Message from the BLiSS organisers

Have you ever wondered what your peers do in their lab? What field they study? What fancy technique they are an expert of? Then found yourself bored out of your mind during a general conference because the talks are too specific and you still don’t get what the research is about?

BLiSS is a one-day symposium made for ECRs, by ECRs. This event will provide a unique opportunity for Life Science ECRs from all the major Universities and research institutes in and around Brisbane to:

- **meet** their peers
- **share** their research in an interesting and engaging format (digital interactive posters, short, punchy talks focusing on research impact and significance, showcasing cutting-edge technique)
- **grow** as a researcher (build meaningful connections, jump-start collaborations)

Other program highlights include a stellar plenary talk from Prof Marylin Renfree, panel discussions on “How to survive as a scientist” and “Gender equity in science”, and a fun-filled social mixer.

BLiSS Steering Committee members

**Chair:** Florence Cotel
**Vice Chair:** Kirsty Short
**Treasurer:** Ilaria Stefani
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Ronan Kapetanovic
David Poger
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Ashik Ullah
Natalie Prow
Todd Shelper
Nathan Boase
Christiane Lang
Nela Durisic

**Design:** Nick Valmas
BLiSS 2016 themes
The overall theme for BLiSS 2016 is “Our Next Challenges”. We want to gather all of the Brisbane Life Sciences ECR community together for an opportunity to share their research in an effort to create new collaborations and research projects to help solve today's leading global issues.

Fighting disease and managing healthcare
This theme is aimed at research that aspires to prevent, better manage and develop innovative therapies to improve clinical and public health outcomes for both the population and the individual.

Sustaining the earth for 2100
Build Queensland’s and Australia’s capacity to respond to environmental change and integrate research outcomes from biological, physical, social and economic systems.

A head start on ageing and mental health
With census projections indicating the proportion of the population >65 years reaching 25% in the next 40 years, research on improving the physical and mental well-being of the ageing population in society is a major goal. This theme is aimed at research promoting a better lifestyle to the adult and senior population.

The new frontier:
technical and interdisciplinary advances
Breakthrough research often transcends the scope of a single discipline. This theme is aimed at research that integrates information, data, techniques, tools, and/or theories from two or more disciplines or bodies of specialized knowledge to accelerate scientific discovery.
## Program

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| 10:00    | Panel Discussion: **How to survive as a scientist** *(Chair: Dr Kirsty Short)*  
A/Prof Kirsten Spann, Prof Bill von Hippel, Dr Amy Jennison, A/Prof Christian Gruber |

### 10:45 Morning tea + poster session 1

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|       | Oncology drug discovery in the next dimension  
Dr Carrie Lovitt |
|       | Rethinking the role of antibodies in infectious diseases  
Dr Charles Armitage |
|       | The underestimated potential of ultrasound  
Dr Marie-Luise Wille |
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Ms Signe Christensen |
|       | The antimicrobial effect of zinc  
Dr Cheryl-Lynn Ong |

### 11:30 The Forum

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|       | Microbiome and blood pressure in early pregnancy  
Dr Marloes Dekker Nitert |
|       | How mutations in sequence-specific transcription factors cause disease  
Dr Kevin R. Gillinder |
|       | Murine model to study macrophage contributions to prostate cancer  
Dr Andy Wu |
|       | Using transplantations to study chronic diseases and therapies  
Dr Danielle Borg |
|       | Dissecting immunological networks in HPV-associated cancers  
Dr Zewen Kelvin Tuong |

### 12:40 Lunch

### 13:45 The Auditorium

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|       | Paying attention to sleep in fruit flies  
Dr Leonie Kirszenblat |
|       | Can our diet AGE us? Oral uptake and trafficking of dietary AGEs  
Ms Amelia Fotheringham |
|       | Two hundred million years in the making of brain circuits  
Dr Rodrigo Suárez |
|       | The contribution of neural crest to phenotypes in Down syndrome  
Ms Anu Balachandran |
|       | Concurrent physiological measures to aid clinical psychiatric diagnosis  
Mr Saurabh Sonkusare |

### 14:25 Afternoon tea + poster session 2

### 15:40 Panel Discussion: **Gender equity** *(Chairs: Dr David Poger & Prof Marilyn Renfree)*  
Prof Bob Williamson, Dr Wafa El-Adhami, Prof Melissa Brown, Ms Julienne Clifford

### 16:25 Concluding remarks & prizes

### 17:30 End of the symposium
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Universities Australia Chair, Professor Barney Glover, National Press Club, Mar 2016

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Any questions you want to ask during the panel discussions or the general discussion of each oral "Big challenge" session? Tweet and tag your burning question!
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What's your BLiSS? the competition
We are excited to announce an Instagram/Twitter competition themed ‘What’s your BLiSS at work?’ Is it the perfect experiment, a publication acceptance or just hanging out with your group over that steaming cuppa? Upload a photo and tag #ecr_bliss16 any time before or during BLiSS for a chance to win prizes on the day!

