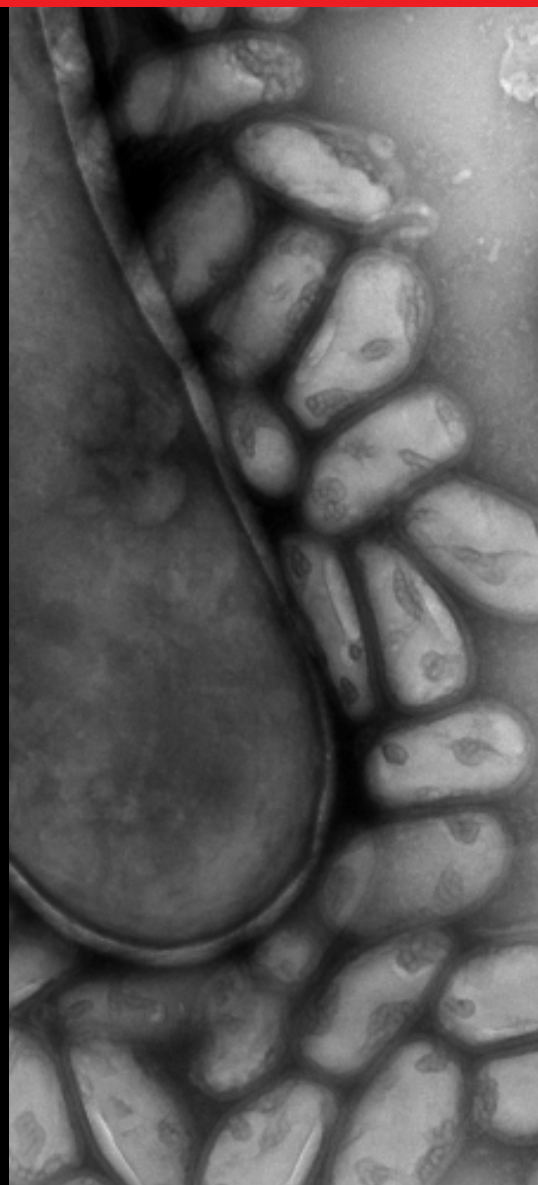
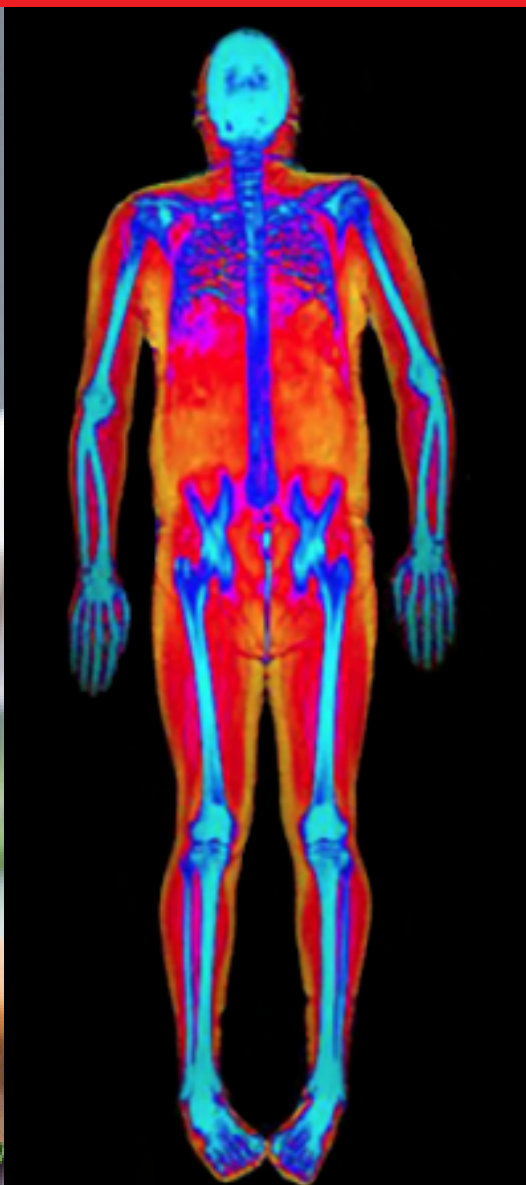


