milk has evolutionarily developed as the primary source of nutrition in infants. It is highly dynamic in composition, consisting of EVs, protein fragments, amino acids, nucleic acids, antimicrobials, antibodies, cytokines and chemokines. Previously, we observed that bovine milk EVs (MEVs) are enriched with a bioactive cargo with roles in immune regulation and

Publications with Impact

Bovine milk EVs are a double-edged sword.

growth. Thus, in this study we began by determining the ability of MEVs to survive the gut conditions, followed by their bioavailability and biodistribution. Interestingly, MEVs survived extreme conditions including acidic pH and boiling temperature. Further, we observed that MEVs were bioavailable and reached various peripheral tissues including liver and heart in spite of oral delivery. Our findings indicated that MEVs, due to their intrinsic stability, could be the vehicles that sequester bioactive cargo and aid in its systemic uptake and delivery. These preliminary findings led us to investigate whether MEVs could have a functional role in the consuming individual. We did so by understanding their role in controlling cancer progression in mice, orthotropic and xenograft, models. Intriguingly, we observed that MEVs were able to impede the growth of primary tumors upon oral administration in mice. However, the rate at which the tumor cells metastasised was accelerated in these mice. However, in mice which were subjected to surgical resection of the primary tumor, administering MEVs led to reduction of the metastatic burden. We observed that MEVs were able to mediate these effects by inducing senescence and epithelial-mesenchymal transition in tumor cells. Our findings highlighted that MEVs are a double-edged sword in the context of cancer progression.

The novel findings in our study emphasise the potential utility of dietary EVs from milk in developing novel therapeutic regimes for treatment of metastatic cancer. Further, these findings pave way for improved understanding of inter-species and inter-kingdom communication mediated by dietary EVs. The study was only possible due to the collective effort of Mathivanan laboratory members over the years, some of whom are highlighted in the laboratory photo, as well as our wonderful collaborators.

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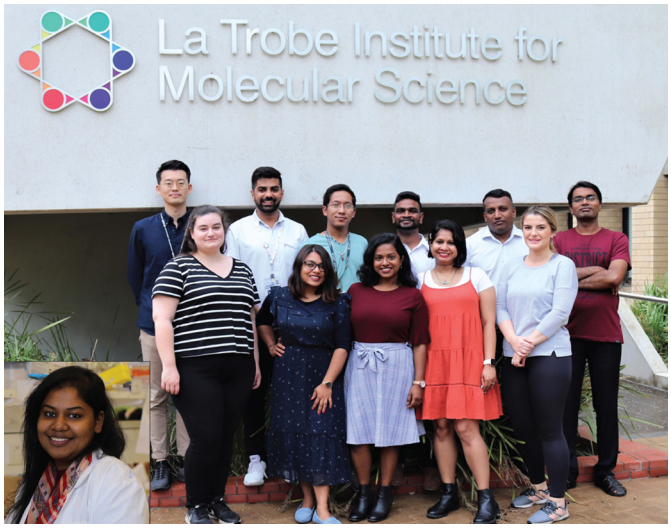


Mathivanan Lab. Inset: Monisha Samuel (lead author). Back row (from left): Taeyoung Kang, Rahul Sanwlani, Sanjay Shahi, Sai Vara Prasad Chitti, Suresh Mathivanan and Mohashin Pathan. Front row (from left): Cassandra Cianciarulo, Akbar L Marzan, Ishara Atukorala, Pamali Fonseka and Christina Nedeva.

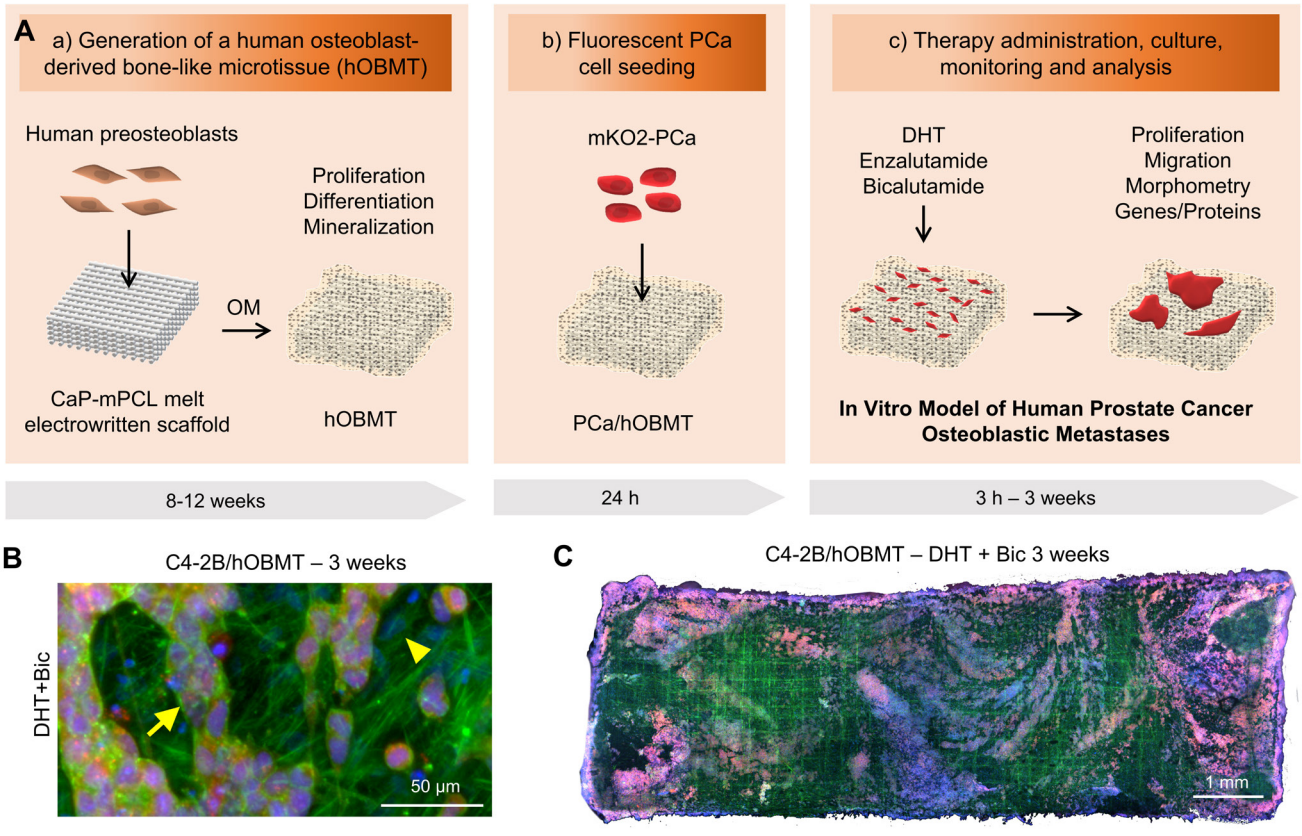
Publications with Impact

Antiandrogen Effects in a Bone Cancer Model

Bock N*, Kryza T, Shokoohmand A, Röhl J, Ravichandran A, Wille ML, Nelson CC, Hutmacher DW, Clements JA. *In vitro* engineering of a bone metastases model allows for study of the effects of antiandrogen therapies in advanced prostate cancer. *Sci Adv* 2021;7:eabg2564.
***Corresponding author: n.bock@qut.edu.au**

Androgen signalling is key to prostate cancer progression, and thus, targetting the androgen axis is the gold standard for recurrent advanced disease. Androgen receptor (AR) antagonists initially inhibit or delay bone metastasis, yet antiandrogen therapies (ATT) ultimately lead to cancer/stroma cell adaptation through AR reactivation and paracrine signalling. The role of the tumour microenvironment as a key modulator of cancer cell response to therapy is still unclear, but recent data suggest that ATT may further promote metastasis progression and adverse outcomes. Specifically, bone metastatic lesions are found in over 90% of patients with metastatic castrate resistant prostate cancer (mCRPC). It is thus critical to delineate the effects of standard ATT in this microenvironment. One challenge however lies in adequately modelling the pathology of the disease *in vitro*.

In our study, we used an all-human microtissue-engineered model of mineralised metastatic tissue combining human osteoprogenitor cells, 3D printing and prostate cancer cells. We assessed the effects of the first- and second-generation antiandrogens, bicalutamide, and enzalutamide, respectively, in this microenvironment. Compared to past models of bone metastases, our model enables long-term cultures (three weeks), combined with quantitative imaging and high throughout processing at a single-cell level. The model was made of primary human osteoprogenitors differentiated in early and mature osteoblasts and osteocytes and matrix biomineralisation, for direct interactions with prostate cancer cells. The presence of human osteocytes in an *in vitro* model is notable, as they are difficult to culture *in vitro* in 2D, yet important. Osteocytes indeed express key bone proteins playing



A *Schematic overview of manufacturing.*
B,C *Confocal microscopy images of the 3D metastatic microtissues after three weeks coculture with C4-2B cells under dihydrotestosterone (DHT, 10 nM) and bicalutamide (Bic, 10 µM) showing cancer cell coverage of hOBMT and formation of micrometastases. Full arrows show cancer cells, full arrowheads show osteoblasts.*
Adapted from Bock et al., Sci Adv *2021;7:eabg2564 Fig. 1, CC BY-NC 4.0.*

Publications with Impact

an important role in the receptor activator of nuclear factor κB/osteoprotegerin (RANK/OPG) pathways, strongly implicated in prostate cancer bone metastasis. The mineralised microtissues were further used in co-culture with fluorescently tagged AR-positive/negative metastatic prostate cancer cell lines (LNCaP, C4-2B, and PC3 cells) and let to grow on the microtissues from three hours to three weeks depending on the targeted characterisation. This approach resulted in a versatile *in vitro* model of human prostate cancer osteoblastic metastases, to assess the effects of androgen deprivation in that microenvironment.

We found that probing the bone microenvironment with Enzalutamide led to stronger cancer cell adaptive responses and osteomimicry than bicalutamide. Enzalutamide presented with better treatment response, in line with enzalutamide delaying time to bone-related events and enzalutamide, extending survival in mCRPC. We learned that enzalutamide administration, although more effective in reducing overall migration and proliferation of AR-dependent LNCaP cells in the bone microenvironment compared to bicalutamide, led to more bone microenvironment gene alterations than bicalutamide. Alterations included osteopontin (OPN), podoplanin (E11), Runt-related transcription factor 2 (RUNX2), bone sialoprotein (BSP), and Dickkopf WNT Signaling Pathway Inhibitor 1 (DKK1), although no significant differences were observed in AR expression between both drugs. This finding implied that the effects of enzalutamide triggered more response than bicalutamide in cancer/bone stroma interactions and with less dependence on AR expression. Antiandrogen treatments also failed to reduce prostate specific antigen (PSA) expression in the bone microenvironment and contributed to increased bone production/maturation and neuroendrocrine/transdifferentiation markers (such as dopa decarboxylase (DDC)). This is in line with cancer cell osteomimicry and increased osteoblastic activity, which is correlated with lesions seen in the radiological data of men with bone mCRPC and through serum markers.

Importantly, our work enabled to decouple the effects of osteoblasts in the bone tumour microenvironment without the confounding factor of osteoclasts. Osteoclasts are indeed often considered responsible for the initiation of the vicious cycle of metastasis. However, it was not currently known whether and how osteoclasts or osteoblasts affect enzalutamide resistance and reciprocally, whether the effects of enzalutamide on those cells contribute to drug resistance. Here, it was shown that the presence of osteoclasts was not necessary to activate such pathways. These pathways were firstly activated by direct interactions between human osteoblasts and cancer cells and then accentuated by ATT, with worse outcomes with bicalutamide, yet stronger genomic dysregulation using enzalutamide. This suggests that combining enzalutamide with approaches that also target osteoblasts and/or osteoclasts may lead to better therapies and flags osteoblasts as another valid source of antiandrogen resistance in mCRPC.

Ultimately, the all-human microtissue-engineered model of mineralised metastatic tissue we presented represents a substantial advance to dissect the role of the bone tumour microenvironment and responses to therapies for mCPRC.

Nathalie Bock, Thomas Kryza, Dietmar W Hutmacher and Judith Clements.
Institute of Health and Biomedical Innovation and Translational Research Institute
Queensland University of Technology

Some of the team involved in this study at QUT, from top left, clockwise: Nathalie Bock, Thomas Kryza, Dietmar W Hutmacher and Judith Clements.

Mapping Human Breast Tissue Heterogeneity During Development and Cancer

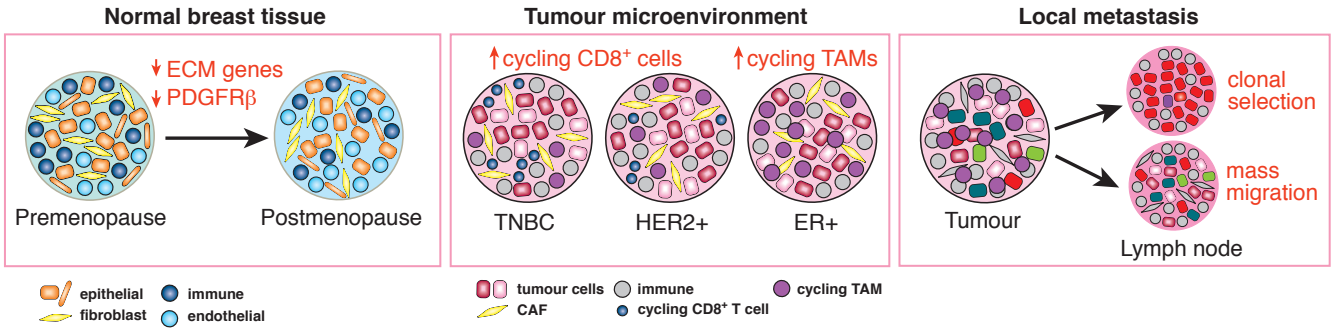
Pal B, Chen Y, Vaillant F, Capaldo BD, Joyce R, Song X, Bryant VL, Penington JS, Di Stefano L, Tubau Ribera N, Wilcox S, Mann GB; kConFab, Papenfuss AT, Lindeman GJ, Smyth GK*, Visvader JE*. A single-cell RNA expression atlas of normal, preneoplastic and tumorigenic states in the human breast. *EMBO J* 2021 Jun 1;40(11):e107333.
***Corresponding authors: smyth@wehi.edu.au, visvader@wehi.edu.au**

Normal breast is a highly heterogeneous tissue comprising an elaborate ductal epithelial network embedded in a stromal environment. In breast cancer patients, neoplastic changes in the epithelium and evolving changes in the tumour microenvironment further define tissue composition. Our recent study published in *EMBO J* provides novel insights at the single-cell level into the molecular events that unfold during different physiological and malignant states of breast tissue. In this study, we examined the single-cell transcriptomes of 340,000 cells extracted from 65 clinical specimens representing normal breast (pre- and post-menopause), the preneoplastic state (BRCA1$^{+/-}$ tissue), the major breast cancer subtypes, including male breast cancers and locally advanced lesions (lymph node infiltrates).

The analysis of normal breast tissue revealed subtle changes in epithelial transcriptomes associated with menopause. Conversely, the stromal cell compartment showed striking compositional and molecular changes, in which fibroblasts expressed lower levels of typical markers, including *PDGFRA, PDGFRB, POSTN* and *COL* genes. These molecular changes may lead to alterations in the extracellular matrix and the immune-stromal composition of breast tissue in postmenopausal women.

Neoplastic progression was shown to globally impact cellular and molecular heterogeneity within the breast immune-stromal microenvironment. A direct comparison of healthy preneoplastic tissue and tumours from BRCA1$^{+/-}$ mutation carriers revealed dramatic infiltration of transcriptionally distinct lymphocytes and myeloid cell types. Extending this analysis to 34 treatment-naive primary tumours (ER$^+$, HER2$^+$ and TNBCs) unveiled a unique immune microenvironment composition for each cancer patient. Integration of immune cell profiles across multiple patients identified a significant population of 'cycling' CD8 T cells (T_{RM}- and T_{EMRA}-like) expressing proinflammatory cytokines and effector molecules in TNBC and HER2$^+$ cohorts. In contrast, ER+ tumours were enriched with proliferative tumour-associated macrophages (TAMs) with distinct immunosuppressive M2 phenotypes (*CD163$^+$, MRC1$^+$* and *CX3CR1$^+$*). Collectively, these results provide a basis for developing novel strategies targeting tissue-resident immunosuppressive cells to improve the efficacy of current standard-of-care immunotherapies.

Focussing on EPCAM$^+$ tumour cells, we observed marked intra- and inter-patient heterogeneity across each tumour subtype. Interestingly, a discrete subset of cycling cancer cells was detected in all tumours, with the highest proportion detected in TNBCs, which show more aggressive behaviour. Surprisingly, putative cancer stem cells or cells with EMT-like properties were not associated with any specific transcriptional cell cluster in any subtype.



Schematic diagram showing characteristic features of single cell transcriptome of normal breast tissue, treatment naïve breast tumours (TNBC, HER2$^+$, ER$^+$), and local metastatic lesions. Pre- to post-menopause transition is associated with decreased PDGFRb and matrix-associated genes in fibroblasts. Comparison of tumour microenvironments show infiltration of specific cycling immune cells i.e CD8$^+$ T-cells in TNBC and HER2$^+$ and TAMs in ER$^+$ tumours, suggesting different immunoregulatory pathways operating in these subtypes. The matching pairs of ER$^+$ tumour and lymph node (LN) samples showed both clonal selection and mass migration of tumour cells during lymph node metastases.

Publications with Impact

Lastly, we completed integrated scRNA-seq and single-cell copy number variation (CNV) analyses of paired ER$^+$ breast tumours and lymph node biopsies, which allowed us to study tumour clones and their transcriptional profiles at the single-cell level. Indeed, the presence of different seeding patterns of genetically distinct clones of primary tumour cells into the axillary lymph nodes confirmed the involvement of multiple mechanisms of tumour progression, i.e., monoclonal, polyclonal or the mass migration of tumour cells.

Our comprehensive single-cell RNA expression data provides a global view of heterogeneity within normal breast tissue, tumours and their surrounding microenvironment. These data will complement future single-cell spatial-transcriptomics studies aimed at correlating expression with spatial organisation and intercellular relationships.

Bhupinder Pal[1,2,3,4] and Jane Visvader[1,2]
[1] Walter and Eliza Hall Institute of Medical Research
[2] University of Melbourne
[3] La Trobe University
[4] Olivia Newton-John Cancer Research Institute

Jane Visvader and Bhupinder Pal.

2021 Prime Minister's Prize for Innovation

The ASBMB congratulates Professor Tony Weiss AM on being awarded the 2021 Prime Minister's Prize for Innovation. On 3 November 2021, the Australian scientific, research and science teaching community came together online to celebrate achievements of the country's leading scientists, research-based innovators and science teachers at the 2021 Prime Minister's Prizes for Science.

Professor Weiss, from the University of Sydney, received the 2021 Prime Minister's Prize for Innovation in recognition of his pioneering research and commercialisation of synthetic tropoelastin-based biomaterials, which can accelerate and improve the repair of human tissue.

Professor Weiss is considered the world's leading authority on tropoelastin, the protein building-block that gives human tissue its elasticity. For the past two decades, he has pioneered global research into tropoelastin and elastic fibres, which are found in human tissue ranging from the skin to the lungs and arteries. Elastic fibres play a significant role in the generation and regeneration of tissues found in the human body.

In 2008, he founded the company Elastagen to commercialise his research and inventions. The company raised $35 million in venture capital and grant funding, completed clinical trials and scaled-up production. Ten years later, Elastagen was sold to one of the world's largest biopharmaceutical companies for $334 million – one of the largest transactions ever completed in Australia's life science sector.