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Drug discovery and development programs depend on disease-relevant in vitro models. In the field of oncology, cells cultured in monolayer conditions are often employed, however these pre-clinical models do not always mimic the complex milieu of cancer (Figure 1) and drug candidates for this disease may lack clinical efficacy. The objective of this research was to increase the relevancy of in vitro pre-clinical models for cancer drug discovery through development of advanced three-dimensional (3D) cell culture models suitable for examination novel chemical compounds, profiling drug candidates and elucidation of drug resistance mechanisms. For this research, cutting-edge technology including liquid handling robotics and automated high content imaging and analysis methodology was utilised to evaluate drug candidates and deconstruct molecular mechanisms in advanced 3D cellular models.

Figure 1. The complex, heterogeneous microenvironment of tumours. The main elements of a tumour are tumour-specific and tumour-associated cells, structural components and chemical gradients. Modelling tumours utilising 3D cell culture technologies facilitates recapitulation many pertinent tumour elements.

1 C Lovitt, T Shelper, V Avery. Expert Opinion Drug Discovery. 2016, 11, 885-
Rethinking the role of antibodies in mucosal infections

Charles W Armitage¹, Richard S Blumberg², Kenneth W Beagley¹

¹Institute of Health and Biomedical Innovation, QUT, Brisbane, QLD, AUS
²Brigham and Women’s Hospital, Harvard Medical School, Boston, MA, USA

How your research fits into the bigger picture: The majority of successful vaccines rely on antibody-mediated protection targeting a pathogen’s surface proteins, yet many pathogens also have an intracellular niche. *Chlamydia trachomatis* is an intracellular bacterium that replicates inside host cells allowing it to hide from the immune system, thus the vast majority of vaccines have targeted the extracellular phase of infection. We have demonstrated that antibodies to the extracellular phase bind *Chlamydia* and paradoxically enhance epithelial uptake and infection¹⁻². Furthermore we provided the first evidence that antibodies travelling through epithelia can bind and neutralise intracellular chlamydial growth¹⁻³. These data provide evidence that targeting intracellular antigens is an interesting avenue in vaccine design.

The key questions that you are trying to answer: Identifying additional antigens and the mechanism of intracellular antibody neutralisation, and how the immune system clears infection represents a novel approach in vaccine design to intracellular pathogens.

The unique techniques you use in your experiments: GMO cells and mice, protein production and purification, flow cytometry, confocal microscopy, microbiology and immunology techniques.

Figure 1. Antibodies play an intracellular and extracellular role in pathogen clearance. Immunoglobulin G (IgG) trafficking through the epithelial cytoplasm can interact with chlamydial inclusion membrane and Type 3 Secretion System (T3SS) proteins which upregulates lysosomal fusion, protein degradation and flagging infected cells for killing by cytotoxic CD8+ T cells.

¹C Armitage, C O’Meara, M Harvie, P Timms, R Blumberg, K Beagley. *Immunol Cell Biol.* 2014 92(5) 417-26
³C Armitage, R Blumberg, K Beagley. 2016 In preparation
The underestimated potential of ultrasound

Marie-Luise Wille, Christian M. Langton, Scott Wearing
Institute of Health and Biomedical Innovation, Queensland University of Technology, Brisbane, Australia

In a clinical context, ultrasound is commonly known as an imaging modality and primarily used in monitoring the developing foetus in obstetrics. Other applications include monitoring of the blood flow in the heart, guiding a biopsy needle in oncology, and assessing musculoskeletal tissues after injury. However, we are far from having exploited the full potential that ultrasound has to offer and while innovation and technology are focussing on improving X-ray, PET, and MRI, the feasibility and associated costs for the patient are usually ignored.

In my research I take advantage of the fact that ultrasound is a mechanical wave and therefore highly dependent upon density and structure of the propagated material. By applying a novel ultrasound signal processing technique, I am exploring new avenues to find alternative and cost-effective methods to predict osteoporotic fracture risk or to monitor tissue composition changes in the diabetic foot in order to prevent ulceration.

Figure 1. Prototype design of an ultrasound heel scanner which can measure the bone density or the tissue composition of the plantar fat pad. This handheld device may be easily transported in a carry bag and transmit the ultrasound signals via Bluetooth to a tablet computer.