2027 Honours
in the School of
Agriculture,
Biomedicine
& Environment



**Visit our LMS site for up-to-date information
and upcoming information sessions:**

<https://lms.latrobe.edu.au/course/view.php?id=104895>



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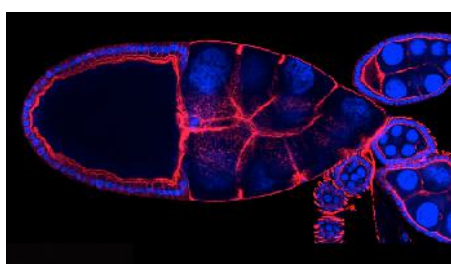
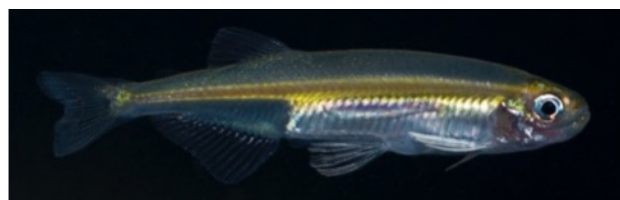
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General Information

Welcome to SABE

Congratulations on selecting the Honours program within the School of Agriculture, Biomedicine and Environment!

The School of Agriculture, Biomedicine and Environment (SABE) plays a large part in the strategic endeavours of the University, and generates a significant proportion of the University's research outputs and income across a broad range of disciplines. These include: Agriculture, Botany, Soil Science, Animal Physiology and Health, Plant Science, Agronomy, Ecology, Evolution, Genetics, Conservation Biology, Zoology, Neurobiology, Microbiology, Physiology and Pharmacology, Anatomy, Biochemistry, Cell Biology, Chemistry, Cardiovascular Physiology and Translational Science.

Doing a Honours research project in SABE will place you at the leading edge of scientific knowledge in your area of interest, which I hope will be both exhilarating and satisfying. Creating new knowledge and sharing this with your colleagues will allow you to appreciate the scientific method and instill in you a curiosity that can be quite addictive. On your path to discovery, you will be supported by academic supervisors with years of experience and expertise to guide you through your research project and state-of-the-art infrastructure. I wish you only success in your research endeavours during Honours and hope you consider joining our postgraduate student body in the future.



Prof. Robyn Murphy
Dean, School of Agriculture,
Biomedicine and Environment (SABE)



Dr. Keith White
Honours coordinator for SABE

Hello, my name is Keith and I am the coordinator for the SABE Honours program.

The addition of an Honours year to your Bachelor's degree adds many strings to your bow. As an Honours student, you get to:

- Be trained by experts and work within a professional team
- Develop management skills as you take on a new and exciting research project
- Learn how to overcome adversity/troubleshoot when things aren't working
- Communicate the findings and real-world implications of your research
- **AND** learn more about a discipline you enjoy

An Honours year is different to your prior studies. Most of your time is dedicated to research rather than classwork. No set timetable directs you where/when to be and you receive close mentorship from talented scientific researchers who train you in becoming an expert in your field of interest. You will find Honours fun, exhilarating, frustrating, intense, and like nothing you have ever done before!

The purpose of this information booklet is to (1) help you decide if you want to do Honours, (2) direct you to academic supervisors whose field of expertise interests you and (3) understand how to apply for Honours. If you have any questions or just need some guidance, please email us: sabehonours@latrobe.edu.au.

Important information about SABC Honours

What is Honours?

As an Honours student in SABC you will embark on an experience that is very different to your undergraduate studies. Honours students fully immerse themselves in a research topic and experience first-hand what a career in research is like. Our students work alongside world-leading researchers in a variety of discipline areas, ultimately, becoming experts in data analysis, critical thinking, and the use of cutting-edge scientific techniques. Our goal in Honours is to transform you from an undergraduate student (who learns about science from a textbook) into a successful researcher (who rewrites textbooks).