Tony Weiss AM

Professor Weiss is also an ambassador for Australian innovation and has given his time to mentor Australian researchers. He offers insight on every aspect of science commercialisation, inspiring both Australian investors and incubators to support the next generation of life science technologies.

His Prime Minister's Prize follows on from a slew of other awards including the Order of Australia, NSW Premier's Prize, ASBTE Clunies Ross Medal, Eureka Prize, RACI Weickhardt Medal, RACI Applied Research Medal, ASBTE Award for Research Excellence and ASBMB's AMRAD Pharmacia Biotech Medal.

He encourages other researchers to share in the journey.

"To receive the Prime Minister's Prize for Innovation means a great deal to me. It's an extraordinary process to reach the point where innovation succeeds. The process of innovation is a roller coaster; there are ups and downs, but it's always a journey forward. This recognition is testament to the many people who have been part of this journey with me. Most importantly, it's a celebration of science and innovation in our country."

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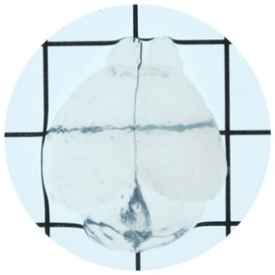

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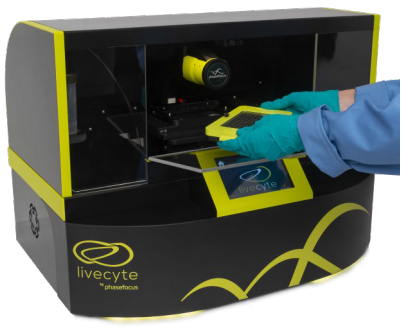

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ASBMB 2021 Education Symposium

On Tuesday 28 September, the ASBMB Education Symposium returned to inspire our academics online, with the theme of Sharing Practice: a Focus on Assessment and Academic Integrity.

This year's ASBMB Education Symposium was a showcase of the quality and commitment of our educators and revealed how resilient and strong the biochemistry education community is. Over 160 educators, professional staff, researchers and students from Australasia and beyond connected virtually to share good practice, focusing on assessment and academic integrity.

The Symposium was opened by ASBMB President Professor Jacqueline Matthews (University of Sydney) and Professor Roger Daly (Head, Department of Biochemistry and Molecular Biology, Monash University), followed by a keynote address from Professor Phillip Dawson (Centre for Research and Digital Learning [CRADLE], Deakin University) whose presentation was titled 'If we aren't physically with students, how can we be sure they are completing tasks in the circumstances we require – and how can we verify their identity?' His presentation explored what educators can do to detect and deter cheating in the online environment and argued that addressing cheating "will require an uneasy balance between positive 'academic integrity' and adversarial 'assessment security' approaches." Our second keynote address, presented by Associate Professor Ann Rogerson (University of Wollongong), focussed on shifts in student behaviours during COVID affecting academic integrity. Ann's research demonstrated a sudden spike in the reliance of technology, use of purchased subject materials and students forming their own study networks and increased online communication about exams in real time, thereby influencing academic integrity. Ann's presentation highlighted the need for educators to reconsider how we assess and manage academic integrity with students.

Through three symposium sessions, educators from institutions far and wide shared their expertise on the approaches they have implemented to enhance student learning, achieve academic integrity and enhance academic skills. The atmosphere was lively as educators also shared the challenges they experienced with robust discussions, post presentation and via the chat function, including questions such as: What does best-practice in assessment look like in a post-COVID era? Do we expect to revert back to our assessment practices pre-COVID, or do we see ourselves on a new path? Are exams still fit for purpose, and if not, what are the alternatives we value? How do we assess laboratory skills in an online forum? What is the role of technology? How do academic integrity issues challenge us and how do we respond as we adapt to this new normal?

This year's Symposium highlight was once again our student panel discussion, on the topic of assessments and academic integrity. The student voice was heard through three panellists: third year student Taku Chitambo (Monash University), second year student Eleanor Lawton-Wade (University of Melbourne) and second year student Ella Scott (University of Sydney). These students – who did their universities proud – shared their perspectives on assessments (online and in-person), how they uphold academic integrity, their concerns about academic integrity with online assessments and their recommendations for the design of online assessments. Their insights were timely reminders to educators of the importance of our ultimate audience, our students.

The recordings of the Symposium sessions and the abstract booklet are available on the ASBMB website. It is now incumbent on the broader education community to reflect upon, adapt and apply this learning to our specific student cohorts in a post-COVID world. However, we must ensure to keep in mind the richness of the student voice and weaving this into our practice – after all, it is their lives and learning that is most affected by the changes happening around us.

We thank the ASBMB for their support and encouragement. We also send a big thank you to Justine Olcorn and Ester Villvanathan (Department of Biochemistry and Molecular Biology, Monash University) for assisting with the symposium organisation and for their expert support on the day. Our sincere thanks to our student participants, our presenters who shared their insights and to all of you who attended on the day. Your participation is evidence of our collective commitment to inspire each other in our efforts to nurture the future biochemists.

ASBMB 2021 Education Symposium Organising Committee
Nirma Samarawickrema, Monash University
Tracey Kuit, University of Wollongong
Amber Willems-Jones, University of Melbourne,
Matthew Clemson, University of Sydney
Maurizio Costabile, University of South Australia

ASBMB Education Feature

The ASBMB Education Feature is coordinated by Nirma Samarawickrema (nirma.samarawickrema@monash.edu) and Tracey Kuit (tracey_kuit@uow.edu.au).

Student Panel: Perspectives on Assessment and Academic Integrity at the 2021 ASBMB Education Symposium

Tracey Kuit (University of Wollongong) and Amber Willems-Jones (University of Melbourne) talk to undergraduate Biochemistry students Taku Chitambo, Eleanor Lawton-Wade and Ella Scott.

At the ASBMB 2021 Education Symposium, a student panel discussion was held with three undergraduate students: Taku Chitambo, a third year Bachelor of Science student from Monash University, Eleanor Lawton-Wade, a second year Bachelor of Biomedicine student from the University of Melbourne, and Ella Scott, a second year Bachelor of Science student from the University of Sydney. Eleanor, Taku and Ella shared their experiences and perspectives on online assessment and academic integrity. Responses to questions have been paraphrased and condensed with permission.

Do you think online and in-person assessments are equivalent? Can you describe any specific examples?

Eleanor – In-person and online assessments are not equivalent, but that doesn't mean there is a difference in competence or validity, they are just assessing different things. For example, in-person exams often focus on recall rather than application of knowledge, whereas online assessments have a stronger focus on data analysis. Online assessments that include questions based on clinical application and data interpretation are preferred; though they should not be overly complex or too clinical to the point that course material is not actually examined.

Taku – No, they are not the same, but that is not a bad thing, they simply have a different focus. In in-person assessments, exams often relied on recalling lecture content and specific words. Online assessments however, focus on understanding ideas and topics, and applying these to key concepts. Case studies are a great way to assess biochemistry topics and scenarios that require application to real life situations; they can assess concepts that students do not properly understand. Conversely, quizzes – if designed to require basic knowledge recall – are not that helpful in terms of assessing complex concepts because while the student may be able to recall certain words, they may lack the understanding of the underlying principles.

How do you uphold academic integrity as a student, both individually and in a group?

Taku – When I have worked in a group, we would ensure that we split up the work evenly, and use software that records history and contribution (such as Google Docs). It is often easy to tell if someone has breached academic integrity because their assessment begins to sound different from how they speak and write. The best way to be able to maintain academic integrity in a group is by having regular meetings to gauge each member's work ethic, and to ensure each member conveys ideas inline with their contribution to the group's Google Doc, etc.

Ella – My approach to upholding academic integrity is essentially the same whether I'm working in a group online or in-person. In some ways it is easier to uphold academic integrity online because everything is recorded, e.g. through access to each other's contributions via version history on Google Docs, or through Zoom meeting attendance, etc. Personally, I also ensure that I am honest when completing the peer review component of group assignments, where each group member assesses their own and everyone else's contribution to the assignment. Such peer review is useful for ensuring academic integrity because it encourages group members to contribute equally to an assignment and ensures that everyone gets the marks they deserve based on their contribution. If any issues with academic integrity arise, it is important to communicate openly and early with the subject coordinator to try to resolve any potential issues from developing further.

Is academic misconduct openly discussed by students and do you have any specific concerns about academic integrity that you'd like to share?

Taku – As a third-year student, I have had the opportunity to see the transition of university education from in-person to online. In-person cheating or breaches in academic integrity in examinations were often active acts that required the individual to actively breach them. This made it easy for students to identify what constitutes cheating

Biochemistry students, from left: Taku Chitambo, Eleanor Lawton-Wade and Ella Scott.

in an exam – the line was clear. In online examinations and assignments however, the line is blurred, resulting in uncertainty for both students and teaching staff as to what counts as a breach of academic integrity and how to handle a breach. Personally, my concerns do not necessarily pertain to whether academic integrity has been breached by students but rather, to ensuring students properly and clearly understand what they can and cannot do in assignments and online examinations, and the steps they can take to stay within the bounds of academic integrity.

Ella – Student concerns relate to:

1. Transparency. The need for universities to clearly define what academic integrity means in a digital world and how collusion is defined in terms of student contact.

2. Fairness and equity. When students pre-prepare answers to questions compared to those who type them out during an exam, there is inequity and a lack of fairness. There is the sense that this can influence how much knowledge an individual can demonstrate during the exam under time constraints.

3. Productive dialogue: Academic integrity benefits both students and academics alike. Engaging in productive dialogue, rather than fear tactics is likely to elicit more responsive and positive engagement from students, and improve relationships between academics and students.

What was your experience with proctored exams this year? Do you have feedback you'd like to share with those considering using proctored exams in a unit of study?

Ella – My experience with ProctorU included exams in both Biochemistry and Pharmacology. For both disciplines, the settings included recording, and no internet access. In Biochemistry, we had access to local files, while this was prohibited for Pharmacology. Overall, sitting a proctored exam is slightly more stressful than an unproctored exam, for two main reasons (aside from having in the back of your mind that you are being watched):

1. Technical issues. The responsibility is on the student to ensure the technology is working correctly. This can be challenging and stressful if it is not clear what to do, who to contact or how to provide sufficient proof of the technical difficulties encountered.

2. Maintaining exam conditions. Responsibility is again on the student, which can cause additional anxiety as you often worry about accidentally doing something wrong, e.g. will reading a question aloud or a rubbish truck driving past outside trigger the AI?

Open-book exams with ProctorU seem to provide a good balance between upholding academic integrity and giving students the best chance of focusing on the exam because the monitoring does not feel quite as strict as the closed-book exam, so it is less distracting.

If you could design an online assessment what would it look like?

Ella – I would embrace the opportunities presented by online exams rather than trying to recreate an exam room. In an online setting, it is impossible to achieve conditions like those of past in-person exams, and the more you try, the more stressful and distracting it becomes for the student. My tips for an online assessment include:

- Set open-book proctored exams to ensure that the individual who is sitting the exam is the person who is meant to be sitting it. Set a time limit and provide access to local files and the internet (where possible).
- Use open-book to everyone's advantage by ensuring all students have access to their notes so that questions can be higher-level, e.g. set questions on content taught across the semester, but relate it to a disease/biological situation that hasn't been explicitly explored. This will rely on students drawing on their knowledge to link the content, while still being able to search for definitions etc. where needed.
- Less is more: Reduce the number of separate documents/images required to upload, or if possible, keep it all in one quiz, so that there's less that can go wrong technically.

Taku – In my ideal online examination, there would be:

- Continual 'case-study' style questions that are built upon each other.
- A small section of multiple-choice questions on a broad range of topics that require deductive reasoning as compared to recall capability.
- Problem solving questions that centre around the ability of students to properly apply theory, in addition to extended response questions where students can

demonstrate their knowledge on mechanisms that underpin the development of disease.
- No 'drag and drop' style questions as they can often get messy and make the exam harder to navigate.

Online exams should be open-book. Students will almost always find a way to cheat so if the exam is open-book then all students are on the same playing field. The more points of control you add in an exam the more points of possible failure you add, with an increased likelihood of collusion. Instead of exam questions being taken directly from lecture content examples, they could be based on fictional diseases or applications to ensure that 'googling' the answer isn't an option. Alternatively, students could be assigned different case studies to help reduce collusion.

Finally, instead of assessing a whole semester in the final exam, there would be a mid-semester exam on topics covered in the earlier half of semester, with the final examination involving questions that pertain directly to the overall learning outcomes of the subject (in the format described above).

Eleanor – In an ideal world, it would be good to have an exam in two parts (similar to the two forms of learning/processing papers that many Physical Sciences departments run):
- Part 1, closed-book exam with questions on content recall. This could be a proctored exam as long as there is transparency about the technology. While I understand why academics have moved away from recall questions, the reality is that to be a successful student you still need to know many specific details/terms and there simply isn't time in an exam to look everything up.
- Part 2, open-book exam with authentic application-style questions. This could include scenario-based or data interpretation questions. Importantly, sufficient time would be provided to answer these types of questions, thereby emphasising the importance of the care and consideration required to craft a well written response; something that is hard to achieve when you have unrealistic time pressures.

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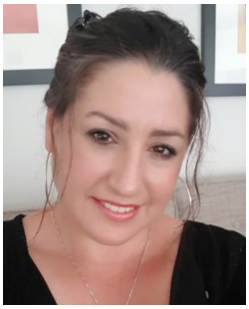
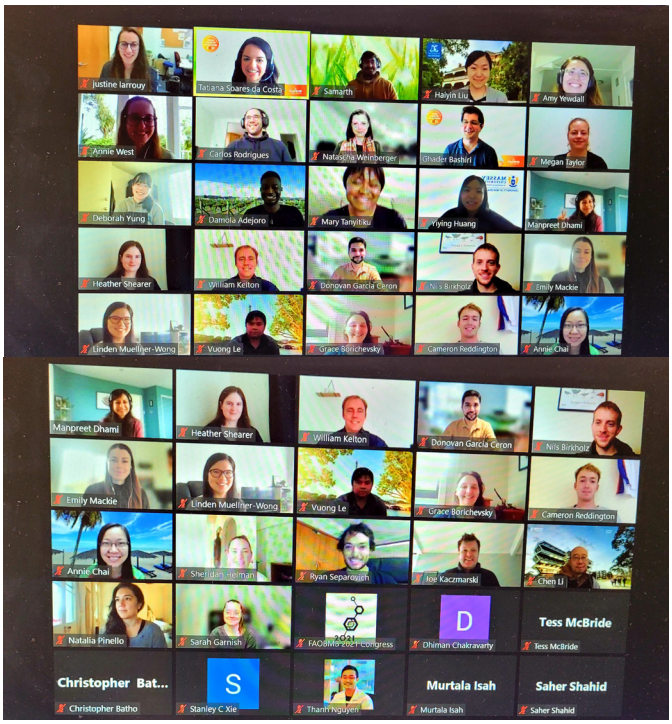


2021 FAOBMB Young Scientist Programme

The COVID-19 pandemic has completely changed the world and the way we live. The FAOBMB Young Scientist Programme (YSP) 2021 was scheduled to take place in the beautiful South Island of New Zealand from 19–21 November, prior to the 16th FAOBMB Congress. Unfortunately, as with most other events since the pandemic began, the YSP had to be held virtually. In spite of the challenges, the YSP organisers, especially the Chairs, Tatiana Soares da Costa and Ghader Bashiri, successfully made the event as interesting and engaging as in-person meetings. Over 50 young scientists participated in the YSP, including attendees from Asia, Africa and Europe, despite different time zones. I attended the YSP as a recipient of one of the two 2021 FAOBMB Young Scientist Awards.



YSP participants on Zoom.

Following the welcome address by the Chairs, the first invited speaker was Peter Mace, an Associate Professor at the University of Otago. Peter shared his inspiring journey from a PhD student at Otago, followed by two postdoctoral fellowships in the US and eventually became a lab head back at Otago. In addition to an example of a successful academic career, the organisers also invited scientists who pursued careers outside academic research. Michael Baker is the current CEO of an ASX listed company, Arovella Therapeutics. Michael completed an MBA after his PhD degree and a few years of postdoctoral research. The biggest lesson from his experience is "never stop learning." The skills we acquired from a PhD degree are also useful for non-academic careers. Krish Jayatilleke started to work as a clinical research associate immediately after completing his PhD. He coordinates a number of clinical trials across Australia. Their stories were insightful for those interested in pursuing alternative career paths.

There were five YSP sessions that covered a wide range of research topics, including molecular and structural biology, microbiology, immunology, plant biochemistry, drug discovery and computational biology. Every attendee was given a chance to present their work and share new ideas. The extensive discussion after each session by fellow young scientists clearly demonstrated the interest and enthusiasm we had for each other's work.

The event provided a great platform for exchanging scientific experiences, which might lead to fruitful collaborations in the future. This is particularly important given the networking opportunities we have lost because of the pandemic. I even got to know colleagues who work in the same building as me for the first time through the YSP. What strange times we live in! Workshops on science communication and interview preparation were certainly the highlights of the event. As young scientists, we often have difficulties in conveying scientific concepts to the general public. The workshops showed us to the keys to reach broader audiences.

The YSP provided a precious opportunity for us to keep connected with colleagues. Workshops and talks from the guest speakers are immensely helpful for us to identify and build our career paths. I would undoubtedly recommend this programme to students and early career scientists.

Stanley Cheng Xie, Bio21 Molecular Science and Biotechnology Institute, University of Melbourne

Australian 2021 YSP Awardees

Naveen Vankadari (Monash University), Sarah Garnish (WEHI), Haiyin Liu (University of Melbourne), Pramod Subedi (La Trobe University), Natalia Pinello (University of Sydney), Joe Kaczmarski (Australian National University), Laura Ciacchi (Monash University), Jia Jia Lim (Monash University), Jennifer Payne (Monash University), Linden Muellner Wong (University of Melbourne), Carlos Rodrigues (University of Melbourne), Donovan Garcia (La Trobe University), Emily Mackie (La Trobe University), Christopher Batho (QIMR Berghofer Medical Research Institute), Sheridan Helman (QIMR Berghofer Medical Research Institute), Natascha Weinberger (Western Sydney University), Chen Li (Monash University), Thanh Nguyen (Monash University), Fuyi Li (University of Melbourne), Praveena Thirunavukkarasu (Monash University), Ryan Separovich (UNSW)

16th FAOBMB Congress

Terrence Piva reports on the fully online FAOBMB Congress hosted in Christchurch, New Zealand and the virtual FAOBMB Council meeting.

As a result of the COVID-19 pandemic, the 16th FAOBMB Congress was held online. This Congress incorporated the annual meetings of the New Zealand Society for Biochemistry and Molecular Biology (NZSBMB), Australian Society for Biochemistry and Molecular Biology (ASBMB), New Zealand Microbiological Society (NZMS) and New Zealand Society of Plant Biologists (NZSPB). Initially, this meeting was scheduled to be held from 22–25 November 2021 in Christchurch, New Zealand, as a face-to-face meeting, but due to travel restrictions imposed by the New Zealand Government, it was scheduled in mid-2021 to be a hybrid meeting with New Zealand residents in attendance and all other participants online. However, a COVID outbreak in Auckland resulted in internal travel restrictions in New Zealand and a decision was made in October to hold the Congress as a fully online meeting. Sincere thanks must be given to the Local Organising Committee chaired by Wayne Patrick (NZSBMB) along with the Professional Conference Organisers, Arna Wahl Davies and Nerida Ramsay from Composition Limited, for running this Congress online so efficiently. In conjunction with the FAOBMB Congress, the Young Scientist Programme was held online from 19–21 November 2021 (see report on page 20).