Dr Marie-Luise Wille
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Since 3/2015 Postdoctoral Research Fellow, IHBI, QUT
Research interests: ultrasound, medical imaging, signal processing, astrophysics
A new way to fight bacterial infections

Signe Christensen¹, Morten Grøftehauge¹,², Begoña Hera¹,³, Róisín McMahon¹ and Jennifer L. Martin¹,⁴

¹Division of Chemistry and Structural Biology, Institute for Molecular Bioscience, University of Queensland, St. Lucia, Queensland 4072, Australia
²School of Biological and Biomedical Sciences, Durham University, Durham DH1 3LE, UK
³La Trobe Institute for Molecular Science, La Trobe University, Melbourne, VIC 3086, Australia
⁴The Eskitis Institute, Griffith University, Brisbane Innovation Park, Nathan QLD 4111, Australia

The rise in antibiotic resistance is undermining our ability to treat an increasing range of bacterial infections and is a huge threat to public health worldwide¹. Disulfide bonds provide structural bracing to numerous proteins including those involved in bacterial pathogenesis². Bacterial disulfide bond (DSB) proteins catalyze the formation of disulfide bonds and thus are potential targets for drug development. The primary enzyme in the DSB family is DsbA. DsbA enzymes share the same overall fold but have subtle variations on their surface³. A broader knowledge of the diversity of DsbAs supports the development of broad and narrow spectrum inhibitors of DsbAs. Here I present the characterization of the DsbA from the intracellular pathogen Chlamydia trachomatis (CtDsbA). The structure of CtDsbA was solved by X-ray crystallography and reveals a typical DsbA fold (Figure 1). Functional assays shows that CtDsbA is an oxidase, although the least oxidizing DsbA studied to date.

Figure 1. The structure of CtDsbA was solved by X-ray crystallography to a resolution of 2.7Å. CtDsbA has a typical DsbA structure with a thioredoxin fold (dark blue) containing the active CXXC motif (yellow). In light blue is the inserted helical domain. CtDsbA has an additional, non-catalytic, disulfide (orange) only seen in three other DsbAs, as well as an unpaired cysteine (red), which has not been previously reported in a DsbA.


Oral presentations

Fighting disease and managing healthcare
Zinc deficiency is associated with increased susceptibility to bacterial infection. Here, we investigated the role of zinc in innate immune defense against Group A *Streptococcus* (GAS), a Gram-positive bacterial pathogen responsible for a wide spectrum of human diseases. We found that deletion of the *czcD* gene (encoding a zinc efflux pump) reduced the ability of GAS to grow in the presence of zinc and increased accumulation of internal zinc. Furthermore, the mutant displayed attenuation in the mouse and neutrophil assays and show that zinc at the site of infection is critical for host immune defense. We also demonstrated the mechanisms by which zinc exerts its toxic effect in GAS. As such, zinc efflux is an important contributor to GAS pathogenesis and zinc may play a direct antibacterial role in innate immune defense against infection. To date, our data has provided new insight into the potential use of zinc as therapeutics against bacterial infections.
O-06

Microbiome and blood pressure in early pregnancy

Luisa F Gomez–Arango, Helen L. Barrett, H. David McIntyre, Leonie K. Callaway, Mark Morrison, Marloes Dekker Nitert for the SPRING trial group

1School of Medicine, The University of Queensland, Brisbane Australia
2UQ Centre for Clinical Research, The University of Queensland, Brisbane Australia
3Obstetric Medicine, Royal Brisbane and Women’s Hospital, Brisbane Australia
4Mater Research, The University of Queensland, Brisbane Australia
5Diamantina Institute, Faculty of Medicine and Biomedical Sciences, The University of Queensland, Brisbane Australia
6School of Chemistry and Molecular Biosciences, The University of Queensland, Brisbane Australia

Background: Obese pregnant women have a higher risk of developing pregnancy-induced hypertension and preeclampsia. Outside pregnancy, the gut microbiome of obese individuals is different from normal-weight individuals. Low-grade inflammation is a hallmark of obesity. Metabolites excreted by bacteria in the gut microbiome may contribute to hypertension and inflammation. This study aimed to investigate if blood pressure and level of the inflammatory marker PAI-1 are associated with altered gut microbiome composition in overweight and obese women in early pregnancy.

Methods: The composition of the gut microbiota was determined in 205 women at 16 weeks gestation from the SPRING study with 16S rRNA sequencing. The expression of butyrate-producing genes in the gut microbiota was assessed by real-time PCR. PAI-1 levels were measured in fasting serum of a subset of 70 women at 16 weeks gestation.