What skills will you obtain by doing Honours in the School of Agriculture, Biomedicine & Environment (SABC)?

Students who undertake Honours in SABC will work on an exciting, research-based project. You will learn a multitude of practical laboratory or field skills, access state-of-the-art technology, analyse data, think critically and develop skills in communicating your research. Our Honours graduates are highly sought-after by employers from all sectors. Skills include:

- A range of important scientific technical skills (fieldwork, animal, cellular, biochemical and/or molecular laboratory techniques) that are required to perform everyday research.
- Skills to manage a research project, from effective time-management to the detailed planning and execution of experiments.
- Critical thinking: learn to interpret and evaluate scientific literature and your own data.
- Communication skills (both written and oral) required to present your research to scientific and generalist audiences.

What are the entry requirements for Honours in SABC?

Honours is a 4th year of your undergraduate degree, meaning you need to have finished your Bachelor's degree before you start. Our requirements for entry are:

1. **Completed Bachelor's degree** (or at least will be completed by the time Honours begins). There are two Honours courses offered in SABC: the Bachelor of Science Honours and the Bachelor of Biomedicine Honours. To be eligible for the Bachelor of Biomedicine Honours you need to have completed a Bachelor of Biomedicine.
2. Achieve an **average mark (WAM) of 60 or better across all third-year subjects.**
3. Achieve a **WAM greater than 65 in four discipline-specific 3rd year subjects.**
4. Obtain the approval of a research supervisor.

The final selection of students into Honours projects is at the discretion of the research supervisor. This means that even if you meet all the other criteria, the most important eligibility requirement is that you select a research supervisor AND they agree to take you on.

When is Honours in SABC offered?

Honours in SABC has two entry points. You can commence your Honours year:

- February, concluding mid-November
- July, concluding mid-June the following year.

No matter when you start Honours, the year is structured so that it ends with the submission of a thesis detailing your research accomplishments.

Can I study full-time or part-time?

Honours in SABC is available for both full-time and part-time study. However, this is dependent on the nature of the research project and willingness of the supervisor. We have indicated in this booklet whether research projects are available for full-time study, part-time, or both.

What is the time-requirement for Honours?

Honours should be thought of as an intensive work-experience placement. Students studying full-time should expect a time commitment of 40 hours per week, while part-time students should expect a time commitment of 20 hours per week. Students will also have to spend additional time working towards coursework subjects and research assessments such as the preparation of presentations or thesis writing.

Where will my project be located?

Honours projects in SABC are supervised by scientists in a variety of state-of-the-art research facilities. Where you conduct your project will depend on where your supervisor is located - you may even not have a fixed location and spend your time in the field! Our Honours projects are available at the Bundoora and Albury-Wodonga La Trobe University campuses; within institutes such as the La Trobe Institute for Molecular Science (LIMS) or AgriBio; or at external research sites such as the Olivia Newton-John Cancer Research Institute (ONJCRI) in Heidelberg, and Baker Heart and Diabetes Institute in Prahran. No matter where you do your Honours project, you will have access to superb facilities and interact with a large number of groups with similar scientific interests.

Scholarships and financial aid

La Trobe Access Scholarships

Honours can be a demanding year, often requiring students to balance employment, personal commitments and the significant time investment needed to complete a research project. La Trobe's Access Scholarships and Bursaries are designed to help students overcome barriers to study and achieve their academic goals. These scholarships and bursaries support students who have experienced:

- Financial hardship
- Personal hardship or challenging life circumstances
- Disadvantage or underrepresentation in higher education

All new and continuing domestic La Trobe University students are eligible to apply. Unfortunately, international students are not eligible. Access scholarships provide funding of at least \$5,000 per year, while Bursaries are typically awarded as a one-off payment of at least \$1,000.

Applications for Semester 1

Applications for Access Scholarships and Bursaries for Semester 1 are processed through the VTAC SEAS and Scholarships Scheme.