The theme of the meeting was Molecules, Life, Diversity. The Congress was very successful and attracted over 740 delegates as well as 58 sponsors/exhibitors from 28 countries. The Congress web portal allowed registrants to view all sessions in real time, as well as move easily between the online presentations. Registrants were also able to view posters and meet the presenters online in the relevant time slots, meet the exhibitors as well as be part of the online welcome reception on Day 1. The Congress ran extremely well in the online format for presenters and participants.

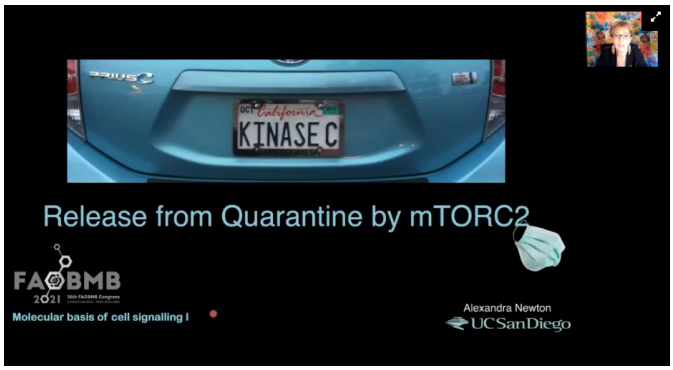
The Local Organising Committee assembled an excellent program of 15 plenary and nine award lectures, and three Education Symposia. There were a further 50 symposia sessions covering broad aspects of molecular sciences including cell signalling, proteomics, microbiology, immunology, bioinformatics, cell biology, plant biology, virology, metabolism and enzymes. These sessions were populated by 57 invited speakers (including various award winners) and 195 speakers who were selected from abstracts. There were 300 posters delivered online at different times during the day. There were five to six concurrent sessions held in the mornings, while 11 to 12 sessions ran in the afternoons of the meeting. The first day of the Congress concluded with the online welcome reception and a poster session.

Congress Chair, Wayne Patrick.

Registrants were able to switch online rooms to view the presentations, which apart from the Plenary lectures were pre-recorded before the Congress. Presentations given by the Plenary lecturers were delivered live online. Registrants can access the presentations online for 30 days after the Congress.

There were five Australian plenary speakers: Ricky Johnstone (2021 FAOBMB Award for Research Excellence), Paul Young (Takashi Murachi Memorial Lecture), Merlin Crossley (ASBMB Lemberg Medal Lecture), Adrian Davin and Victoria Korolik.

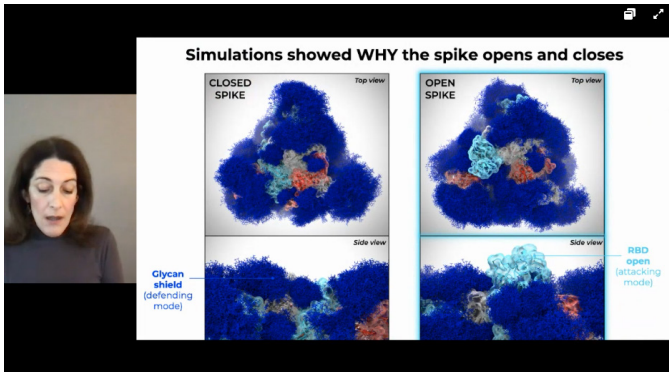
Following the Opening Ceremony, including the welcome delivered by Wayne Patrick (Congress Chair) and Akira Kikuchi (President FAOBMB), Julia Horsfield (NZSBMB Award for Research Excellence winner) delivered the Jisnuson Svasti Lecture. Her talk was on the effect cohesin mutations have on cell signalling pathways in cancer cells. Her talk set



Alexandra Newton's symposium talk on PKC.

the scene as a great start to the online meeting. Immediately following this lecture, the first of the nine parallel sessions were run. We were treated to a great presentation from the IUBMB President, Alexandra Newton (USA), on protein kinase C (PKC) in the first of the cell signalling sessions. Newton detailed the interactions between mTORC2 and PKC and how the former assists in activating the latter. This talk generated much interest from the audience and was one of the standout presentations at the Congress.

Both the 2020 and 2021 winners of the FAOBMB Awards for Research Excellence, Masayuki Yamamoto (Japan) and Ricky Johnstone, delivered their award lectures. The FAOBMB Award for Research Excellence is given annually to a distinguished biochemist or molecular biologist for work carried out in the FAOBMB region. Yamamoto's presentation was held over from the cancelled 28th FAOBMB Conference in 2020. He spoke about the interaction between KEAP1 and NRF2 and the role they play in the cell's response to environmental stressors. KEAP1 acts a sensor for external stresses while NRF2 is a transcription factor, which plays a key role in the induction of cellular defence enzymes. Johnstone's presentation was delivered on the last day of the Congress. His lecture was on the role played by the transcriptional CDKs (CDK7-9,11–13) in driving POLII transcription in cancer cells, and how the disruption of which can be used as therapeutic strategies to treat certain cancers. These lectures were amongst the highlights of the Congress.



Rommie Amaro delivered the Kunio Yagi Lecture.

Paul Gleeson chaired the FAOBMB Awards session, which included presentations by the 2021 Young Scientist Award winners Sakowan Kuhadomlarp (Thailand) and Stanley Cheng Xie (Australia), as well as this year's Ramachandran Lecture by Valakunja Nagaraja (India). Kuhadomlarp spoke about the development of glycomimetics inhibitors to prevent binding of *P. aeruginosa* to host cells via LecA lectins. Xie spoke of his work of identifying amino-amide boronates that target proteasome active sites and how these studies have assisted in furthering our understanding of the proteasomal system of *P. falciparum* and in the design of specific inhibitors thereof. Nagaraja discussed the effect epigenetic changes, as well as modifying the topology of the genome, had on mycobacterial survival.

Ricky Johnstone was presented the FAOBMB Award for Research Excellence 2021 by Paul Gleeson (in Melbourne).

Masayuki Yamamoto (in Sendai, Japan) was virtually presented the Award for Research Excellence 2020 by FAOBMB President, Akira Kikuchi, as part of an online meeting of the Japanese Biochemical Society.

The most outstanding Plenary was the Kunio Yagi Lecture delivered by Rommie Amaro (USA), which was on computational microscopy studies of the interaction of the COVID-19 spike protein binding to the cell membrane and the protection afforded by its glycan shield. The videos shown in this presentation depicted the movement of the glycan shield that helps make the spike protein virtually invisible to the

Stanley Cheng Xie was presented the FAOBMB Young Scientist Award (Male) 2021 by Paul Gleeson (in Melbourne).

Sakhon Kuhaudomlarp was presented the FAOBMB Young Scientist Award (Female) 2021 by Jisnuson Svasti (in Bangkok, Thailand).

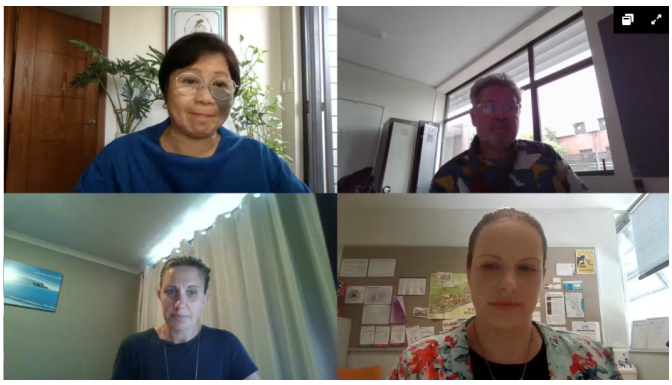
immune system until it is exposed to bind the target ACE2 receptor. Other glycans play a crucial role in the binding of the spike protein to the cell surface. The last part of the lecture covered studies under way on how COVID viruses are able to survive in aerosols encased in lung fluid, a key aspect of their transmission between humans.

This year there were three FAOBMB Education Symposia all chaired by Sarah Kessans (NZSBMB), which were devoted to the use of virtual reality (VR) in education. The first two sessions looked at using VR to help teach undergraduates about proteomics and to school students about forest pathogens. The third session dealt with VR more broadly in teaching, and examined different aspects of online teaching to enhance laboratory skills. The sessions generated questions from the virtual audience on how these technologies can be used to help students learn aspects of biochemistry online. Gareth Denyer (Australia), in his two talks, was one of the most inspiring educational presenters.

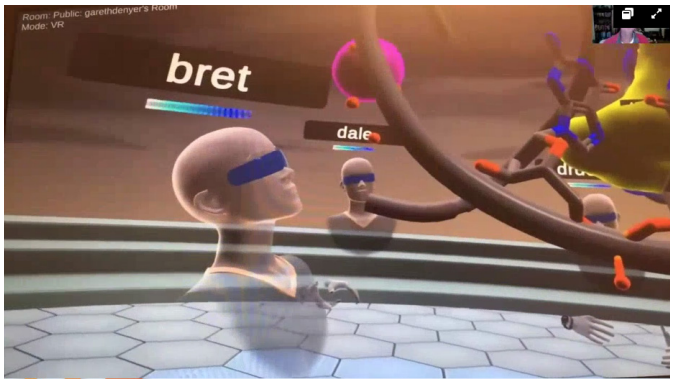
Merlin Crossley's ASBMB Lemberg Medal lecture was on the transcriptional regulation of globin genes, in particular, the use of CRISPR to edit gene sequences, which could help in overcoming a number of erythrocyte disorders. This was a thought-provoking lecture and very well delivered. Other ASBMB awardees delivered lectures at the Congress: Erinna Lee (Shimadzu Research Medal), Lois Balmer (SDR Scientific Education Award), Antonio Calabrese (Boomerang Award) and Lahiru Gangoda (Eppendorf Edman ECR Award).

Paul Young gave the Takashi Murachi Memorial Lecture on the delivery of vaccines using a high-density microarray patch, to replace the conventional use of syringes. He detailed how the patches are constructed and demonstrated their effectiveness in eliciting immunity at the dermal layer. The last part of his talk was on his team's new vaccine, Hexapro, which contains the SARS-Cov-2 spike protein. The ongoing lab trials have yielded very positive results.

A number of microbiological plenary talks were delivered at the Congress, including: microbial evolution (Adrian Davin), microbial ecosystems on plant leaves (Stephen Lindow, USA, FAOBMB Lecture), overcoming microbiological contamination of foods (Steve Flint NZMS Orator Lecture) and inducing bacteria to fix atmospheric carbon (Ron Milo, Israel). Other plenary talks were on chromatin organisation during the cell cycle (Gerd Blobel, USA), use of



The third Education Symposium, chaired by Grace Yu (Philippines; top left), with three of the speakers.



Gareth Denyer spoke about virtual reality in education.

genomics to track the spread of COVID-19 in New Zealand (Jemma Geoghegan, New Zealand), and the role played by chemosensors in *C. jejuni* biology (Victoria Korolik, Australia).

Presentation Prize Winners

FAOBMB Poster Prizes
Annie Wai Yeeng Chai (Malaysia)
Simab Kanwal (Thailand)
Jennifer Jaeun Lee (South Korea)
Junyeop Lee (South Korea)
Madushika Perera (Sri Lanka)

IUBMB Poster Prizes
Markus Brent Arevalo (Philippines)
Dhiman Chakravarty (India)
Afeez Ishola (Taiwan)
Madinat Hassan (Nigeria)
Kai Xin Ooi (Malaysia)

ASBMB Poster Prizes
Christopher Batho
Hudson Coates
Emily Mackie
Catia Pierotti
Pramod Subedi

NZSBMB Poster Prizes
Claudia Allan
Grace Borichevsky
Laura Dillon
Josh Scadden
Heather Shearer

American Society for Microbiology Poster Prizes
Hannah Klaus (New Zealand)
Arrafy Rahman (New Zealand)

NZMS Student Speaker Awards
Mareike Erdmann (first place)
Giselle Wong (second place)
Kelsey McKenzie (third place)

FAOBMB Council meeting

The FAOBMB Council meeting was held via Zoom on 8 November 2021, with Australian participants Terry Piva as the ASBMB delegate, Paul Gleeson as Chair of Fellowships Committee and Phillip Nagley as the FAOBMB Archivist. The meeting was attended by delegates from 19 of the 21 constituent member societies/countries, along with the six members of the Executive Committee. The Council meeting was chaired by the FAOBMB President, Akira Kikuchi (Japan) and the Secretary-General, Sheila Nathan (Malaysia). In his President's report, Kikuchi discussed the effect COVID-19 has had on FAOBMB's activities, especially the cancellation of the 2020 FAOBMB Conference in Colombo, Sri Lanka. He thanked the organisers for the 2021 Congress. He also mentioned: the role FAOBMB may play in the region in the post-COVID era; strengthening FAOBMB's interactions with IUBMB; and the role that biochemistry and molecular biology should play in overcoming issues that affect our region. The FAOBMB President Elect is Joon Kim (South Korea), who will take office in 2022, and will become President from 2023–2025. Elections held in 2020 had led to three Executive members extending their terms of office from 2021–2023: Sheila Nathan (Secretary-General), Grace Yu (Education Chair) and Paul Gleeson (Fellowship Chair).

FAOBMB President, Akira Kikuchi.

Reports on the previous FAOBMB Council Meeting (August 2020) and the FAOBMB Executive Committee Meeting (June 2021) were tabled. There were discussions on the Council's finances, as well as reports from the Education Committee, Fellowships Committee, IUBMB matters, as well as discussions on the FAOBMB Awards. Reports were also tabled for the 16th FAOBMB Congress (2021), 29th FAOBMB Conference in Shenzhen (2022), 17th FAOBMB–26th IUBMB Congress in Melbourne (2024) and 30th FAOBMB Conference in Bangkok (2023). There were two bids from South Korea and Hong Kong to host the 31st FAOBMB Conference in 2025. Following a vote, Busan, South Korea, was chosen as the venue for this meeting, hosted by KSBMB. Extensive revision of the FAOBMB's Standing Orders were agreed to by the delegates, specifically concerning Congresses and Conferences, and Fellowships.

The next FAOBMB Conference will be held in Shenzhen, China from 19–22 October 2022. This Conference will celebrate the 50th anniversary of the foundation of FAOBMB. Everyone hopes that this will be a face-to-face meeting, but contingencies will be in place for online options.

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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 Protein Biochemistry to Reviewing Public Policy

Sarah Atkinson, Assistant Director, Industry, Innovation and Science Agency Advice Unit, Department of Finance, Australian Government

I loved science and maths at high school. I loved learning new things and solving problems by pulling them apart. That enthusiasm carried me through a Bachelor of Science, Honours and a PhD in protein biochemistry that I completed at the University of Melbourne in 2013 with Associate Professor Matt Perugini and Professor Ren Dobson.

As I approached the end of my PhD, I wasn't really sure what to do next. Running my own academic research lab didn't feel right for me, but I didn't really know what my other options were. Everyone around me encouraged me to stay in academia and do a postdoc, and I enjoyed being at the bench, so I took what I thought would be a 12-month position with Dr Natalie Borg at Monash University in 2012. I'd learn some new skills, recover from being a poor PhD student and work out what to do next.

Over the next eight years, a pattern developed where I would approach the end of my postdoc funding, begin to consider what my move out of academia might look like and then receive more funding and decide to stay for "just a bit longer". This approach took me though a six-month contract extension (2013), an NHRMC Early Career Fellowship (2014–2017), a Monash University Faculty of Medicine Senior Postdoctoral Fellowship (2018) and an ARC DECRA (2019–2020).

There were no epiphanies on what my next career move should be during that time, but what I was able to work out was what I enjoyed doing and what I needed to feel satisfied and fulfilled. That moment of seeing a new protein structure for the first time was actually about solving a problem – hard work leading to an answer. The enjoyment I got from optimising a protocol was about making something better – more efficient, more suited for its purpose.

I started to see policy work as an option because it had those features: understanding a problem, planning a solution and making something better. When I heard about the Science Policy Fellowship (SPF) program, a 12-month program run by the Office of the Chief Scientist to give researchers experience in policy development and engagement, it felt perfect for me. I reached out to a couple of past fellows online and at Science meets Parliament in 2019, and decided I wanted to apply.

Sarah Atkinson

Choosing to leave my DECRA was a difficult decision. But I was lucky my boss and other colleagues were so supportive. It felt, for the first time, that I was making a proactive decision about my career. Finding out I had been accepted into the SPF was just as exciting as those positive NHMRC and ARC Fellowship emails.

The SPF placed me in the Department of Finance, which doesn't sound like a natural fit for a biochemist. But I love the work that I'm doing. I've been a Budget and Policy Officer in the Industry, Innovation and Science Agency Advice Unit for 12 months now. We provide policy and financial advice on a range of programs within the Industry, Science, and Resources portfolios. On any given day, I might be writing a Ministerial Brief, assessing the costs for a proposed government program, drafting a Budget measure or discussing a new policy proposal with colleagues at the Department of Industry, Science, Energy and Resources, or the Departments of Prime Minister and Cabinet or Treasury.

I don't think about biochemistry a lot these days, but a lot of the skills I developed have been invaluable in my new role. Multitasking, learning new things quickly and the resilience to keep moving when work changes at the last minute are vital in the fast-paced lead up to policy proposals being considered by government. Scientific writing skills are very similar to the work we do summarising complex information for government briefing. Mentoring junior staff is very similar to supervising a student. I don't expect to ever solve a crystal structure or purify a protein again, but I apply a scientific approach to everything I do.

Off the Beaten Track

I like that my role is dynamic and fast paced. I am constantly learning about new policy issues. The work we do contributes to government decisions and policies, and it's satisfying to see the impact. It has been an adjustment being a cog in a much larger machine, where government priorities decide the work I do rather than what I feel like doing on any given day. My step count has also drastically decreased now I'm not moving around a lab all day!

After my year as a Science Policy Fellow, I secured an ongoing role in the Department of Finance and was recently promoted within my team. The public service offers a lot of opportunities to expand your skills and responsibilities. It feels like a meritocracy where people are rewarded for being good at what they do. The SPF is a great way to get a taste for what a career in policy is like. But it is not the only entry into a career in the public service for a scientist. The APS Jobs website has jobs advertised all the time and most government departments have graduate programs for recent graduates.

I think the utility of a PhD is viewed far too narrowly in academia. We become specialists in a particular research area, but the skills and approach we develop along the way are highly valued everywhere – we just need to get better at seeing those skills in ourselves and at telling others that we have them.

SDS Page: Short Discussions for Students Page

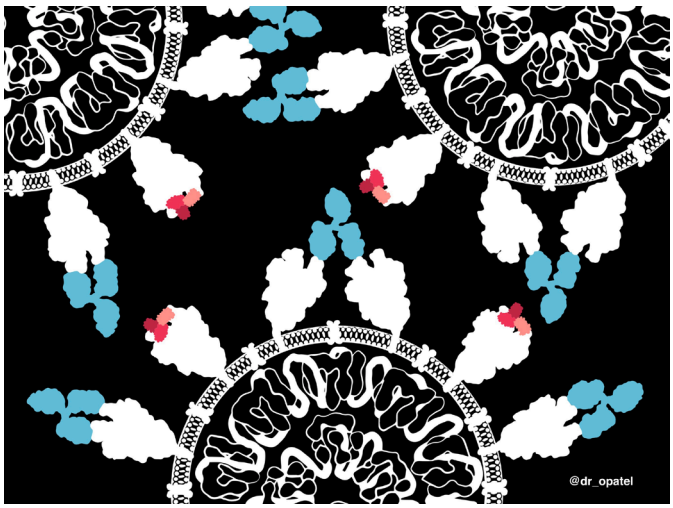
How Art Helps Bring Science Closer to Community

Onisha Patel, Walter and Eliza Hall Institute of Medical Research

I am a scientist who also likes to escape into the world of arts when time permits. Over the years, I have used visual art for science communication, engagement, education and outreach. From creating scientifically accurate illustrations to more abstract illustrations using scientific data, I like being creative in my approaches. I have exhibited my work at the Art of Science exhibitions, public art galleries, outreach events at schools and community events. My interactions with artists, teachers, students and people who visit the exhibitions have taught me a few things that I keep in mind as I refine my SciArt practice (integrating science and art) practice.