Results: Obese women had significantly higher systolic and diastolic blood pressure than overweight women in early pregnancy. Systolic blood pressure was negatively correlated with abundance of the butyrate-producing genus Odoribacter in the gut microbiome. Butyrate production capacity by the bacteria in the gut microbiome was decreased in women with higher blood pressure. PAI-1 concentrations were increased in obese pregnant women. PAI-1 was inversely correlated with expression of butyrate kinase and abundance of Odoribacter.

Conclusion: The results of this study show that in overweight and obese pregnant women at 16 weeks gestation, the abundance of butyrate producing bacteria and butyrate production in the gut microbiota is significantly negatively associated with blood pressure and with PAI-1. Increasing butyrate-producing capacity may contribute to maintenance of normal blood pressure in overweight and obese pregnant women.
How mutations in the DNA-binding domain of sequence-specific transcription factors cause disease

Kevin R. Gillinder¹, Graham W. Magor¹, Andrew C. Perkins¹,²

¹Mater Research – University of Queensland, Translational Research Institute, Brisbane, QLD 4102, Australia
²The Princess Alexandra Hospital, Brisbane, QLD 4102, Australia

The average human genome contains nearly 100 missense mutations within the DNA-binding domain (DBD) of various sequence-specific transcription factors (TFs). Missense mutations in the DBD of TFs can alter both the affinity and the specificity of DNA-binding leading to disruption of gene regulation. Despite their medical importance, the consequence of these mutations remains largely unknown. To investigate this, we have generated missense mutations, modeling human disease, in critical DBD residues of Krüppel-like factor-1 (KLF1), an essential TF required for nearly every aspect of red blood cell formation. Combining Next-Generation sequencing techniques including chromatin immunoprecipitation (ChIP), chromatin conformation capture (Capture-3C), ATAC-seq, and 4sU-labelled RNA-seq, we aim to understand how these mutations alter the affinity and specificity of DNA-binding, and distort transcription of direct target genes.

Figure 1. A missense mutation in KLF1 confers an altered DNA specificity leading to anemia. During normal red cell formation KLF1 regulates target genes like β-globin and Alas2, through binding the sequence GGT-[CT]G-GGN in the promoter or enhancer of genes. However, the E339D mutation, also known as Neonatal Anemia (Nan-KLF1) alters the specificity and affinity of this sequence, leading to dysregulation and ectopic gene expression.

3MR Tallack & AC Perkins. IUBMB Life. 2010 62, 886–890

Dr Kevin Gillinder
Affiliation: Mater Research – University of Queensland, Australia:
Phone: +61 73343 7531 E-mail: kevin.gillinder@mater.uq.edu.au
Personal History: 1999–2002 BSc. Science (Hons)
2009–2012 PhD in Stem Cell Science, Newcastle University UK
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O-08
Murine model to study macrophage functional contributions to prostate cancer lesion development

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Prostate cancer (PCa) is the most commonly diagnosed cancer in Australian men with high propensity to metastasise to bone which disrupt bone homeostasis and leads to tumour growth and development of pathological osteoblastic/osteolytic lesions. Bone metastasis and associated skeletal complications increase mortality risk in PCa patients. Identification of approaches to disrupt the interplay between PCa cells and cells of the bone marrow environment will lead to additional treatment options for men with skeletal metastasis. Immune cells in particular macrophages have been implicated in tumour development and its number correlate with disease progression in primary PCa. We have developed a murine immune-competent PCa bone growth model that mimics lesions observed in human PCa bone metastasis and this model permit us to explore macrophage functional contributions to PCa lesion progression. Our research will provide foundation knowledge toward the development of macrophage-targeted therapies that may improve responses of established bone tumour to chemotherapy.

Figure A. Immune competent mouse model of PCa growth in bone exhibit both osteoblastic and osteolytic lesions, a clinical feature commonly observed in patient samples. (i) Immunohistochemistry staining for collagen type I shows pathologic woven bone (WoB) within the medulla adjacent to original cortical bone (CtB) and interspersed in regions of both dense tumour and haematopoietic tissue. (ii) Enzymatic staining of TRAP, showing region of extensive osteolysis on existing bone surfaces (white arrowhead). Tm, tumour; Tb, trabecular bone.