- Applications are free.
- Applications generally open in August and close in early October each year.
- Visit [Applying for equity schemes and scholarships](#) for current application dates, eligibility requirements, and application instructions. Use the blue Login button on the top right of the website to begin.

Applications for Semester 2

Applications for Access Scholarships and Bursaries for Semester 2 are processed directly by the La Trobe Scholarships Office.

- Applications generally open in May and close in late June each year.
- Visit the [La Trobe Scholarships home page](#) for current application dates, eligibility requirements, and application instructions. You can also use the filters to explore any other opportunities you may be eligible for.

School-level Awards & Scholarships

Merit-based scholarships are also offered to recognise academic achievement. Students who undertake a project in one of the School's Departments are automatically considered for one of several merit-based scholarships:

- R.D. Schnagl Award: Award of \$500. Available to students who completed a major in Microbiology.
- Peter Rawlinson Award: Award of \$500. Available to students with a research topic in field-based animal ecology.
- David Ashton Prize: Award of \$1000. Available for students with a research topic on the ecology of Australian flora.
- Richard Zann Memorial Bursary: Award of \$3000. Available to students from a regional area with a research topic in animal studies.

These awards/scholarships are automatically awarded to students based on their 3rd year marks and the appropriateness of the research project. Students do not need to apply and will be notified if successful.

Career outcomes

Our Honours graduates are highly employable, being sought after by other universities, research institutes, hospitals and biotechnology companies. The majority of our Honours graduates develop a love for research during their placement, and decide to continue in research by undertaking further postgraduate study (Masters/PhD). Our graduates then go on to undertake further postdoctoral research, within Australia or overseas. Others, including those listed below, pursue diverse non-academic roles in industry, medicine, biotechnology and others:

- Dr Josh Vido (Honours 2019) is now a Nature Repair Coordinator with *Nyamba Buru Yawuru*.
- Jayde Higginbottom (Honours 2023) is the Monsoon Vine Thicket Project Coordinator with *Kimberly Land Council*, Broome.
- Ella Johnston (Honours 2016) is an ARC Early Career Industry Fellow working at La Trobe University, supported by *VivaZome Therapeutics Pty Ltd*.
- Rebecca Grinter (Honours 2023) is working at *Corangamite Catchment Management Authority (CMA)*, an agency for integrated catchment management.
- Gianna Lishmund (Honours 2015) is an Inside Sales Specialist at *Tecan*.
- Matthew Brewer (Honours 2015) is a Senior Supply Planner at *MARS petcare*.



**How
do you choose
a project?**

SABE research overview

Our research topics

The most important selection criteria for entry into Honours is the approval of a research supervisor. **This involves students selecting a research project they want to do AND the research supervisor agreeing to supervise the student.** The first step in this process is for students to make a shortlist of the Honours projects that they find interesting. This can be overwhelming for students as our researchers work on such a large variety of exciting and important research topics. This word cloud was generated from the projects available in this booklet - you can see how many things we research!

Your first job is to identify areas of science or 'research discipline(s)' that are most appropriate to your undergraduate degree and interests.



Location, location, location!

We also conduct our research in many different ways, and at a variety of locations. The location of your Honours supervisor is likely to be where your project is located. Therefore, this may be something you want to consider when choosing a Honours project. Our researchers are located at:

- La Trobe University **Bundoora** campus, (variety of buildings);
- La Trobe Institute for Molecular Science (**LIMS**), a research institute located within the Bundoora campus;
- **AgriBio**, a biosciences institute also located within the Bundoora campus;
- Centre for Freshwater Ecosystems, located within the La Trobe University **Albury-Wodonga** campus;
- **Baker Institute**, located next to the Alfred Hospital in Prahran;
- The Olivia Newton-John Cancer Research Institute (**ONJCRI**), situated next to the Austin Hospital in Heidelberg.

In this booklet, the project location is indicated in the heading of every supervisor's information page.