Art helps to simplify the message

We have all heard that a picture is worth a thousand words. I will reiterate this point, especially when creating visuals for a lay audience. The message must be clear and understandable. Last year I participated in #CellSpace, a virtual event by David Goodsell, a scientist and an artist, and a personal role model for creating art to communicate about Covid-related research. A lot of research was being published at the time, including in preprints on how the SARS-CoV-2 virus looks structurally, how it gains entry to the cell, and how it was spreading. Our goal was to go through this information and create art to communicate about Covid-related research for community exhibitions. Given my interest in drug discovery, I summarised the research from David Baker's group (Institute of Protein Design) on the *de novo* design of synthetic small viral proteins (minibinders) against SARS-CoV-2 with a piece of art. Read more about this work here. I kept the background and the SARS-CoV-2 virus in black and white to highlight the key message on differences between minibinders and antibodies. The size of the virus, spike proteins, antibodies and minibinders are relative to each other and based on structural information.



Onisha's artwork depicts the contrast between minibinders (small antiviral proteins in shades of red) and antibodies (blue) that bind to the spike proteins on the surface of the SARS-CoV-2 virus.

SDS Page: Short Discussions for Students Page

Onisha's Vaxxed t-shirt design.

First impressions matter

Humans are visual creatures, and first impressions matter. Some people are attracted to colours, composition, light and dark elements, focal point, technique, medium, underlying meaning (if there is one) and much more. All of these can be very subjective, of course. Like science, art involves a lot of trial and error, from the initial idea to the final image. I was keen to promote vaccination messages creatively that would welcome a conversation out of curiosity and 'first impression'. My 'Vaxxed' design on a t-shirt (available on the Redbubble-search for dropatel) is a conversation starter about my own vaccination experiences, especially with those who are hesitant to be vaccinated. This design was also selected for the 'Creative Resilience' exhibition which is part of the UNESCO's 75th Anniversary exhibition, 'Transformation'. The exhibition will be on display at the UNESCO Headquarters in Paris in November 2021 and at the Dubai World Expo in 2022.

Building community connections through art

I regularly exhibit my SciArt at art galleries or public exhibitions. The conversations that I have with people range from wanting to know about the research, why is it important, underlying story behind the work, my journey as a scientist, why I do art and much more. These conversations have helped me refine how I talk about science and its connection to our lives rather than it being purely information focused. I do feel these conversations have helped me build more compassion and empathy for others. At WEHI, we are lucky to have the annual Art of Science exhibition, which has been going for over 20 years now! This exhibition brings the beauty of medical research out in the real world through art and provides an opportunity for scientists to connect with the community through conversations. You can enjoy the WEHI virtual exhibition here.

STEM engagement

During school visits, I regularly speak about the power of structural biology and how it reveals the molecular world. While I have shown beautiful images of protein structures, I wanted to do something more 'hands on' rather than 'show and tell'. Subsequently, I have collaborated with PDB Europe and Viewbank College (Melbourne) to bring the #PDBArt exhibition to Australia over the last two years. The PDBArt project aims to get students excited about the molecular world of proteins using art as a tool and highlights why understanding protein structures is important. This project has helped students who don't like science engage with science. In addition to learning about proteins, this project has helped students build other skills, including working independently, conducting research, developing ideas, sourcing materials and communications. You can hear more from students and teachers about the #PDBArt project here and a guided tour of the exhibition here.

Dr Onisha Patel is a senior scientist at the Walter and Eliza Hall Institute of Medical Research.
patel.o@wehi.edu.au

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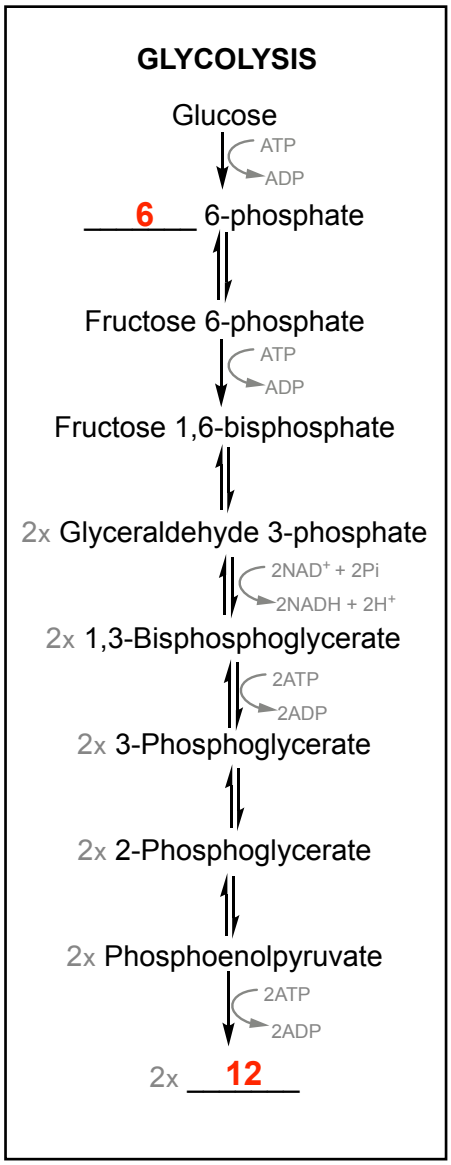
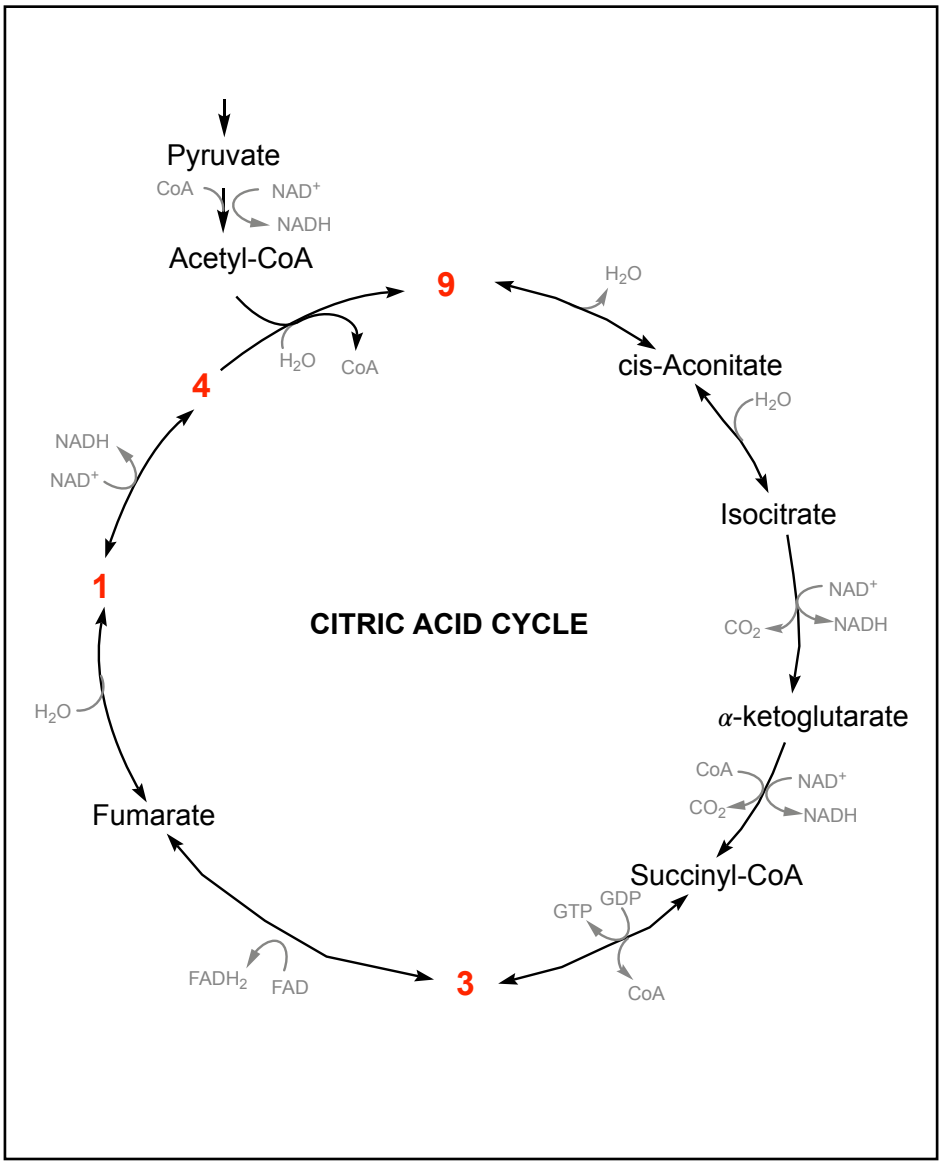
Competition:
The Missing Intermediates

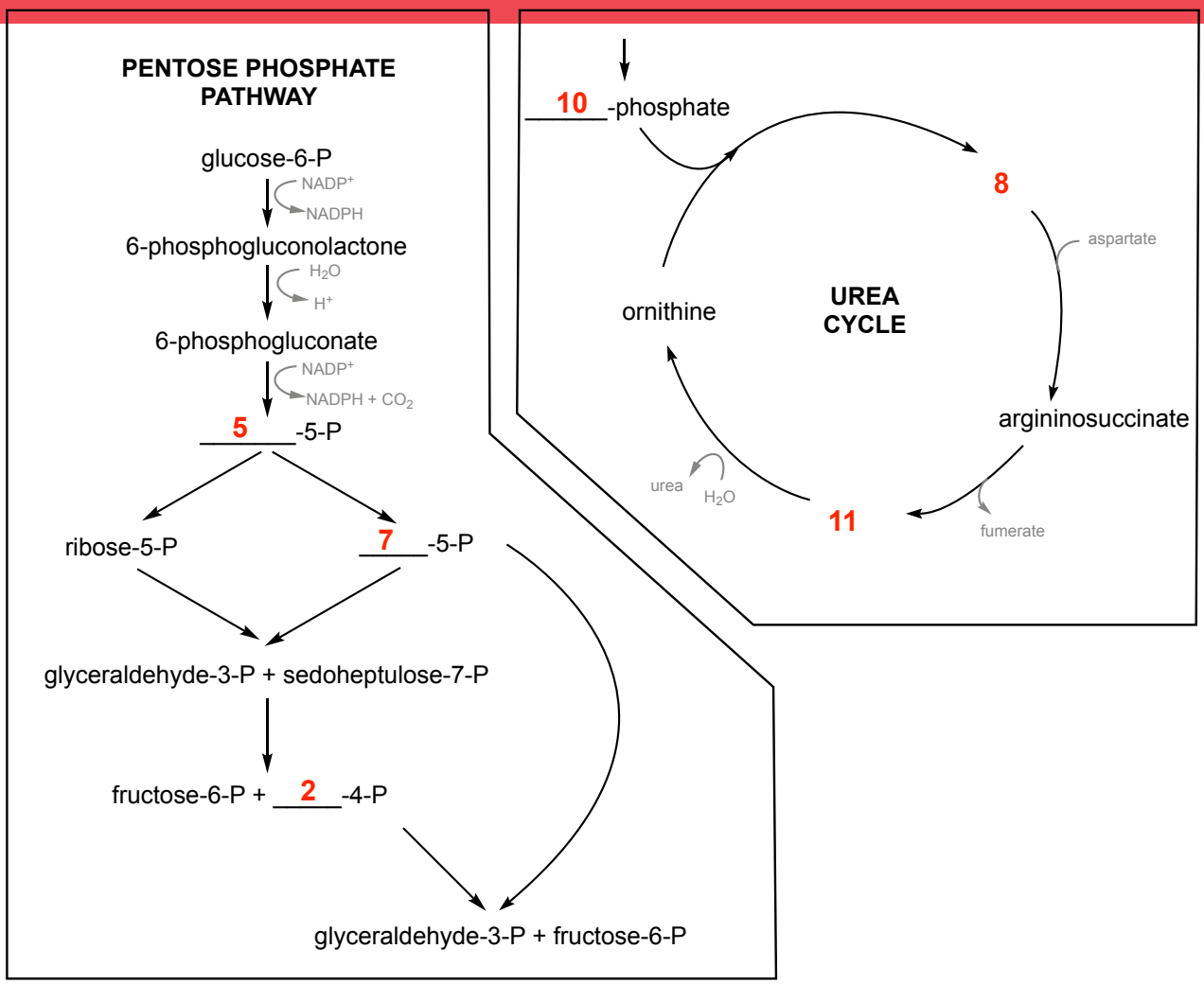
Presenting the latest competition for the members of ASBMB. All correct entries received by the Editor (editor@asbmb.org.au) by 28 January 2022 will enter the draw to receive a voucher. With thanks to Joe Kaczmarski.

The following biochemical pathways are missing some key intermediates (numbered 1–12). Complete the answer key (on the next page) by filling in the missing gaps. The highlighted letters will spell out the answer phrase.

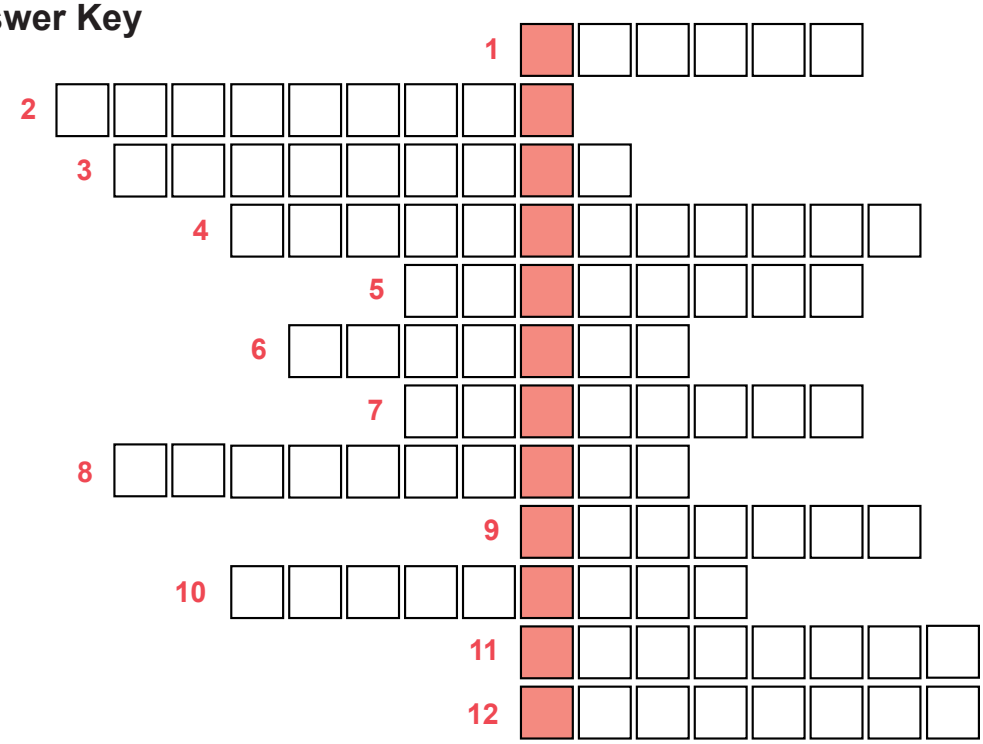




Competition: The Missing Intermediates



Answer Key



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The COVID-19 Patent Landscape

In this issue, Sheila Barbero and Sarah Hennebry from FPA Patent Attorneys analyse the landscape of recent patent filings relating to COVID-19, and discuss some of the implications for researchers seeking to commercialise in this area.

Sheila Barbero (top) and Sarah Hennebry.

Given the impact of the COVID-19 pandemic over the past two years, it comes as no surprise that there has been a tremendous surge in COVID-19 related research. This has resulted in a flood of scientific literature relating to COVID-19 and the development of potential therapies.

The surge in COVID-19 research has also led to a significant increase in patent filings in this area. We thought it would be interesting to take a closer look at the recent trends in COVID-19-related patent filings by conducting a patent landscape search.

In this article, we provide a high-level analysis of a patent landscape search which focuses on coronavirus patent filings over the past five years. We then discuss some considerations for those interested in seeking patent protection or commercialising their research in this area.

The coronavirus patent landscape

To get a snapshot of the current coronavirus patent landscape, we conducted a search for patent documents, in particular PCT applications, published since 2016 relating to human coronavirus.

Unsurprisingly, there has been an upward trend in patent filings since 2020, correlating with the emergence of COVID-19 and the pandemic. About 100 patents per year published over 2016–2020, and this increased to about 200 patent publications in 2020. This year, the number of patent publications has jumped to about 780 to date.

The majority of identified patents relate to the treatment and prevention of coronavirus infection. Modalities are wide ranging and include small molecule drugs, antibodies, RNA technologies, and vaccines including peptide-based, viral vector and DNA-based vaccines. The biological targets are also broad and include the SARS-CoV and/or SARS-CoV-2 spike protein as well as others. The variety of targets is in part because many of the patents identified in the search relate to existing anti-viral technologies that have been 'repurposed' as COVID-19 therapies – a trend that is also happening on the research front.

Other major categories of technology include methods of detecting or diagnosing infection, including nucleic acid detection and protein detection; and medical devices, including protective clothing and ventilation machines.

As shown in the figure, the majority of patent filings originated from the US, followed by Europe, China and other countries in Asia. Patent applicants span all sectors including universities and research institutes, pharmaceutical companies and government institutes.

Nonetheless, a takeaway from this snapshot of the coronavirus patent landscape is that this is clearly a hot area for patent filings – and therefore innovation – and will likely continue to be for some time.

With the surge of coronavirus-related patent filings, you may be wondering how to navigate this increasingly crowded landscape if you are interested to commercialise your research in this field. We discuss some of the implications below.

How does the coronavirus patent landscape affect my ability to get a patent?

The increasing number of patent and non-patent publications relating to COVID-19 means that securing a novel and inventive position in this area is becoming more challenging.

If you are in the early stages of research and are considering patent protection, a **novelty search** (also called a **prior art search**) can help to identify patents relevant to your research that could be potential roadblocks to obtaining a granted patent.

Conducting a novelty search can help to inform a decision about whether investing in patent protection would be worthwhile. For example, if a novelty search identifies a patent describing an invention that is similar or very close to your invention, this could provide an early indication that there may be challenges for you to obtain patent protection of broad or commercially relevant scope. University commercialisation offices will often conduct novelty searches for invention disclosures they receive, or engage a patent attorney to do this.

Landscape searches are also increasingly being used as a way to guide or focus research, particularly for researchers interested to patent their research. For example, landscape searches can be used to identify potential 'vacant' patent space. This can help to guide how you prioritise what to investigate next.

When analysing novelty and landscape searches, it is important to remember that the standard of science that goes into patent applications is not necessarily the same as a peer review articles, and disclosures in patent specifications can be speculative. Nonetheless, any disclosure in a patent specification, including a speculative one, could potentially be relevant to the novelty and inventiveness of your invention. For example, if a patent specification describes a hypothesis or proposes a

mechanism that is key to how your invention works, that disclosure could make it difficult for you to achieve grant of a broad claim for your invention.