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Using transplantations to study chronic diseases and therapies

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Cellular transplantation is a viable therapy for several diseases. Cellular transplantation can be performed preclinically in murine hosts via various site-specific injection sites to further improve cell therapies and understand disease processes. The subcapsular space, located between the renal capsule and kidney is an ideal site for cellular transplantation due to its accessibility, containment of transplanted material, and ease of angiogenesis. With the aim to improve functional outcomes for islet transplantation, a cell therapy used for individuals with unstable type 1 diabetes, we used the renal subcapsular space as a site for autologous, murine islet transplantation. Specifically using a chemically-induced model of diabetes, hyperglycaemic recipient mice were transplanted with a syngeneic islet mass under the kidney capsule. Islets were treated with a compound known to reduce islet stress or PBS (vehicle control). Post-transplant, this model allows for continual monitoring of graft function. Further processing of the graft can be performed after anephrectomy.

Figure 1. Illustration of renal subcapsular transplantation in anaesthetised mice. A small incision is made in the renal capsule, tubing containing cells is inserted into subcapsular space, cells are released using a microsyringe into the renal space, tubing is retracted and small incision is cauterised.

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Dissecting the immunological networks that changes in HPV-associated cancers

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HPVs are epitheliotropic double-stranded DNA viruses that infect the basal keratinocytes on skin and mucous membranes. Most HPV infections are cleared rapidly by the immune system but extended virus persistence, especially by ‘high-risk’ HPV types, is associated with the induction of local immunosuppression and increasing risk of dysplastic transformation of normal epithelium. We are interested in understanding the immunological consequences of HPV infection in cancers, including cervical cancer and oral cavity cancer. We combine molecular, immunological and bioinformatics approaches to investigate the alterations to immune networks in transgenic mouse models of cervical pre-cancer. In addition, we have recently used high-throughput sequencing technology to investigate the impact of HPV on the mutation burden during cancer and to uncover critical components that may influence the immune landscape in HPV-associated skin and mucosal malignancies (Figure 1). We hope that our research will one day assist in better informing immunotherapy design and strategies.

Figure 1. Alterations to complex genetic and immunological networks underscore the consequence of HPV infection during cancer. Identification of the main pathways involved will aid in tailoring immunotherapy options for patients.

Paying attention to sleep in fruit flies

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The benefits of a good night’s sleep seem obvious, yet we still know little about the functions of sleep. One consequence of sleep deprivation is the degradation of attention. Interestingly, attention seems to be intimately linked with sleep throughout the animal kingdom, as studies in humans and other animals suggest sleep is crucial for attention while attention processes drive sleep need. We are investigating the relationship between sleep and attention in the model organism Drosophila, using novel behavioral paradigms to study visual attention and sleep, and state-of-the-art microscopy techniques to examine how these processes affect synaptic connectivity in the brain. We have found that sleep deprivation makes flies more distractible, while genetically activating a molecule involved in sleep and plasticity makes flies less distractible. By studying relatively simple circuits of the fly brain, we aim to discover fundamental plasticity mechanisms of sleep that optimise attention.

Figure. Evolution of sleep and cognitive capacities. Sleep has several functions that appear to have evolved as nervous systems became more complex. In simple nervous systems such as the nematode, C. elegans, sleep-like states are triggered by developmental stages and environmental stress, suggesting these are primitive functions of sleep. In animals with more complex nervous systems (such as flies and mammals) a daily need for sleep emerged, most likely to cope with the plasticity demands of cognitive processes such as operant learning and selective attention.

Figure. Evolution of sleep and cognitive capacities. Sleep has several functions that appear to have evolved as nervous systems became more complex. In simple nervous systems such as the nematode, C. elegans, sleep-like states are triggered by developmental stages and environmental stress, suggesting these are primitive functions of sleep. In animals with more complex nervous systems (such as flies and mammals) a daily need for sleep emerged, most likely to cope with the plasticity demands of cognitive processes such as operant learning and selective attention.


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Can our diet AGE us? Exploring oral uptake and trafficking of dietary AGEs modified proteins in healthy mouse models

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Advanced Glycation End Products (AGEs), are post translational modifications to proteins, commonly seen in western diets. AGEs are known to affect glycaemic control, cause inflammation, accumulate with aging and associate with disease. Little is known about gastrointestinal absorption of dietary AGE modified proteins and their subsequent localisation to different tissues. Therefore, we used a near infrared (near–IR) labelled AGE–modified model protein (near–IR AGEs), deliver edit intra–gastrically to healthy adult mice and analysed their tissues, from 15min to 8 hrs after delivery to localize the near–IR AGEs. AGE modified proteins were present in the circulation, duodenum and liver as both intact protein (66kD) and cleavage products (<20kD) within 15 minutes. Only cleavage products were found to be present in the kidney and urine. The presence of intact dietary derived AGE modified protein in the circulation and tissues may have a role in exacerbating inflammation and disease pathology.

Figure 1. Schematic of oral delivery, uptake and trafficking of near infrared tagged model AGEs. Healthy adult mice were delivered AGE modified proteins into the stomach to mimic ingestion. The near IR labelled AGEs appeared within the bloodstream, duodenum and liver as a mix of un–cleaved, intact product, or smaller digested products. The cleaved digested products were also found to be present in the kidney and the urine.

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Two hundred million years in the making of brain circuits

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Several psychiatric and neurological conditions are due to malformations of neuronal circuits in the cerebral cortex, a region of the brain only present in mammals. What general rules have guided brain formation across evolutionary time remains unknown. To address this, we compared magnetic resonance imaging, mapping of neuronal circuits, and gene expression analyses across mammalian species. Our findings reveal a 200 million years old template of cortical connections, with shared genetic programs, neuronal architecture, and wiring features between hemispheres. Such an ancestral map predates the origin of the corpus callosum for more than 40 million years, and suggests the corpus callosum evolved in early placentals by exaptation of evolutionary-old mechanisms. These results reveal conserved developmental features that could be exploited to re-route cortical connections in congenital defects of cortical miswiring, and offer new insights to inform biomedical strategies aimed at improving mental health in individuals with neurodevelopmental disorders.

Figure 1. Ancient origin of a mammalian program cortical connections. The cerebral cortex is only present in mammals, and consists of neurons organised in layers at the brain surface. The brain of other vertebrates, such as birds, is instead organised in clusters of neurons. The pattern of connections between hemispheres differs dramatically between birds and placentals (such as mice and humans). However, whether monotremes and marsupials share such patterns is currently unknown. Here we combined magnetic resonance imaging of the brains of platypus and dunnarts, with gene expression and circuit connectivity analyses and revealed an ancient map of bilateral connections that arose more than 200 million years ago.

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Investigating the contribution of neural crest to phenotypes observed in Down syndrome

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Neural crest cells (NCCs) are transient, multipotent progenitors that emerge 3 weeks into human embryonic development. They migrate within the embryo differentiating into craniofacial bone and cartilage, craniofacial and enteric neurons and glia, pigment and smooth muscle cells. Abnormal NC development results in neurocristopathies including Hirschsprung’s disease, craniofacial and cardiac abnormalities. Infants with Down syndrome (DS) have >300 times higher risk for developing these congenital malformations warranting a closer examination of NC development in DS.

We developed a SOX10 reporter line using CRISPR/Cas9 genome editing technology which along with an optimised protocol to differentiate human pluripotent stem cells (hPSCs) into SOX10+ NCCs allows us to efficiently isolate these cells. A multi-omic study on SOX10+ cells combined with bioinformatics tools was used to primarily identify unique cell surface markers as well as heterogeneity amongst SOX10+ cells. Currently, we are examining the molecular profile and migratory capacities of neural crest from DS-hPSCs.

*Figure 1.* Differentiation of SOX10 reporter hPSC line to cells that express SOX10:mMaple which can be enriched for under puromycin selection.

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**Research interests:** CRISPR/Cas9 genome editing, patient derived human pluripotent stem cell culture and differentiation, neural crest cells, multi-omic analyses combined with bioinformatics, in-vitro cell migration assays
Multiple concurrent physiological measures to aid clinical psychiatric diagnosis

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Descriptions of affective disorders clearly recognize some distinct changes in physiological features, yet in most clinical practice and research there is little actual use of physiological measurement. The use of such measures to aid clinical diagnosis has been limited by poor reliability, validity and methodological advances. These physiologic changes could provide an objective method to aid a clinician in diagnosis or even monitoring treatment responses in patients with neuro-psychiatric disorders.

I am validating and characterising the pattern of these changes underlying various emotions by employing multi-modal set of tools that measure physiological changes. Furthermore, this study will also generate data for facial expression tracking study which further compliments the eventual aim of objective diagnosis of neuro-psychiatric disorders.

Figure. LabNeuro: Multimodal data acquisition laboratory. This image shows the subject wearing an EEG cap with electrodes attached to the fingers and arms (for measuring skin conductance and heart rate respectively) and thermal camera and video camera are focussed on the participant’s face. LabNeuro is running on the left monitor while the stimulus is displayed on the right monitor.
Developing new mass spectrometry tools for the analytical chemistry toolbox

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Analytical chemistry is fundamentally concerned with identifying and quantifying molecules in complex matrices. Even with modern instrumentation and software, analysis of structurally diverse molecular targets presents a significant challenge. This daunting task is exaggerated for the non-specialist researcher tasked with determining molecular function and requires an interdisciplinary approach to maximise data quality.