What impact does the coronavirus patent landscape have on my freedom to operate?

Those who are closer to product launch should consider conducting a **freedom to operate (FTO) search** (also called an **infringement search** or **clearance search**).

As discussed in our previous article, FTO searches involve identifying pending and granted patents relevant to your product in each country where you are planning to 'use' the product (for example, where you are planning to manufacture, import or sell the product) and determining whether or not a third party's rights may be infringed by your commercial activity.

When assessing FTO, it is ultimately the claims of a patent that will determine the legal monopoly of the patent applicant. Therefore, it is important to consider what the scope of the granted claims will be, and whether there is enough supporting data in the patent specification to ensure the granted claims are valid. This is different from assessing novelty, in which the entire disclosure of a patent specification is considered, and any statement made in that specification could potentially destroy the novelty of a claim.

In order for a patent to be granted, the patent application must not only claim an invention that is new and inventive, but also include sufficient information for someone to be able to perform the invention and provide a reasonable expectation that the claimed invention will work. The latter are referred to as 'enablement' and 'support' requirements, which we have discussed in an earlier article.

Given the urgent need for therapies to combat the COVID-19 pandemic, it is likely that some patent filings were rushed and the patent specifications may not contain sufficient data demonstrating the treatment of coronavirus infection. For example, some patent specifications may only contain preliminary data for a disease model that may not be directly relevant to COVID-19 or coronavirus infection. In these cases, patent applicants may find it challenging to convince patent examiners that enablement and support requirements have been met for their patent applications. This could mean that the patent applicants may not be able to obtain patent protection for the broadest positions disclosed in their patent application, but may only be able to obtain limited protection based on what is supported and enabled – or may not be able to achieve grant of their patent applications at all.

Therefore, even though there has been a flux of patent applications filed in this area, it is likely that not all of these patent applications will be granted, and the scope of any granted patents may be narrower than the broadest position described in the patent specification.

Take home messages

- There has been a recent surge in publications relating to COVID-19, including patent publications, and this is likely to continue for the next few years.
- For those interested in seeking patent protection in this area, the increasing number of publications means it is becoming more difficult to secure a novel and inventive position; conducting a novelty or landscape search can help you to identify potential roadblocks to obtaining a granted patent.
- For those considering FTO, it is important to remember that the entire disclosure of a patent specification does not necessarily dictate FTO, because the claim scope that is ultimately granted may be narrow or not granted at all.

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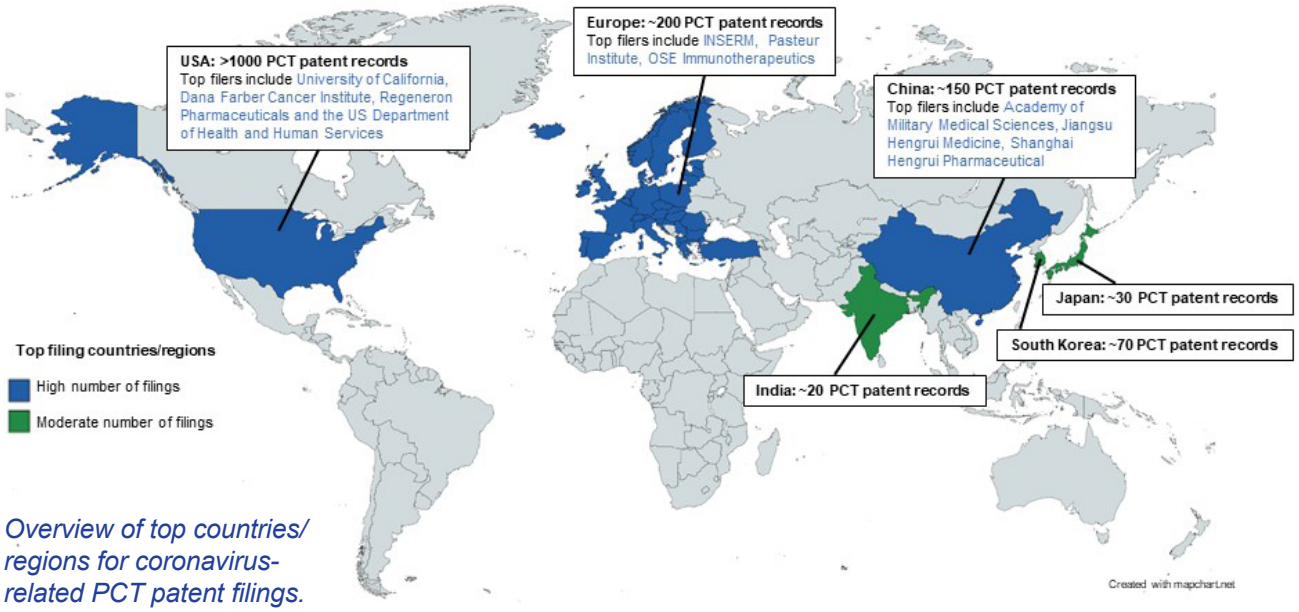


Overview of top countries/ regions for coronavirus-related PCT patent filings.

News from the States

Compiled by Melissa Pitman

Australian Capital Territory

Contributed by Christina Spry

The Canberra Protein Group, which brings together researchers from across the ANU campus and CSIRO, resumed face-to-face meetings in February 2021. The first meeting and those held subsequently were well attended with more than 50 participants per meeting and showcased the protein work of students and postdocs. Unfortunately, face-to-face meetings were put on hold once Canberra went into lockdown in August, but the group looks forward to when events can recommence.

The winner of the Canberra Protein Group logo competition was recently announced. Congratulations to Joe Kaczmarski (Research School of Chemistry, ANU) for his winning design.

The Australian Biochemistry Lunch Seminar Series, initiated by Thomas Huber (Research School of Chemistry, ANU) in 2020, continued in 2021, now coordinated by the Canberra Protein Group. The seminar series, which is held weekly on Mondays at noon, has seen leading biochemists from across the country share their work on Zoom with an audience of researchers also spanning Australia. This series has enabled Australian biochemists to stay connected throughout the extended lockdowns, and with a minimal carbon footprint. A list of past speakers, recordings of past presentations and the schedule can be accessed here. To join upcoming meetings, simply follow this Zoom link.

In the last 12 months, the Centre for Advanced Microscopy (CAM, ANU) have established an NCRIS-supported cryo-EM suite featuring two high-end transmission electron microscopes for screening and automated data analysis of frozen samples for single particle analysis, MicroED and tomography (JEOL JEMF200 and JEOL 200kV CryoARM) and a ZEISS Crossbeam 550 FIB-SEM. The latter comprises a Leica cryo stage and transfer system which facilitates cryo block face imaging, as well as the production of on-grid and lift-out TEM lamella for viewing in the JEOL 200kV CryoARM. For a correlative workflow, additional upgrades include a new Linkham Scientific cryo stage (CMS196) for the ZEISS LSM800 with Airyscan and ZEISS Atlas 5 and ZEN Connect software, which facilitate an enhanced workflow for correlative cryo-light microscopy and tomography/3D cryo volume imaging.

In 2020, the ANU ASBMB Prize, awarded to the ANU undergraduate student who achieves the two highest average marks in three of four courses with a Biochemistry and/or Molecular Biology focus, was awarded to Callie Madeline Spooner. Congratulations Callie!

New South Wales

Contributed by Laura Sharpe

2021 has been another pandemic year, with several months spent in lockdown town for NSW. However, I am pleased to report on the awards that were sponsored by ASBMB NSW in this challenging year. We continue to reward our excellent undergraduate students and high school students across NSW.

The Charles Sturt University – ASBMB Biochemistry Prize ($300) was awarded to Paviska Sivashanmugarajah earlier in the year when in person award ceremonies were possible! Congratulations to Paviska.

Charles Sturt University ASBMB Biochemistry Prize awardee, Paviska Sivashanmugarajah, with Associate Professor Linda Deravin, Head, School of Nursing, Paramedicine and Healthcare Sciences.

The University of Newcastle – ASBMB Prize for Biomedical Science ($300) was presented to the student with the best overall performance in the Bachelor of Biomedical Science program, and this year was awarded to Sophie Lewis. Congratulations to Sophie and we wish her all the best in her future career goals as a forensic pathologist!

University of Newcastle ASBMB Prize for Biomedical Science awardee, Sophie Lewis.

ASBMB NSW has been sponsoring the NSW Science Teachers Association Young Scientist Awards ($300) award for several years. The ASBMB Award is given for the best high school student project with a biochemistry or molecular biology theme. Our

News from the States

involvement in schemes like this helps to encourage our future scientific stars and ignite their passion for research, which is particularly important during another year in which there have been limited opportunities for high school students.

Queensland

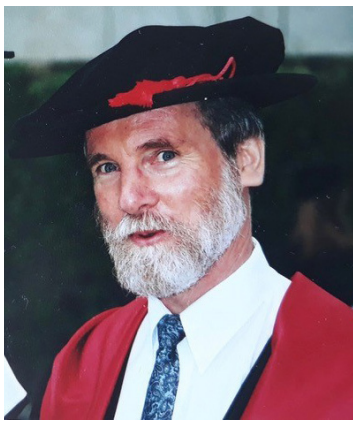
Contributed by Michael Landsberg

After a relatively quiet 2020, biochemists around Queensland are gearing up for a return to 'COVID-normal' and have been looking forward to participating in regular activities again. 2021 has been a little bit stop–start, but we hope to build on this momentum as we move into 2022.

The Queensland branch of the ASBMB continues to sponsor prizes for high achievers in undergraduate Biochemistry programs at most universities around Queensland. Award winners announced so far in 2021 are David Salles, who was awarded the ASBMB prize from Griffith University and Ulrik Horn, who was awarded the ASBMB prize for academic excellence in third year Biochemistry. ASBMB Queensland congratulates both David and Ulrik on their achievements and we hope to see you both continue on with careers in biochemistry and as future members of our Society!

ASBMB Queensland also continued its annual sponsorship of the Queensland Science Contest, organised by the Science Teachers Association of Queensland (STAQ). We awarded ASBMB bursaries in six, year level categories from Year 2 all the way through to Year 12 (unfortunately, no entries were submitted in the Prep–Year 1 Division so if any parents out there have budding young scientists in their households, then please keep an eye out for this contest in 2022!). The prize winners were formally recognised at a ceremony to be held in November 2021, and needless to say, the standard of entries was incredibly high and the judging panel was suitably impressed with the enthusiasm for scientific discovery that was clear across the board. Many thanks to Adam Walker (Queensland Brain Institute) and Conan Wang (institute for Molecular Bioscience) for assisting with judging these.

On 17 November, the ASBMB Queensland Branch co-hosted the first annual Ross Smith ECR Award Symposium with the Queensland Protein Group. Many members of the ASBMB will know Ross – an Emeritus Professor at the University of Queensland – from his numerous roles throughout the years within the ASBMB. Perhaps most significantly, Ross played a key role in organising the first ever meeting of what would soon become the Queensland Protein Group in 1987, subsequently serving as its inaugural Chair. Ross continued to enthusiastically support the activities of the QPG and the ASBMB in Queensland over the years that followed, most recently serving as the Queensland State Representative from 2011 to 2014, just prior to his retirement. In recognition of these contributions to the Society, the QPG and ASBMB Queensland established an award in his name that will be awarded annually to an outstanding ECR working in the broad field of protein biochemistry. In addition to presentations from the finalists, the inaugural symposium featured a keynote presentation from Smith Lab alumnus and current Director of the National Biologics Facility, Professor Trent Munro, along with several student talks. The Ross Smith ECR Award (sponsored by ATA Scientific) was awarded to Yu Shang Low, University of Queensland. The winner of the best student presentation was Michael Healy, University of Queensland. The winners were announced by Dr Lisa Smith, who joined us via Zoom from the University of Sheffield.



Professor Ross Smith received a QU award for outstanding research higher degree supervision in 2001.

South Australia

Contributed by Melissa Pitman

This year, the ASBMB SA branch sponsored a number of local events, many of which were lucky enough to be face-to-face.

Annually, we sponsor two events that are focussed on secondary school students: the Oliphant Science Awards and the Cochlear Aurora STEM photo contest. This year we continued to both sponsor and judge these events, that are focussed on supporting and encouraging students to pursue science.

For the Oliphant Science Awards, we awarded a prize for Dinan Perera from Year 12 at Prince Alfred College with a project titled CAR-T Cell Therapy. The judging for the Cochlear Aurora STEM Photo Contest has just commenced and winners will be announced at a ceremony scheduled for December 2021.

At an undergraduate level, the SA state branch sponsored a second-year biochemistry prize at the University of Adelaide. This year, the prize was awarded to Jesse Kennedy for her outstanding efforts in biochemistry and molecular biology courses.

The ASBMB SA branch also sponsored a number of researcher prizes for best publications at both the University of South Australia (Centre for Cancer Biology) and the University of Adelaide. The winners for the best PhD student publications (UniSA) were Julian Carosi (Carosi *et al.*, *Autophagy* 2021;17(9):2217–2237) and Alicia Byrne (Byrne *et al.*, *Journal of Medical Genetics,* 2020;57(7):454–460). The best publication was awarded

News from the States

Second year University of Adelaide ASBMB Biochemistry Prize awardee, Jesse Kennedy.

Professor Stuart Pitson awards Julian Carosi, winner of the 2020 Centre for Cancer Biology Best PhD Student Publication Prize.

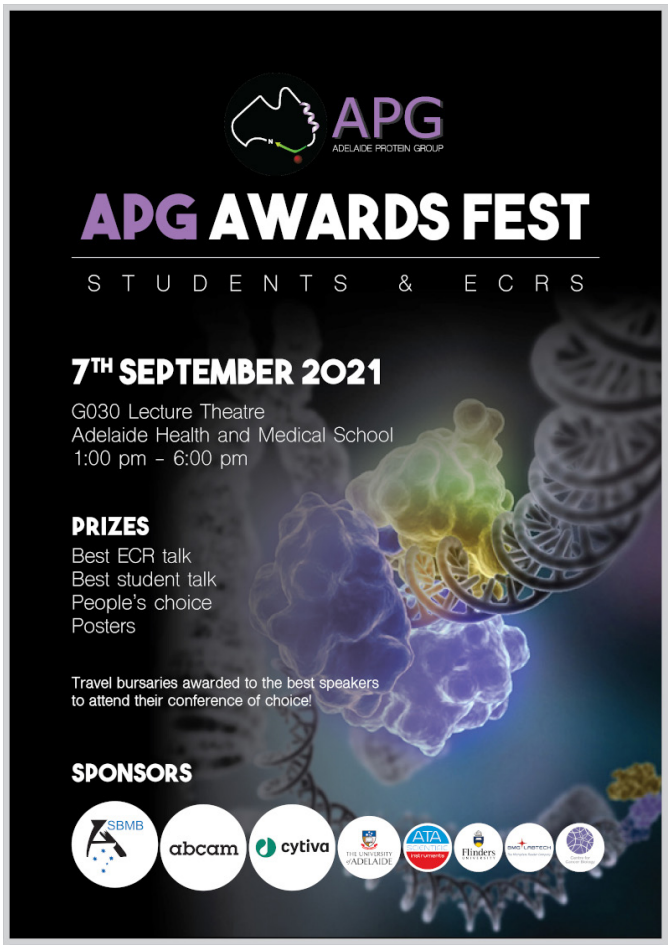
Professor Stuart Pitson awards Alicia Byrne, winner of the 2020 Centre for Cancer Biology Best PhD Student Publication Prize – Clinical.

to Michael Samuel and Marina Kochetkova (Boyle *et al.*, *Nature Cell Biology* 2020:22;882–895). At the School of Biological Sciences at the University of Adelaide, the best Early Career Researcher publication was awarded to Cameron Bastow (Bastow *et al.*, *PNAS* 2021:118(17): e2025763118).

In September, the Adelaide Protein Group ran its first merged Awards Fest event that combined both the student and ECR awards events. This event featured the keynote speaker Professor Trevor Lithgow (Monash University), who was the 2020 ASBMB Lemberg medallist. The newly formatted event was a great success with good attendance and awards for one ECR, two PhD student presentations and two poster prizes, as well as a People's choice award.

In October, the RNA Special Interest Group ran a seminar and networking event with presentations from Professor Robyn Meech and Dr Julie-Ann Hulin from Flinders University and Dr Cameron Bracken from the Centre for Cancer Biology. This event was co-sponsored by the ASBMB SA branch.

We look forward to another year of invigorating events!



Adelaide Protein Group inaugural merged Awards Fest.

Victoria

Contributed by Laura Osellame

The ASBMB Victoria Branch has continued its commitment to a wide range of scientific events for all researchers at all stages of their career in Victoria. Now more than ever before, it is important that we all stay connected, especially students who may have found COVID-19 a very isolating experience. In what has been another challenging year for our state, ASBMB Victoria, has, where possible, continued to sponsor biochemistry and molecular biology events, both hybrid and online.

2021 began brightly with the annual Lorne Conference on Protein Structure and Function. ASBMB Victoria again supported Women in Science through the promotion of bursaries with the aim of helping women with children attend the conference. The 2021 bursary was awarded to Marija Dramicanin (Walter and Eliza Hall Institute). Owing

News from the States

to the ongoing COVID-19 pandemic, the conference was run in a hybrid capacity with a strong online presence and limited in-person attendance, with international speakers presenting online. The 2021 Leach Lecture was presented by Professor Mike Lawrence (WEHI).

In May, the fourth conference on Cell Signalling and its Therapeutic Implications (CSTI) was held as a virtual event. This year's theme was Focus on Cancer. The meeting highlighted outstanding signalling work and its translation into the clinic. Topics ranged from from Cancer Cell Biology to Clinical Translation (session sponsored by ASBMB Victoria). A highlight of the conference was the presentation of Andrew Wilks (SYNthesis Research), the awardee of the 2021 Martin Lackmann Award for Translational Research.

The Melbourne Protein Group Student Symposium was held virtually this year on 15 July. Keynote speakers were Associate Professor Wai-Hong Tham (WEHI), Dr Sarah Gordan (Florey Institute of Neuroscience) and Dr Derek Lacey (Bluestone Yeast). The two Tilley award winners for best oral presentations were Wessel Burger (Monash) and Bronte Johnson (University of Melbourne). This event, sponsored by ASBMB Victoria, was a great success and a wonderful opportunity for the students of Melbourne to get together in lockdown.

The 2021 Science Talent Search was once again moved online in 2021, with Victorian schools operating in home schooling mode. ASBMB bursaries were awarded to the following schools: Melbourne Girls Grammar (Merton and Morris Halls), Serpell Primary School, Sirius College, St Leonard's College, Templestowe Park Primary and Tintern Grammar. The titles of some of the students research projects included: Under which conditions do carrots grow best?, Which commonly used surfaces contain the most bacteria? and Enzymatic browning.

The MPG organising committee working behind the scenes.