The QUT Mass Spectrometry Development Laboratory advances novel instrumentation for the analytical chemistry community, especially for resolving impasses where conventional techniques are unable to provide a complete picture. Differentiating isomeric lipids (e.g., omega-3 and omega-6 fats) is difficult when identification is primarily based on molecular mass! We study the interaction of ionised lipids with laser radiation or gaseous reagents inside a mass spectrometer to discern subtle structural differences. By studying the dissociation of multiple isomers in the presence of ozone, we have shown that Drosophila produce only a single isomer of a pheromonal triacylglycerol (Figure 1).

Figure 1. Sequential collision-induced dissociation (CID) and ozone-induced dissociation (OzID) of triacylglycerols inside a modified mass spectrometer unequivocally identifies the molecular structure of a pheromone, and demonstrates that only a single isomer is produced.

Beyond pretty models: how single particle cryo-electron microscopy is used to understand macromolecular complexes

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Since its development, cryo-electron microscopy (cryo-EM) has been a promising technique accompanying X-ray crystallography and NMR for the structural investigation of protein complexes. The recent advances in imaging with Direct Electron Detectors (DED) and single particle analysis software have dramatically improved the resolution of 3D reconstruction starting the so-called “resolution revolution”. Here I describe how we optimised single particle cryo-EM analysis for the characterisation of two different macromolecular complexes: The vacuolar protein sorting 4 (Vps4) oligomer, a key enzyme hijacked by enveloped viruses (HIV, Ebola and Herpes simplex) to mediate their infection and the Bluetongue virus core-like particle (BTV-CLPs) a RNA free viral capsid used for encapsidating foreign proteins with therapeutic potential. The cryo-EM study of both of these particles will aid the therapeutic development of new anti-virals targeting host proteins, as well as the design and modification of virus-like nanoparticles for biomedical and nanotechnology applications.

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Mucosal associated invariant T-cells (MAIT cells) are an abundant population of innate-like human T cells in the blood, liver and gut mucosa. Their activation via the T cell receptor (TCR) upon presentation of bacterially derived antigens by an MHC class-I related molecule (MR1) has been implicated in pathological processes such as inflammatory bowel disease and the immune response to pulmonary bacterial infection. Although the identity of the antigen(s) had been elusive, we recently discovered that an unstable riboflavin-type metabolite binds to MR1 and then activates MAIT cells. It is formed in vivo via the condensation of 5-amino-6-D-ribitylaminouracil (5-A-RU) and pyruvaldehyde (2), a metabolite of glycolysis. Through chemical synthesis, MS and NMR characterization, the solution structure of this unstable antigen was determined unambiguously as 5-(2-oxoethylideneamino)-6-D-ribitylaminouracil (5-OP-RU), which readily undergoes degradative cyclization to give lumazine. The MAIT TCR-MR1-antigen crystal structure revealed the formation of a Schiff base between MR1 Lys43 and 5-OP-RU stabilizing the antigen. Together, these show an unexpected mechanism of generating T-cell antigens by using disparate chemicals from different metabolic pathways.
One of the grand challenges of modern biophysical science is to understand how intrinsically disordered peptides (IDPs) can fold into a unique, biologically functioning protein structure from the myriad conformations of the unfolded state. We combine the inherent power of high performance computing and advanced molecular dynamics simulations algorithms to capture the conformational changes in IDPs that typically occur on the millisecond time scale. Malfunction of a key IDP called Tau is the likely culprit behind Alzheimer’s disease. It’s misfolding promotes aggregation and are toxic to the brain. Experimental methods alone are generally too limited to provide the atomistic level of detail that is needed to characterize the molecular interactions that are involved. The combination of modelling with NMR techniques paves the way towards understanding how information encoded in amino acid sequences of Tau governs its molecular function, contributes to organization of protein interaction networks and modulates the mechanisms of protein self-assembly.

Figure 1. Molecular dynamics simulations of structural characterisation of IDPs. Step 1 consists of defining a molecular mechanics force-field to calculate the potential energy of the protein as a function of the atomic coordinates. In step 2 a simulation box is defined that contains the coordinates of the Tau peptide, water and salt to mimic the experimental condition. Step 3 consists of numerical integration of Newton’s equations of motion defined by the positions, forces and velocities of every atom in the simulation box. These equations are solved using the high performance computing facility. Steps 4, 5 and 6 involve the analysis and molecular interpretation of the terabytes of data produced by the simulation of the peptides leading to characterisation of their structural features.

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The Australian National Fabrication facility was established by the Australian Government to provide access to the most advanced micro and nanofabrication tools to the Australian research community. Across our 8 nodes we provide support for projects that span every aspect of Australian research efforts, from food and agriculture through to astronomy and archaeology. This talk is a brief introduction to the capabilities that you can find here in Queensland and some examples of the diverse and exciting research that we facilitate.

**Dr Jane Fitzpatrick** is the Facility Manager of ANFF-Q. Jane has a background in biotechnology where she worked in industry and academia, including a 3 year spell with an innovative biotech start-up company. She brings experience in business development and operations management from her previous roles and has a wealth of experience of the ANFF organisation through her involvement since 2010. She also has a focus on the development and support of the female members of our industry to ensure that the talent that we nurture is fully realised. As with all our staff, she is dedicated to the principles of open access, centralised facilities that support Australian researchers to achieve on a global scale.
Poster presentations

- Sustaining the earth for 2100
- A head start on ageing and mental health
- The new frontier: technical and interdisciplinary advances
- Fighting disease and managing healthcare

P-1 Antibiotic treatment at delivery shapes the initial oral microbiome in neonates

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P-02 Copper in bacterial physiology and pathogenesis

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P-03 Hardening up: metal composition in aculeate ovipositors

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P-04 Investigating Plasmodium falciparum histone deacetylase 1 complex proteins

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P-05 Ureaplasma spp. multiple banded antigen (MBA) size variation is associated with altered immune responses in vivo and in vitro

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P-06 Identifying cellular and molecular events leading to agenesis of the corpus callosum during brain development

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P-07 Melt-electrospun polycaprolactone-strontium-substituted bioactive glass for bone regeneration

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P-08 Toward destabilizing multidrug resistant plasmids in E. coli

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P-09 Genetic network of non syndromic intellectual disability

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P-10 How sunflower makes a ring from a string

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P-11 Characterising visually responsive ensembles in the zebrafish tectum

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P-12 Molecular regulation of adult neural stem cells

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P-13 An integrated molecular analysis of invasive lobular carcinoma

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P-14 The endopeptidase PepO is essential for the pathogenesis of the global M1T1 clone of Streptococcus pyogenes


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P-15 Suppression of the pelo protein by Wolbachia and its effect on dengue virus in Aedes aegypti

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P-16 Fine-tuning erythropoiesis by competition between Krüppel-like factors for promoters and enhancers

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P-17 Optimisation of multicomponent systems for the targeted delivery of oligonucleotide therapeutics

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P-18 Engineering Escherichia coli for the production of propionic acid

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P-19 Development novel tissue targeted nerve growth factor: fibronectin chimeric fusion proteins for stimulation of peripheral nerve regeneration

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P-20 In vivo activity of clinically approved anti-cancer HDAC inhibitors in a murine model of malaria

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**P-21** Zoonotic agent lurking in the environment: *C. psittaci* infection impacts on animal and public health in Australia

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**P-22** Genetic risk for schizophrenia is associated with where you live

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**P-23** Why do the axons cross the brain? To get to the other side!

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**P-24** Zinc against group A *Streptococcus*

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**P-25** Functional hypomorphic ATM variant effects DNA damage response and repair pathways

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**P-26** Wnt signalling regulates the cytokine response to the natural killer T cell antigen, α-galactosylceramide

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P-27 Molecular cloning designer simulator (MCDS)
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P-28 Elucidating neuropathologies with the help of human induced pluripotent stem cells
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P-29 The assassin bug Pristhesancus plagipennis produces two distinct venoms
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P-30 Use of genome–wide association studies and polygenic scores to examine the genetics of ADHD
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P-31 Using light-activated channel rhodopsin to study neuronal networks involved in sensory input
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P-32 Examining a novel visual task for identifying individuals at increased risk of developing mental illness
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**P-33** Virulence determinants in West Nile virus

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**P-34** Profiling at the single-cell level reveals evidence for antigen-driven oligoclonal expansion within the TCR repertoire of citrullinated vimentin-specific CD4⁺ T cells in peripheral blood of Rheumatoid Arthritis (RA) patients

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**P-35** Lifestyle factors among Vietnamese women after breast and/or gynecological cancer

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**P-36** Hypercholesterolemia is a danger signal of increasing risk for osteoarthritis

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**P-37** Efficiency of UV-induced DNA damage repair in normal skin melanocytes, genotypic variants associated with melanoma and dysplastic naevi

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**P-38 The role of EphA3 in leukemia stem cell renewal**

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**P-39 Parasite-origin Kunitz type protease inhibitor with anti-cancer properties**

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**P-40 The development of a genetic tool for detecting the malaria parasite in mosquito populations**

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**P-41 Enrichment of SNPs in functional categories reveals genes affecting complex traits**

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**P-42 A blueprint for building the Nicotiana benthamiana genome biology**

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**P-43 The University of Queensland Library**

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