RNA Network Australasia: an ASBMB Special Interest Group

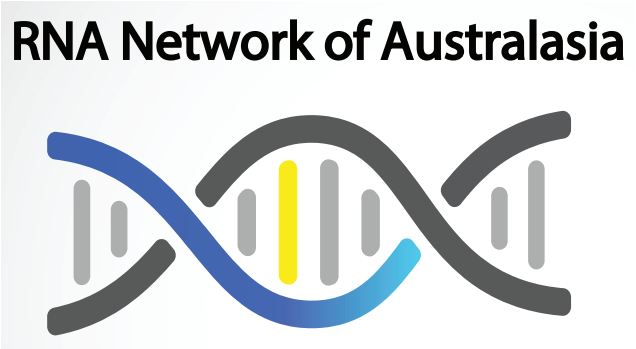
The RNA Network of Australasia was initiated by Thomas Preiss (ANU) in 2008 as the ASBMB's RNA Special Interest Group. The aim of the group is to support Australian and New Zealand RNA-related research and create a network to share ideas around RNA. The current Chair is Archa Fox (UWA) and the State Representatives are Minni Änkö (VIC), Cameron Bracken (SA), Archa Fox (WA), Nigel McMillan (QLD), Gyorgy Hutvagner and Nham Tran (NSW) and Nikolay Shirokikh (ACT). ASBMB funding supports various state-based activities and also pays for an ECR to speak about RNA research at each ComBio conference.

What a time to work on RNA! If there is one silver lining of this pandemic it is that suddenly the world is getting to know about the importance of RNA – as an RNA genome for the virus causing all our problems, and the mRNA vaccines that are a main solution to the crisis. Members of the RNA SIG have been busy using their knowledge of RNA to help the general public understand the mRNA vaccines as well as trying to explain to funders and policymakers the future potential of this area.

One highlight was a national roundtable to identify Australia's RNA science and technology priorities, held on 29 July 2021, which was hosted by the Australian Academy of Science and the newly-formed Australia and New Zealand RNA Production Consortium. A key outcome from the discussions included, "Considering the uniquely Australian problems that stand to be solved by RNA science, including sensing new biosecurity threats, and supporting climate change adaptation in agriculture, the group determined a list of research priorities by balancing Australia's strengths against emerging global trends. These research priorities were highlighted in the National Roundtable Statement and included:

- RNA vaccines, including vaccines for people with autoimmune disorders
- RNA therapeutics
- RNA sensing tools
- The role of RNA in plant and animal development
- The role of RNA in brain function and disorders
- RNA chemistry
- Stability and advanced manufacturing of RNA therapeutics
- RNA delivery technologies

Meanwhile, organisation has been going on for over a year for the first Australian RNA Biology and Biotechnology conference, A-RNA. The event was originally planned for mid-November 2021, in Thredbo, NSW, however given the ongoing COVID-19 lockdowns, the decision was made to postpone the conference to 15–18 May 2022. This conference is being organised by Nikolay Shirokikh (JCSMR, ANU), Rob Weatheritt (Garvan Institute), John Mattick (UNSW), Minni Änkö (Hudson Institute) and Archa Fox (UWA). We have a stellar lineup of speakers who will join by Zoom – Melissa Moore (Moderna), Dan Peer (Tel Aviv University, Israel), V Narry Kim (Seoul National University, South Korea), Yue Wan (Nanyang Technological University, Singapore), Amy Gladfelter (University of North Carolina at Chapel Hill, USA) and Howard Chang (Stanford Univeristy, USA) – and invited speakers from Australia – Sue Fletcher (PYC Therapeutics), Tim Bredy (Queensland Brain Institute), Damian Purcell (University of Melbourne) and Eduardo Eyras (ANU). We are determined for this to be an in-person event.



At the same time, various state-based traditional research gatherings have been continuing, either in virtual or in-person format. Most of these seminar series are also supported by the international RNA Society through the RNA Salon program. Victoria has the Monash University meRNA Club, where monthly speakers from around the country have been speaking in a Zoom seminar series. There are awards and prizes for student presenters. The meRNA convenors are Peter Boag, Minni Änkö, Jacki Heraud Farlow and Fionna Loughlin. The meRNA Club is supported by the RNA Society RNA Salon Initiative, Lexogen and Custom Science. RNA Victoria is another RNA-focussed seminar and symposium series that started in 2021. RNA Victoria highlights RNA-related events and introduces lab heads and senior postdocs working on RNA in Victoria. Contact Minni Änkö if you would like to be added to the website. There is a face-to-face mini-symposium scheduled for 2 December 2021 at Monash University convened by Chen Davidovich, and a second symposium is planned to take place at Peter MacCallum Cancer Centre, convened by Vi Wickramasinghe. Going forward, RNA Victoria will have three to four face-to-face mini-symposia per year across the different research precincts to bring RNA-minded researchers together.

ACT has continued to host The ACT RNA Club. This monthly seminar series is convened by Attila Horvath and co-organised by Nikolay Shirokikh, Jean Wen, Thomas Preiss, Marina Reixachs-Sole, Yoshika Janapala, Anthony Millar and Ming-Bo Wang, and continues from strength to strength. They do a great job of cross-posting different RNA science seminar series nationwide and are always supportive of students, making sure they

RNA Network Australasia: an ASBMB Special Interest Group

are included in sessions with renowned and influential thinkers of the field, such as in the recent meeting with Professor Peter Doherty. The ACT RNA Club serves the community by hosting recordings of its seminars, enlisting the ACT RNA groups and jobs, connecting with the RNA Research and Development Hub at the ANU, and is set to finalise its inaugural round of student talk competition in 2021, honouring winners with awards and prizes.

The Sydney RNA Salon holds monthly seminars, with Rob Weatheritt (Garvan) and Irina Voigneau (UNSW) organising the series. Highlights from the past year have included Yue Wan, a group leader at the genome Institute of Singapore, A*STAR, talking about her work on direct RNA sequencing with nanopore long read technology. South Australia RNA has continued their monthly meetings, sharing the space with the Epigenetics Consortium of South Australia (EpicSA), with whom they alternate seminars each month. This has been driven by two postdocs in Greg Goodall's group, Melodie Migault and Dawei Liu.

All in all, there is lots of great stuff going on in the RNA world at the moment. We appreciate the support of the ASBMB in getting us kick-started as a network.

Archa Fox
Chair, RNA Network of Australasia
Website https://www.asbmb.org.au/special-interest-groups/rna-network-australasia/

FAOBMB Award for Research Excellence 2021

The ASBMB congratulates Professor Ricky Johnstone on being named the winner of the FAOBMB Award for Research Excellence 2021. He presented the FAOBMB Lecture the 16th FAOBMB Congress.

Professor Johnstone completed his BSc (Hons) degree from the University of Melbourne in 1988 with a double major in Pathology and Immunology. In 1993, he completed his PhD at the Austin Research Institute. In 1994, he was awarded a CJ Martin Fellowship from the NHMRC to perform postdoctoral studies in the Department of Pathology at Harvard University Medical School in Boston, USA. He returned to Australia in 1996 to take up a position as a Senior Research Officer at the Austin Research Institute and was made an associate of the University of Melbourne. In 1999, he was awarded an RD Wright Research Fellowship from the NHMRC and in 2000, won a Welcome Trust Senior International Research Fellowship. He moved to the Peter MacCallum Cancer Centre in February 2000 to establish the Gene Regulation Laboratory.

From 2008, Professor Johnstone held the position of Assistant Director Cancer Research and in 2015 was appointed Associate Director Laboratory Research. In 2018 he was appointed Executive Director Cancer Research at the Peter MacCallum Cancer Centre overseeing approximately 700 staff and students and plays a key role in strategic decision making across the organisation. He was also appointed Head of Department, Sir Peter MacCallum Department of Oncology within the Faculty of Medicine, Dentistry and Health Science at the University of Melbourne. He runs a laboratory of 15 staff and students, has published more than 250 peer-reviewed papers, was awarded an NHMRC Senior Principal Research Fellowship in 2015 and is a Full Professor in the Sir Peter MacCallum Department of Oncology at the University of Melbourne.


Ricky Johnstone

Professor Johnstone has won several prestigious awards, including the Australian Academy of Science Gottschalk Medal (2005), AMGEN Prize for Excellence (2003) and the Australian Life Science Research Award (1999). In 2015, he was elected as a Fellow of the Australian Academy of Health and Medical Sciences and in 2014, he was listed by Thomson Reuters as one of the world's most influential scientists based on citation rates for his papers.

Professor Johnstone is an internationally renowned cancer researcher who has utilised genetic mouse models of hemopoietic malignancies and solid tumors to understand the epigenetic and transcriptional changes that underpin tumor onset and progression and to develop new therapies that target epigenetic and transcriptional regulatory proteins. He has recently discovered how epigenetic based-agents can engage the host immune system to drive prolonged therapeutic responses.

FAOBMB Young Scientist Award 2021

The ASBMB congratulates Dr Stanley Cheng Xie (Bio21 Molecular Science and Biotechnology Institute, University of Melbourne) on being named the 2021 FAOBMB Young Scientist male awardee. Dr Sakonwan Kuhaudomlarp (Department of Biochemistry, Mahidol University, Bangkok, Thailand) was named the 2021 FAOBMB Young Scientist female awardee. The winners of the Young Scientist Awards presented lectures on their work at the 16th FAOBMB Congress and participated in the Young Scientist Program preceding the Congress.

Stanley completed his PhD in 2016 at the University of Melbourne under the supervision of Professor Leann Tilley. His PhD research focused on the molecular basis for artemisinin action and resistance in the malaria parasite, *Plasmodium falciparum*. His findings were published in journals including *PNAS, PLoS Biology* and *Journal of Cell Science*. In 2016, Stanley was awarded an ASBMB Fellowship, including the Fred Collins Award.

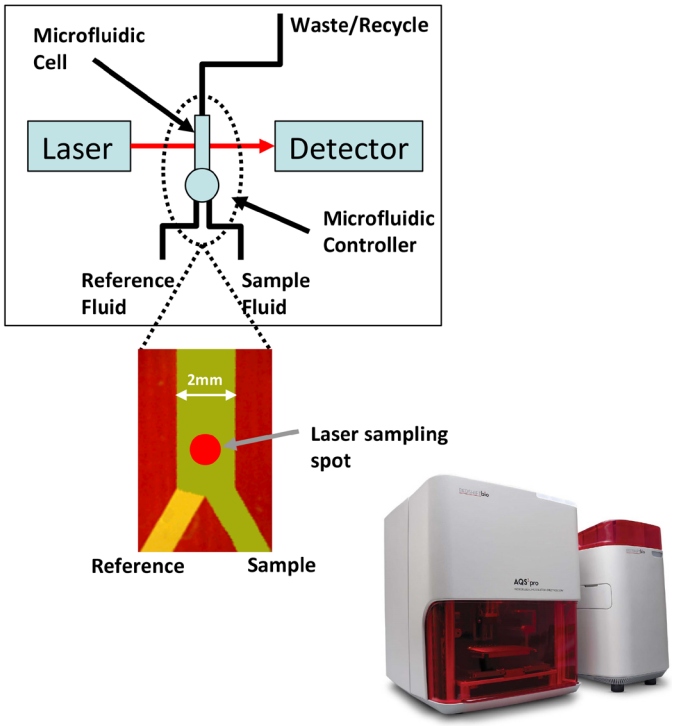
Stanley's postdoctoral research has aimed to translate his basic research findings into preclinical development of potential antimalarial drugs. He has worked with the Japanese pharmaceutical giant, Takeda Pty Ltd, and Swiss not-for-profit organisation, Medicines for Malaria Venture. Stanley travelled to Takeda Boston and worked to discover a new series of proteasome inhibitors to be used in tandem with artemisinin. He also collaborated with GSK Pty Ltd to identify potent and selective inhibitors of the parasite proteasome from GSK's collection of proprietary compounds. In 2018, he relocated to the GSK Tres Cantos Open Labs and worked in Spain for half a year. Stanley has worked in both industry and academia to develop small molecule inhibitors through high throughput screens and hit-to-lead phases to treat malaria.

Stanley Cheng Xie

Stanley's postdoctoral work has resulted in a number of publications, including first author papers in *Nature Microbiology, PNAS* and *Journal of Medicinal Chemistry*. He is also the lead author of invited review articles in *Expert Opinion on Therapeutic Targets* and *Trends in Parasitology*. He co-authored several publications in journals such as *Nature, Nature Communications* and *ACS Infectious Diseases*. Stanley has been invited to speak at international conferences, including the 14th International Congress of Parasitology and the 69th American Society of Tropical Medicine and Hygiene Annual Meeting.

Long-term Protein Stability Prediction Using 'Micro' Changes in Secondary Structure Measured Using Microfluidic Modulation Spectroscopy

Patrick King, RedShift BioAnalytics Inc, pking@redshiftbio.com



Abstract

Microfluidic Modulation Spectroscopy (MMS) is an IR-based technique compatible with almost all biological buffers and additives, including: DMSO, serum, excipients, reducing agents, adjuvants, surfactants and carbohydrates. As a direct result, samples require no dilution, adulteration or transfer into a suitable media for measurement unlike traditional technologies e.g. Circular Dichroism (CD) and Fourier Transform Infra-Red (FTIR), and require no labelling. The AQS3pro is fully automated and generates exceptionally high data quality across an extremely broad concentration range (0.1 to >200 mg/ml), offering more robust and highly-sensitive analysis of free in-solution protein folding irrespective of the background. MMS can confidently be used to enhance Quality by Design (QbD), formulation studies and drug candidate selection where existing technologies are restricted. This report presents 8 protein samples which were studied in pairs, incubated at 4 and 30°C in complex buffers for eight weeks to simulate product stability over years. Structural changes over this timescale were <1% with a sample concentration <10 mg/ml, which would be very challenging to measure using existing traditional technologies. MMS allowed data to be collected rapidly in an automated fashion from well plates, enabling this stability study to be greatly accelerated.

Introduction

The AQS3pro System

The AQS3pro launches a new era in IR spectroscopy for protein characterisation, bringing repeatable, high sensitivity, automated measurements to every stage of the biopharmaceutical pipeline.

Powered by Microfluidic Modulation Spectroscopy

MMS is a unique, patented technology in which the sample (protein) solution and a matching buffer reference stream are automatically introduced into a microfluidic flow cell, and the two fluids are rapidly modulated (e.g. 1–5 Hz) across the laser beam path to produce nearly drift-free background-compensated measurements.

MMS – insulin 'micro' stability study

A set of insulin samples were held below their first Tm at 30°C (measured using DSC) for eight weeks to simulate the effect of degradation in different formulation conditions, at 4°C over several years. Due to the very high sensitivity of MMS and its accommodation to complex buffers, differences in secondary structure that would not have been observed using traditional technologies were measured between samples with little user effort, indicating their relative stability.

A systematic pattern was observed, showing a decrease in alpha helix, turn and disordered structure, with a corresponding increase in β-structured material common to the initial stages of an aggregation process. Only sample 3 showed deviation from this pattern with a reversal in disordered structure behaviour. Each datapoint is averaged from 3–5 replicates, with an internal similarity of >99.5%.

Sample Name	Given Conc. (mg/ml)	Fitted Conc. (mg/ml)	Similarity to 1, 4C (%)	Similarity to 4C sample (%)
Sample 1, 4C	7.2	6.77	100.00	100.00
Sample 1, 30C	7.2	6.77	99.10	99.10
Sample 2, 4C	7.2	6.84	99.65	100
Sample 2, 30C	7.2	6.84	99.10	99.28
Sample 3, 4C	7.2	6.98	99.31	100
Sample 3, 30C	7.2	6.98	99.05	99.50
Sample 4, 4C	7.2	6.70	99.24	100
Sample 4, 30C	7.2	6.70	99.00	99.36
Commercial Insulin Humalog	3.6	3.43	91.87	-

Table 1. *Calculated concentrations and similarity comparisons: to sample 1, and between 4 and 30°C samples. >99.5% internal replicate similarity measured for each sample (3–5 replicates).*

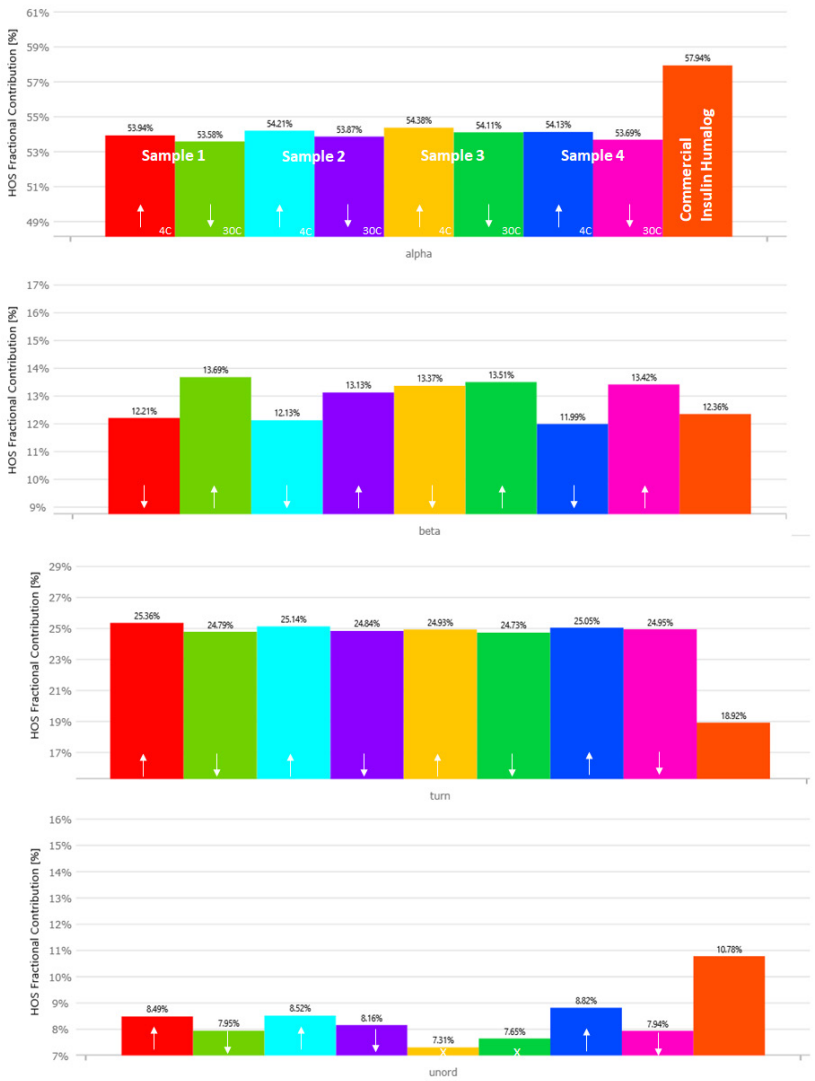


Fig. 1. *Higher-order structure analysis showing changes in four secondary structure elements between pairs of formulated insulin samples held at 4°C and 30°C for eight weeks. Each datapoint is averaged from 3–5 replicates, with an internal similarity of >99.5%. Samples are shown in pairs in numerical order, left: 4°C, right: 30°C. A commercially-available Insulin Humalog is shown on the far right for comparison, measured at 4°C.*

Concentration measurement and similarity analysis

Protein concentrations are calculated automatically using the in-built AQS3delta analytics platform for every sample analysed by MMS, using the peptide backbone as a chromophore, therefore requiring no labelling. Similarity analysis is also performed automatically and determines the variance of each measurement, and so whether differences observed between samples are significant. Sample 3 most retains its secondary structure at higher temperature (right column), whereas sample 1 shows the largest structural difference. Measured changes are very small (<1%), but are significant as internal replicate variance is lower in each case.

Further higher-order structural analysis

Normalised changes in higher-order structure were used to highlight how the four samples in this study changed at elevated temperature in comparison to one another, agreeing well with previous conclusions. Sample 3 showed the smallest alpha to beta transition, indicating this is the most stable sample, least likely to aggregate. Samples 1 and 4 were most likely to aggregate but show slightly different behaviour to one another that may have an impact on their respective mechanisms of aggregation. Sample 2 was like 1 and 4 but showed a lesser degree of destabilisation.

Conclusions

In summary, four pairs of proteins were investigated using MMS to determine whether incubation at elevated temperature for weeks could be used to predict stability at lower temperature over years. Secondary structure changes over this timescale were very small (<1%) but could be confidently measured due to the very high level of spectral sensitivity and reproducibility of MMS. Due to automation this was achieved in one day of experiments and predicted that in decreasing order, sample stability is: 3, 2, 1, 4, which was confirmed by the user to be correct. As part of every measurement, MMS applies inbuilt AQS3delta analytics software to provide several parameters that when considered together are key to giving a more complete picture of structural changes in your samples. Here a combination of concentration, similarity analysis and two types of higher-order structure analysis were combined to rank samples and show that they potentially aggregate via slightly different mechanisms, which may help design a stabilisation strategy for this molecule type. MMS offers a new technology in the Biotherapeutic workspace that provides an invaluable tool for understanding and predicting solution stability behaviour, without the limitations and restrictions of historical technologies. One technique can be applied to all samples, with a level of sensitivity not previously available that here is shown to greatly accelerate long-term protein stability testing.

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ASBMB Annual Reports

President's Report

ASBMB President Jacqui Matthews.

It's been a difficult couple of years for the Society and its members, but I'm being cautiously optimistic about relaxing of major lockdowns in New South Wales and Victoria, the projected opening to interstate and international travel, and the return of international students. I am hoping that we can transition back to focusing on the science and teaching that we love, rather than having to respond to ever-changing regulations...

Meetings

2021: The FAOBMB Congress has gone through many stages of planning, from fully in person with the intention of Australians going to New Zealand as part of a travel bubble, to hybrid with the Kiwis in person and the rest of us online, but has landed on a fully online version. Regardless of the format it's a great program – at the time of writing still a few weeks ahead. The organisers are thrilled that the online aspects have opened up the meeting to students and researchers from countries who would never been able to attend an international meeting.

The East Coast Protein Meeting had been planned as an Australia-based meeting in 2021, to be co-hosted by all of the Protein Groups that are SIGs of ASBMB. Due to rolling lockdowns, the meeting was postponed. We look forward to a return of this student and ECR focussed meeting when expectations of being able to travel are more certain.

In September, in conjunction with Monash University, the Education SIG ran an online Symposium 'Sharing Practice: A Focus on Assessment and Academic Integrity'. Nirma Samarawickrema and the committee put together an excellent set of engaging speakers that stimulated a lot of discussion. There were a lot of strategies shared, and I know I will be implementing some of them in my teaching over the next few years.

2022: ComBio2022 will be held at the Melbourne Convention Centre from 27 to 30 September 2022. This meeting was originally scheduled for 2020, so extra kudos to Jackie Wilce, Mark Hulett and Sally Jay for continuing to lead and organise this meeting. Thanks to their efforts, the main speaker line up remains the same – including two fantastic keynote speakers, Nobel Laureate Jennifer Doudna and the Russell Grimwade Lecturer Cynthia Kenyon. We look forward to seeing you in person.

2023: An ASBMB-focussed meeting has been proposed to be run in Canberra, led by Colin Jackson. Dates and other details will become available closer to the date, but at this stage the intention is that this will be a fairly general meeting and an opportunity to foster collaborations and networks.

2024: Planning for the IUBMB Congress in Melbourne, led by Leann Tilley, is under way.

Special Interest Groups (SIGs)

Active Special Interest Groups (SIGs) play a very valuable role in driving subdisciplinary interactions within our broader community and provide a mechanism for local or distributed groups to network on a regular basis, create opportunities to present and share research and/or teaching practices, and to award prizes or awards to our emerging Society members. Several of the SIGs have been active during the last two years, running local in person symposia where possible and rapidly pivoting to online symposia to provide much needed stimulus during many different types of lockdowns and travel restrictions.

There has been a project in place to consult with and make sure that SIGs are aware of responsibilities towards the ASBMB and, at the recent AGM, some changes to the constitution around SIGs were accepted to make these clearer and to update practices. Some of the key points are that SIGs should be actively organising events or activities, that ASBMB membership should be promoted amongst SIG members, and that SIG-sponsored prize winners or conference speakers should be ASBMB members.

ASBMB Award Recipients

I would like to take the opportunity to congratulate our 2021 award recipients:

The Lemberg Medal
Merlin Crossley (UNSW)
The Shimadzu Research Medal
Erinna Lee (La Trobe Institute for Molecular Science and Olivia Newton-John Cancer Research Institute)
The SDR Scientific Education Award
Lois Balmer (Edith Cowan University)
The Eppendorf Edman ECR Award
Lahiru Gangoda (Walter and Eliza Hall Institute)
The Boomerang Award
Anton Calabrese (University of Leeds, United Kingdom)
ASBMB Fellowships
Pamali Fonseka (La Trobe University) – Fred Collins Award
Edward Kerr (University of Queensland)
Abi Ghifari (University of Western Australia)
Belal Shohayeb (Queensland Brain Institute)

ASBMB Annual Reports

Running the Society

A big thank you to Joel Mackay for his service to the Society – he is stepping down from Council after four years (a year as President Elect, two years as President and a year as Past President). Joel has done a lot of work to strengthen the relationships between SIGs and the Society and to support a focus on Biochemistry Education within the Society. Ross Hannan begins his role as President Elect in 2022, and will take over the Presidency in 2023. I'm looking forward to working with Ross and getting his fresh perspective on issues and initiatives for the Society.

Members of the ASBMB Council put significant amounts of time and effort into the Society. Our Secretary Dominic Ng is doing a superb job of keeping us organised. He and our treasurer Marc Kvansakul have carried out substantial amounts of work behind the scenes to keep the Society functioning and solvent. Tatiana Soares da Costa is our Editor and Chair of Communications, as well as the Biological Sciences representative for the STA and a member of the FAOBMB 2021 International Committee. Terry Piva is the FAOBMB representative, and Nirma Samarawickrema is our Education Representative.

We thank and farewell Monica Murcha, who is stepping down from her role as the WA State Representative, and welcome Alyssa van Druemel to the role. Our other states are ably represented by Christina Spry (ACT), Laura Sharpe (NSW), Michael Landsberg (QLD), Iman Azimi (TAS), Laura Osellame (VIC) and Melissa Pitman (SA).

Supporting the efforts of the Council are Sally and Chris Jay and the National Office; their long-standing service has been essential for the running of ASBMB, working with Sustaining Members, and the organisation of ComBio meetings – as anybody who has been involved on either council or ComBio committees will readily attest. Amongst other activities, Liana Friedman plays a key role as the *Australian Biochemist* Editorial Officer, ASBMB webmaster sending out emails to our members.

Other Initiatives

A Science Advisory Group is under development to be led by Gavin Knott and Laura Murray-Rust. Initially this group will be under the umbrella of Tatiana's Communications portfolio but may expand with a view to developing more science advisory activities.

Professor Jacqui Matthews, President
jacqui.matthews@sydney.edu.au

ASBMB Annual Reports

Treasurer's Report

ASBMB Treasurer Marc Kvansakul.

Relevant summaries of the full audited report (1 July 2020 to 30 June 2021) should be read in conjunction with this statement. Final audit has been completed and will be submitted shortly, and the summary statements on which the report is based were provided by our auditors.

The overall position of the Society has stabilised compared to the substantial loss in 2020. We recorded an operating loss of $5,013 compared to the loss of $66,473 in 2019–2020. The reduction in this year's losses is largely due to the lack of financial activity for ComBio, whereas in 2019–2020 we incurred the costs for co-organizing the event that was ultimately postponed.

The major sources of income for ASBMB are membership revenue, ComBio profits and bank interests. There was $7,655 of advertising income to report. Corporate support for our named awards remains strong and on behalf of the Society, I thank our sponsors for their support of these awards. I would also like to thank Sally Jay for her tireless efforts in securing continuing sponsor support for our awards. Interest on our accounts dropped in 2020–2021 due to the flow-on effect of very low deposit rates based on the official interest rate.

Net expenditure in the 2019–2020 financial year was down $12,400 compared to the previous period, however the operating framework remains atypical. The reduction in expenditure is largely driven by the lack of financial requests from ASBMB state branches and Special Interest Groups, who were unable to mount major initiatives. The distribution of funds to the state and Special Interest Groups was $6,900 below that in 2019–2020. We are fortunate that Sally and Chris Jay manage the National Office with a high degree of effectiveness while keeping their costs relatively stable. Our flagship publication is the *Australian Biochemist* and it is available to members as a PDF. Tatiana Soares da Costa as the Editor of the *Australian Biochemist,* along with Editorial Officer, Liana Friedman, are to be commended for their work in putting the magazine together. Reduced meeting costs were achieved by the Executive and Council holding teleconferences and continue to improve the financial status of the Society.

The overall financial position of ASBMB has stabilised compared to that recorded in 2019–2020. Due to the postponement of ComBio2020, we had to access cash reserves in 2019 ($100,000 was used), thus substantially impacting our current assets. This was required to provide additional seed funds for the operating costs of ComBio2022, and to ensure we maintain sufficient cash to enable the day-to-day operations of the Society and Society-supported activities. However, with expenditure stabilised there was no requirement to access our reserves again this financial year.

With the postponement of ComBio2020 to 2022, we will hopefully benefit from significant income from sponsorship and trade for ComBio2022. For 2021–2022, ASBMB supported the NZSBMB-led FAOBMB Congress, which took place online in November 2021. As part of this support, we provided $10,000 in seed funds, and engaged in a profit/loss share. It is not clear at this stage what the financial prospects of the Congress are. In addition, due to the use of cash reserves, our income from bank interest will also be reduced, however in the current climate of near zero interest rates this is not unexpected. We continue to rely on our cash reserves to support Society activities, and will likely need to innovate again to reduce our cost basis.

In my role as the ASBMB Treasurer, I have many people to thank. Members of the ASBMB Executive who are always constructive and supportive, Sally and Chris Jay (ASBMB National Office), Ian Price (ASBMB bookkeeper), Priestleys (ASBMB accountants) and Brian Hiley (ASBMB auditor).

Professor Marc Kvansakul, Treasurer
treasurer@asbmb.org.au

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

ASBMB Annual Reports

Executive Officers' Report

Your Executive Officers submit herewith the financial statements of the Association for the year ended 30 June 2021, together with the Auditors' Report thereon and in accordance with Section 73 of the Associations Incorporation Act 1991 report as follows.

EXECUTIVE OFFICERS

The Executive Officers throughout the year were: Professor Jacqui Matthews (President Elect to 30/9/20, then President); Professor Joel Mackay (President to 30/9/20, then Past President); Professor Leann Tilley (Past President to 30/9/20); Professor Briony Forbes (Secretary to 30/9/20); Professor Dominic Ng (Secretary from 30/9/20); Professor Marc Kvansakul (Treasurer); Dr Tatiana Soares da Costa (Editor and Chair of Communications); Associate Professor Terrence Piva (FAOBMB Representative).

PRINCIPAL ACTIVITIES

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

OPERATING RESULTS

During the year, the Association produced an operating loss of $5,013 (2020: operating loss $66,473).

STATEMENT BY EXECUTIVE OFFICERS

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

(a) Presents a true and fair view of the financial position of the Association as at 30 June 2020 and its performance for the year ended on that date in accordance with Australian Accounting Standards – Reduced Disclosure Requirements.

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

Signed in accordance with a Resolution of the Executive Officers.

Professor Jacqui Matthews, President
Professor Marc Kvansakul, Treasurer

Independent Auditor's Report

REPORT ON THE FINANCIAL STATEMENTS

We have audited the financial report of the Australian Society for Biochemistry and Molecular Biology Incorporated (the association) which comprises the statement of financial position as at 30 June 2021, the statement of profit or loss, statement of comprehensive income, statement of changes in equity and statement of cash flows for the year then ended, notes comprising a summary of significant accounting policies and other explanatory information, and the certification by members of the committee on the annual statements giving a true and fair view of the financial position and performance of the association.

EXECUTIVE OFFICERS' RESPONSIBILITY

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

BASIS FOR OPINION

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

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

AUDIT OPINION

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

(i) giving a true and fair view of the association's financial position as at 30 June 2021 and of its performance for the year then ended; and

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

IMPACTS OF COVID-19 ON THE ASSOCIATION

The COVID-19 virus has resulted in the Association postponing ComBio2020 to September 2022, and the event is now officially called ComBio2022. Any revenue collected in advance and costs incurred in planning and organising the event have been carried forward to the future event.

The Executive Officers have assessed the Association's ability to continue as a going concern in light of the impacts that the COVID-19 virus has had on the operations of the Association and the community that the Association operates in. Although some aspects of the Association's operations have been impacted by the virus, the Executive Officers are of the opinion that the Association is able to continue as a going concern.

Given the uncertainty of the potential future impacts of the virus on the economy, there is some uncertainty to the future impacts that the virus may have on the operations of the Association.

MC Andreassen (Partner)
Priestleys Chartered Accountants

ASBMB Annual Reports

AUSTRALIAN SOCIETY FOR BIOCHEMISTRY AND MOLECULAR BIOLOGY INCORPORATED

STATEMENT OF FINANCIAL POSITION AT 30 JUNE 2021

	2021 $	2020 $
CURRENT ASSETS		
Cash and cash equivalents	456,848	436,615
Trade and other receivables	89,296	70,729
Other current assets	-	286
TOTAL CURRENT ASSETS	**546,144**	**507,630**
NON-CURRENT ASSETS		
Property, plant and equipment	-	-
TOTAL NON-CURRENT ASSETS	**-**	**-**
TOTAL ASSETS	**546,144**	**507,630**
CURRENT LIABILITIES		
Trade and other payables	140,454	96,927
TOTAL CURRENT LIABILITIES	**140,454**	**96,927**
TOTAL LIABILITIES	**140,454**	**96,927**
NET ASSETS	**405,690**	**410,703**
EQUITY		
Retained surplus	405,690	410,703
TOTAL EQUITY	**405,690**	**410,703**

STATEMENT OF CASH FLOWS FOR THE YEAR ENDED 30 JUNE 2021

	2021 $	2020 $
CASH FLOWS FROM OPERATING ACTIVITIES		
Receipts from members	95,189	73,084
Conference income	-	135,146
Other income	25,091	17,143
Payments to suppliers and employees	(305,031)	(305,031)
Interest received	3,646	10,090
Net cash provided by/(used in) operating activities	**20,233**	**(69,568)**
CASH FLOWS FROM INVESTING ACTIVITIES		
Net increase/(decrease) in cash held	20,233	(69,568)
Cash at the beginning of the financial year	436,615	506,183
Cash at the end of the financial year	**456,848**	**436,615**

REVENUE

	2021 $	2020 $
Operating activities		
Administration Fund		
Subscriptions – ordinary, student, retired and Sustaining Members	75,736	81,217
Conference income – ASBMB2019 *(see note)*	-	122,860
Advertising and insert in proceedings and magazines	7,655	4,280
Other Income	15,000	11,100
	98,391	**219,457**
Non-operating activities		
Interest received – Administration Fund	3,009	8,683
Donations	155	225
	3,164	**8,908**
Total Revenue	**101,555**	**228,365**

EXPENSES

	2021 $	2020 $
Other expenses from ordinary activities		
Affiliate memberships	8,583	12,497
Awards and medals	12,147	18,500
Conference expenses – ComBio *(see note)*	-	174,875
Conference support – other conferences	-	3,398
Council expenses	3,812	4,009
Insurance	-	1,138
National Office costs	44,572	40,501
Magazine costs	10,983	9,179
Other costs	4,389	4,179
State allocations	3,982	8,949
Remuneration of auditor		
- audit or review services	2,900	2,828
- other services	2,700	2,285
ASBMB Fellowship – Research Fund	12,500	12,500
	106,568	**294,838**

CASH AND CASH EQUIVALENTS

	2021 $	2020 $
Cash at bank – Administration Fund	456,848	436,615
	456,848	**436,615**

TRADE AND OTHER PAYABLES

	2021 $	2020 $
Current		
Accrued expenses – Administration Fund	172	809
ComBio/ASBMB conference receivables	53,424	34,220
GST Receivable	-	-
Advances to state committees	35,700	35,700
	89,296	**70,729**

RETAINED SURPLUS

	2021 $	2020 $
Administration Fund		
Retained surplus at beginning of the year	410,703	477,176
Net surplus (deficit) attributable to the Fund	(5,013)	(66,473)
Retained surplus at the end of the year	405,690	410,703

All sums given in Australian Dollars.

Note: Conference Income and Conference Revenue

The ASBMB 2019 conference was solely supported by the Association with revenue of $122,860 and expenses of $174,875, resulting in a net loss of $52,015.

ComBio2020 was postponed due to the impacts of COVID-19.

Our Sustaining Members

ASBMB welcomes the following new Sustaining Member:
LEARNSCI LTD, UK

GenScript's COVID-19 Virus Antigens and Antibodies

From diagnostics to drug discovery and vaccine development, GenScript has developed a comprehensive range of products that scientists may use to accelerate COVID-19 research and development. As the virus continues to mutate, much focus is now being placed on the variants due to their more infectious nature. At GenScript, we provide both wild-type and variant versions (eg. Alpha, Beta, Gamma, Delta, Lambda, etc.) of the SARS-CoV-2 protein, and these have been validated to bind to the human ACE2 receptor and may serve as antigens in both ELISA assays and Western Blot.

To complement these antigens, we also offer COVID-19 antibodies that are specific to the SARS-CoV-2 nucleocapsid protein or the SARS-CoV-2 spike protein. Our new SARS-CoV-2 Spike Neutralizing Antibody Standard (A02087) is particularly useful in the assessment and development of assays for the detection and quantitation of SARS-CoV-2 neutralizing antibodies. Neutralizing antibodies are known to be more effective than regular binding antibodies in decreasing the SARS-CoV-2 viral infection of cells. This antibody standard binds to multiple neutralizing epitopes in the receptor binding domain, and may be used in ELISA assays and in performing neutralization tests.

Contact GenScript's Sales Account Manager now
ap.marketing@genscript.com
www.genscript.com

Abcam Now Available from Fisher Biotec

Fisher Biotec are now authorised to supply the Abcam range of Sample Preparation Products. These include Protein Conjugation Labelling kits, reagents and kits for Western Blotting, Cellular Fractionation, Protein Purification and Quantification.

The addition of the Abcam range will complement our existing portfolio of protein analysis equipment and allow us to offer a complete solution to your protein needs. Currently we are offering promotional pricing on InstantBlue® ultra-fast protein stain, and Lightning-Link® antibody, protein and peptide conjugation kits.

InstantBlue® protein stain is an ultra-fast, one step, non-toxic, ready-to-use stain for polyacrylamide gels. InstantBlue® offers high sensitivity and is mass spectrometry compatible.

Lightning-Link® offers quick conjugation of the included label to your antibody protein or peptide. Lightning-Link® is scalable, efficient and flexible offering over 45 labels. A 100% antibody recovery makes it suitable for a wide range of applications including FACS, ELISA, IHC, WB and Lateral Flow.

Other related products include RunBlue® Precast Gels which offer superior rigidity and stability, a long shelf-life and are compatible with all commonly used electrophoresis equipment. A complete range of prestained and unstained Protein Ladders are also available.

For more information, please contact us.
www.fisherbiotec.com
info@fisherbiotec.com
Freecall – 1800 066 077

The Microplate Reader Company

Development of an AlphaLISA® Protein–protein Interaction Assay to Screen for Re-purposed Drugs as Targeted Disruptors

A major part of pandemic preparedness is our ability to quickly identify the cause of the emerging disease and its route of infection. Taking the example of SARS-CoV-2, it was quickly realised that like other related corona viruses, the point of interaction with cells was angiotensin-converting enzyme 2 (ACE2). With this knowledge, Quinlin Hanson and the team at the National Center for Advancing Translational Sciences (NCATS) employed an AlphaLISA® protein–protein interaction assay in high throughput on the PHERAstar FSX®, to screen for re-purposed drugs as targeted disruptors.

This application highlights recent advances in assay technology and the importance of assay optimisation, and validation. The screen also employs a useful, commercially available counter-assay and demonstrates how improved assay and microplate reader technologies can be leveraged to develop new screens, to improve our ability to respond to emerging diseases.

Read more: here.

If we can help your laboratory's assay development or instrumentation requirements, contact our team on +61 3 5973 4744 or australia@bmglabtech.com.au.

Our Sustaining Members

ScimaR
Life Sciences Solutions

Isolating Primary and Stem Cells? FREE Collagenase Sampling Program!

The demand for safer biologicals and biopharmaceuticals has led Worthington to introduce several *Animal Free (AF)* enzymes for primary/stem cell isolation, tissue culture research and vaccine bioprocessing. Scientists working in regenerative medicine applications including the isolation of stem cells, tissue transplantation, artificial organ development and vaccine production would benefit from AF enzymes since there is no risk of potential BSE/TSE and/or mammalian viruses contaminants. In addition, the use of AF enzymes eliminates many of the quality and regulatory issues and concerns associated with enzymes purified from animal sources.

The lot-to-lot variation which is typical of enzyme preparations makes it important to pre-test a particular lot of enzyme you are planning to use in your experiment. Many years ago we found that the most practical approach for the researcher is to pre-sample several different lots of collagenase at a time and select the best of the group. As the world's leading manufacturer of collagenase, Worthington is able to offer the greatest number of different lots at any given time and recommend specific lots for an application. Regular grades of Worthington *Animal Free* collagenase are also available for sampling.

There is no charge for participating in the collagenase sampling program. Under the program, individual researchers are provided with 100 mg samples of up to three different lots of collagenase for evaluation in their own assay systems. A period of 60 days is allowed for your evaluation of these samples. A minimum of 3 grams of each lot will be placed on HOLD, reserved in your name. When you determine which lot performs best for you, simply specify the lot desired when ordering.

To become part of this program, or to discuss any of the Worthington products, just call **ScimaR** at 1800 639 634, email scimar@bigpond.net.au or visit our website www.scimar.com.au

LearnSci

LearnSci is a specialist technology partner that develops transformative digital resources for university-level science education. Our team consists of scientists, web developers, designers, and education specialists. We strive to enhance practical labs, not replace them. Our resources are based on sound pedagogical principles that improve the lab experience.

Our interactive LabSims make the perfect addition to your students' lab preparation. These learning simulations are created for enhancing practical science, developing key lab skills, and giving your students the capability and confidence that they need.

Our Smart Worksheet Collection offers an advanced assessment solution – supporting students with immediate, personalised feedback. These online, auto-graded resources for data analysis and calculation practice, improve student assessment while drastically reducing your marking burden.

"The fact that LearnSci is a team of scientists and developers means that they understand the types of questions we want to ask and can advise on the best use of technologies." – Dr Andrew Allsebrook, School of Chemistry and Molecular Biosciences, University of Queensland.

To learn more, visit learnsci.com or email info@learnsci.co.uk.

DAINTREE scientific AUSTRALIA

Daintree Scientific Australia presents the Cellcrusher Mini tissue pulveriser and the Cellcrusher tissue pulveriser. The Cellcrushers are simple, innovative devices for fast, effective cell disruption. The cryogenic tissue pulverisers for breaking cells in liquid nitrogen are ergonomic and easy to use.

The Cellcrusher tissue pulveriser reduces most tissues to a fine, easily recoverable powder. Its curved surfaces are designed for fast, easy cleaning and effective cell disruption. The sample size is 20mg to 5g. The key design feature of the Cellcrusher is that it has curved inner surfaces. The recovery spoon is contoured to the curved inner surface of the Cellcrusher, so that minimal sample is wasted. Frozen tissue samples are quickly and effectively pulverised and collected. The curved inner surfaces of the Cellcrusher have no corners, facilitating easy cleaning. The Cellcrusher is suitable for physically tough samples such as cartilage, venous tissue and tumour samples as well as extremely physically tough samples such as seeds, bark or skin (using the Cellcrusher Drill-bit accessory), and RNA extraction.

The Cellcrusher-Mini allows for the recovery of small samples (2mg to 40mg) inside a frozen 'popsicle' of buffer. This neatly combines the sometimes difficult task of collecting miniscule quantities of frozen dust and transferring it into a storage tube before it melts. With six chambers, each only 8mm wide, this tissue pulveriser offers unparalleled efficiency when crushing and recovering tiny samples at liquid nitrogen temperatures.

Contact Daintree Scientific Australia to discuss the Cellcrusher range of tissue pulverisers.

Please contact
Moina Macaskill
Daintree Scientific Australia
www.daintreescientific.com.au
(03) 6376 3335
info@daintreescientific.com.au

Our Sustaining Members

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V5-Trap for the Isolation of V5-Tagged Proteins

ChromoTek has introduced the V5-Trap™ which is a Nanobody or V_HH coupled to either agarose, magnetic agarose or magnetic beads for superior immunoprecipitation (IP) and Co-IP of V5-tagged proteins.

The V5-tag is derived from the P and V proteins of Simian virus 5 (SV5 – a paramyxovirus) and is a popular epitope tag for the capture and detection of V5-tagged proteins in yeast, bacteria, insect and mammalian cells. The V5-tag may be fused to either the N-terminus, C-terminus of a protein or be internal. The short linear peptide sequence of the V5-tag is GKPIPNPLLGLDST which has a size of about 1.4kDa.

Benefit from the V5-Trap advantages for your next IP:

- Very low background
- No heavy and light antibody chains in gel
- High specificity, high binding capacity
- Extraordinarily stable even under harsh washing conditions
- Compatible with N-, C-terminal and internal V5-tag
- Effective elution with V5-peptide
- Recombinant nanobody ensures consistent results

The V5-Trap is a convenient, well characterized, and high-performing tool; it is ready to use, for fast and specific IP of V5-tagged proteins. It is compatible to downstream applications including mass spectrometric (MS) analysis, ELISA, and enzymatic assays. V5-Trap's pulldowns provide pure extracts of V5-tagged protein without contaminating heavy and light chain peptides as can occur with the use of conventional antibodies. Effective elution of bound V5-tagged proteins can be conducted under denaturing conditions (for SDS-PAGE/WB, MS) or under gentle, native conditions using V5-peptide.

BioNovus Life Sciences
David Antonjuk
Ph: (02) 9484 0931
Email: info@bionovuslifesciences.com.au
Web: www.bionovuslifesciences.com.au

ATA SCIENTIFIC instruments

RedShiftBio AQS3pro for Protein Secondary Structure and Drug Development

When developing biotherapeutics, the ability to measure and characterise changes in the secondary structure of proteins is critical. Conventional techniques such as FTIR and Circular Dichroism do not possess the adequate feature set for researchers to accurately assess changes in their proteins within the required conditions. The need for high sensitivity, a wide dynamic range, a simplified and automated workflow, and high repeatability is significant and, until now, has not been adequately provided.

The **AQS3pro** fills the gap for label-free protein analysis with the novel IR technique called Microfluidic Modulation Spectroscopy (MMS). The technique is purposely designed to directly address the limitations of current technologies and provide drift-free, background subtracted, high sensitivity measurements of the protein secondary structure. It is possible to measure protein similarity (fingerprinting), quantitation, higher order structure, protein stability, and aggregation through thermal and chemical denaturation methods using a walk-away automated platform.

The **AQS3pro** allows users to 'see change' in the secondary structure of proteins across a wide concentration range from 0.1mg/mL to over 200 mg/mL, and in the presence of excipients. Samples can be measured with minimal preparation and without dilution to generate data that is reliably representative of drug performance.

The **AQS3pro** measures five key measurements – **aggregation, quantitation, stability, similarity, structure** to support biopharmaceutical development and manufacture.

For more information, contact us at ATA Scientific.
www.atascientific.com.au
enquiries@atascientific.com.au
(02) 9541 3500

SHIMADZU

Food testing for pesticides, herbicides, mycotoxins, vitamins, and other common residues routinely requires the homogenization of the food matrix prior to solid phase extraction. This step produces a sample of uniform consistency, high surface area and easy accessibility for extraction of the required analytes.

The Biotage Lysera is specifically designed for the grinding, lysing and homogenization of biological samples prior to any form of sample extraction. Using sample tubes pre-filled with a variety of beads, the Lysera vigorously and uniformly shakes the tubes providing an efficient, consistent, and quality homogenization usually in less than 40 seconds.

Samples are enclosed in individual vessels to prevent cross contamination and can accommodate dry or wet homogenization of samples from milligram to gram quantities.

Available with a wide range of accessories, the Lysera enables processing of samples in volumes ranging from 0.5 mL to 50 mL. The optional Cryo Cooling Unit is designed to prevent the increase of sample temperature during the homogenization process.

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info@shimadzu.com.au
Freecall 1800 800 950

Our Sustaining Members

Scitech
imaging specialists

Sapphire Biomolecular Imager – Resolution Down to 10 µm

The new Sapphire Biomolecular Imager from Azure Biosystems is a next generation laser scanning system that provides you with exceptional data quality through extremely sensitive detection, ultra-high resolution and broad linear dynamic range. Applications include Blot Imaging eg Western Blots and Southern Blots of 2D DNA gels, Gel Imaging, Tissue and Small Animal Imaging eg whole zebrafish and 96-Well Plate Imaging.

This system supports long and short wavelengths of near infrared fluorescence (NIR), red/green/blue (RGB) imaging, chemiluminescent imaging, phosphor imaging as well as optical densitometry (OD) of proteins in stained gels. It uses up to four solid state lasers (488, 520, 658 and 784 nm) offering ultimate excitation sensitivity and four colour detection of fluorescent westerns.

The Sapphire Biomolecular Imager offers a photomultiplier tube (PMT) for fluorescence and phosphor imaging, avalanche photodiodes (APD) for near-infrared imaging and a CCD sensor for chemiluminescent and visible imaging.

Chemiluminescent Western blotting takes advantage of the enzymatic reaction between horseradish peroxidase (HRP)-labeled secondary antibodies and an enhanced chemiluminescence (ECL) substrate to produce photons of light. The signal enhancement of the enzymatic reaction is useful for detecting small amounts of protein. The Sapphire can deliver chemiluminescent detection with the same sensitivity as film, but with a much broader dynamic range.

The same three detector technology that makes the Sapphire so great for imaging Western Blots is also flexible enough to image a wide range of gels, whether they are ethidium bromide (EtBr)-stained DNA agarose gels, Coomassie-stained protein gels, or even 32P-labeled DNA acrylamide gels and more.

Other key features include image resolution down to 10 microns for high quality image analysis and ultra-wide dynamic range for imaging and quantifying low and high abundance samples simultaneously. This system fully integrates with Sapphire Capture and AzureSpot software programs for perfect imaging and accurate analysis.

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TECAN.

Tecan's **Infinite® F50** and **Sunrise™** are filter based absorbance microplate readers.

Choose the **Infinite® F50** with its **long-lasting LED lamp** for standard ELISAs or the **Sunrise™** with temperature control to additionally run temperature sensitive assays.

Infinite® F50 and **Sunrise™** readers together with our **Magellan™** Tracker data analysis software meet 98/79/EC IVD-D, and provides FDA 21 CFR part 11 functionality.

Our **HydroFlex™** microplate washer can be configured with an 8 or 16 channel head for **strip wise washing** of 96 well plates. **Vacuum filtration** and **magnetic bead washing** are optional modules.

The **HydroSpeed™** can wash complete 96 well and 384 well plates at once with respective **multichannel heads**.

Aspiration and dispense settings can be adjusted for **ELISAs or Cell Based Assays**.

HydroFlex™ and **HydroSpeed™** washers have been designed to meet 98/79/EC IVD-D when configured for ELISA washing. In combination with our **HydroControl™** software, it provides FDA 21 CFR part 11 functionality.

To learn more about these products, visit www.tecan.com. To celebrate the Australian summer, we are offering a **40% discount off** list prices when you purchase an **absorbance reader, and a plate washer together. Offer valid until 28th February 2022.** To take up this offer, call us toll free on 1300 808 403, or email info-aus@tecan.com.

abcam

Knockout Cell Lines and Lysates: Engineered and Ready for You

Target identification, validation and pathway discovery: new CRISPR-Cas9 knockout (KO) cell lines provide reproducible, single gene KOs that support the interrogation of the relationship between genotype and phenotype.

Get high quality KO cell lines and lysates that allow you to identify and validate targets and establish a causative relationship between a target and disease, determine key steps/genes in pathways and confirm pharmacological effects in disease relevant models.

Reliable and ready to use immortalised mammalian cell lines that are well characterised using Sanger sequencing data and proteomics. Parental controls are available.

Cell lines: over 400 gene targets available, parental cell lines: HEK293T, Hela and more, frozen, 1 million cells/vial, 1ML.

Cell Lysates: over 2,600 gene targets available, parental cell lines: A549. HCT116, HEK293T, HeLa, HEPG2, MCF7, lyophilized 100UG, suitable for WB.

More information at www.abcam.com/KOcells

Our Sustaining Members

bio-strategy
delivering technology

High Performance Circular Dichroism Spectroscopy from Technology Leaders JASCO

Circular dichroism spectroscopy (CD) is an essential analytical technique used to analyse chirality in molecules through their optical activity. CD can be applied to a wide variety of molecular structures but has found favour in the scientific community for the elucidation of macromolecular structure, especially proteins and nucleic acids. It is typically used for protein conformation, structural analysis of biomolecules, and chiral discrimination.

JASCO (Japan Spectroscopic Co) is a leading manufacturer of circular dichroism systems and provides a wide range of solutions to meet all analytical and research requirements.

- The JASCO J-1000 series CD spectrometer provides unparalleled optical performance together with versatility and flexibility. It has the latest Quad Lock-in Amplifier which allows the simultaneous acquisition of up to four data channels
- The JASCO FVS-6000 is a high-performance vibrational circular dichroism (VCD) spectrometer. It comes with the most advanced DSP electronics and auto-alignment mechanism, allowing users to obtain high-quality VCD spectra in the infrared region.
- The JASCO CPL 300 is a circularly polarized luminescence (CPL) spectrometer. While circular dichroism provides information about the ground state of chiral molecules, CPL spectroscopy probes the excited states of chiral molecules.

For more information, please contact
Bio-Strategy
1800 008 453
sales.au@bio-strategy.com
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AXT

AXT Bioprinting Solutions

AXT has Australia's most diverse portfolio of bioprinting solutions that caters for different technical and budgetary requirements.

Regenhu

Swiss company, REGENHU focuses on creating advanced bioprinting instruments with user-friendly software that performs tasks with accuracy and repeatability such as the award-winning R-GEN 100. RegenHu's bioprinting platforms provide versatile and fully customisable configurations to cover your biofabrication needs.

Poietis

Poietis specialises in the development and manufacturing of human tissues by 4D bioprinting using their laser-assisted technology. Since its inception in 2014 they have been developing physiological models, particularly in partnership with the world's leading pharmaceutical and cosmetic groups e.g. BASF and L'Oreal.

Fluicell

Fluicell is a public biotech company providing single-cell microfluidic research tools. Their BIOPIXLAR® is a completely new type of bioprinter with the unique capability to position cells in three dimensions with high resolution and precision without the use of bioinks.

UpNano

UpNano's platform of high-resolution 3D printing systems, based on 2-photon polymerisation with sub-micrometer resolution, allows the fabrication of structures and surface textures mimicking the microenvironment of cells. These three-dimensional culture approaches, and especially the results obtained from them are becoming increasingly important in preclinical research into therapeutic strategies.

For more details, please visit https://www.axt.com.au/segments/lifesciences-bioprinting/ or contact info@axt.com.au

SDR SCIENTIFIC
EQUIPMENT · SUPPORT · RESULTS

When it Comes to Drug Discovery, Look No Further…

From Hamamatsu Photonics and SDR Scientific, the FDSS – Functional Drug Screening System – is a family of kinetic plate imagers operating on the principles of fluorescence and luminescence.

Hamamatsu's high-speed and high-sensitivity EM-CCD scientific camera is built into the FDSS series, and enables the readout of calcium flux, mobilisation, and membrane potential changes. It can be used for flash luminescence and enables high speed sampling at 200 Hz for 96 and 384 wells (dependent on the camera binning setting) for all wells simultaneously in the microplate.

Applications include:

- GPCR
- Ion Channel
- Luminescence
- BRET/FRET
- iPS-Cell

The electric field stimulation (EFS) pacing system option enables new applications of the FDSS platform using cardiomyocytes, skeletal muscle cells, and neurons. The CO_2 incubation option enhances the stable status of cell cultures, keeping them at the optimal temperature for study.

SDR Scientific is proud to exclusively represent Hamamatsu FDSS in Australia/New Zealand. Discover the FDSS family by reaching out to your friendly SDR Scientific Technical Sales and Support Specialist on 02 9882 2882/+61 2 9882 2882 or by clicking here.

Our Sustaining Members

That's Love — Spendlove

No, it's not the backdrop of a 1960s spy movie, but the origin of HyClone™ Laboratories definitely has plot twists! It starts in 1967 when Dr Rex Spendlove, then a professor at Utah State University, was studying a viral disease that was fatal to children. Integral to his research was fetal bovine serum (FBS), which at the time, was so poor that Dr Spendlove was forced to develop his own methods to produce a quality serum. The end result was the formation of HyClone™, which pioneered many of the serum collection, filtration, and processing techniques used by cell culture product manufactures.

Cell culture contribute towards today's life-saving therapies, but it fundamentally drives critical research that leads to future breakthrough discoveries tomorrow. At Cytiva, we take this seriously. From off-the-shelf cell culture products to custom cell culture services, our expansive portfolio is designed to accommodate the entire bioprocess workflow.

Learn more about HyClone™: https://cytiva.link/ad1rv

P: 1800 150 522
E: requests.ANZ@cytiva.com

NinoLaf use the latest technology to deliver a range of Class II cabinets which are advanced in design and performance, while easy to clean and maintain.

Designed and built in Sweden, the 'Value' cabinets offer dimmable light, integrated power outlets and segmented table-tops, with a simple and intuitive controller all at a very affordable price. UV light and base stand are optional. Modern fan and filter technology facilitate full protection with the lowest noise levels – down to 46dB(A).

The 'Pro' range offer many additional features and options for customization.

Electronic-adjustable base stands can be controlled via the double-screen touch controller. Optional ethernet connections allow the NinoLaf technical team to support the cabinets anywhere in the world. The back wall is powder-coated to reduce glare and improve illumination.

Gas, vacuum, LAN and USB connections are optional, as are IV bars, hydrogen peroxide fumigation kits, modified table tops etc.

Sizes range from 600 to 1800mm, and all are built to EN12469 standards and fully compliant with Australian Standards.

Also available from NinoLaf are Cytotoxic Cabinets, Laminar Flow Cabinets, Gloveboxes, and an XL version of the Class II cabinet with extra large internal dimensions to accommodate robotics etc.

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Monday 7 February 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 world 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

- **Martin Westwell, Chief Executive** *SACE Board of South Australia*

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

Photos courtesy of MCVB

Siglo Bar on Spring Street by Ben King

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KEY DATES:

Earlybird Registration Deadline:
Friday, 24 June 2022

Abstract Submission Deadline:
Friday, 24 June 2022

Guaranteed Hotel Reservation Deadline:
Friday, 5 August 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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