La Trobe University Bundoora campus



La Trobe Institute for
Molecular Science (LIMS)



AgriBio, Centre for AgriBioscience



Centre for Freshwater Ecosystems
La Trobe University
Albury-Wodonga campus



Baker Institute
Prahran, Melbourne



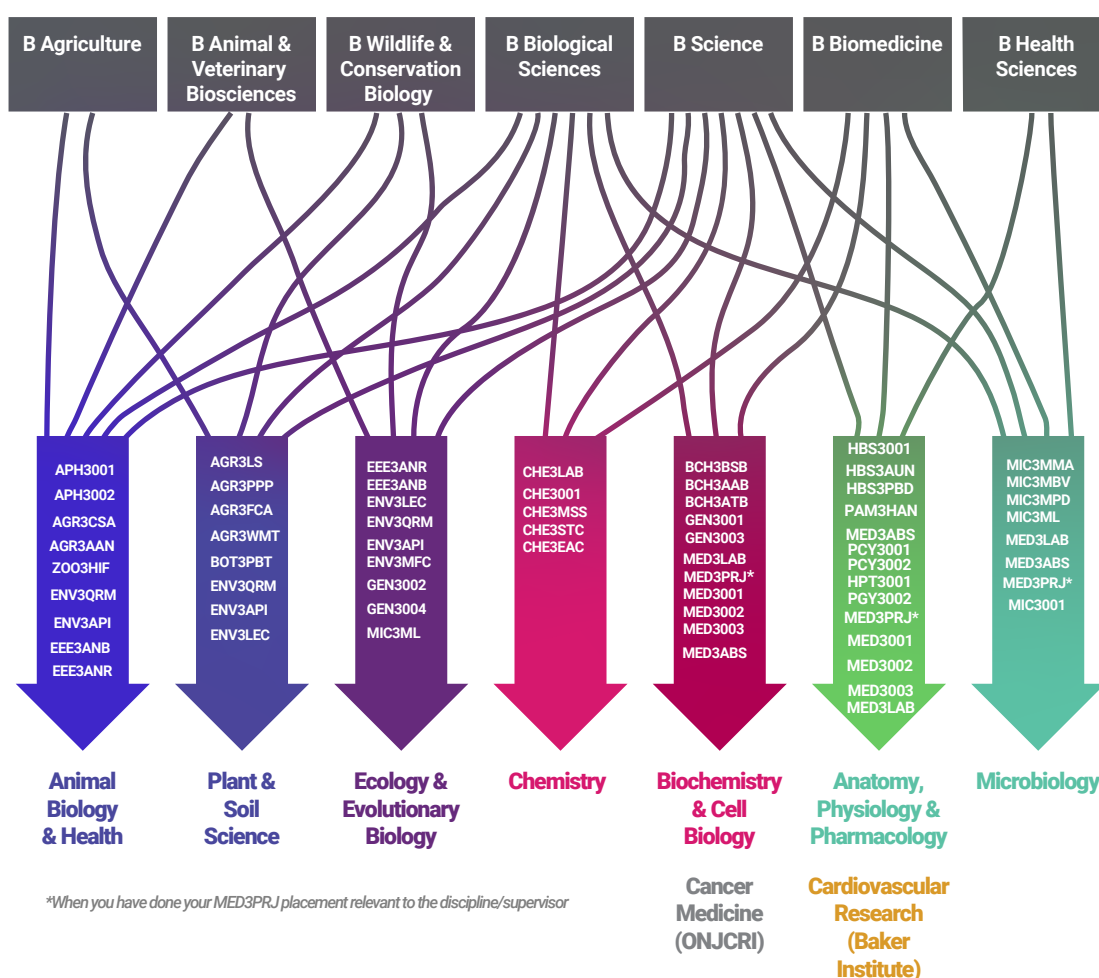
Olivia Newton-John Cancer
Research Institute (ONJCRI)
Heidelberg, Melbourne

How to use this booklet to find your perfect project

In the final year of your Bachelor's degree, you would have taken a number of 3rd year subjects pertaining to a specific scientific discipline. These subjects were probably in an area of science that most fascinated you. You are therefore likely to be most interested in research projects focused on that same area of science.

To help you identify a Honours research project, take a look at the infographic below: find your undergraduate degree and some of the 3rd year subjects that you have taken. These will correspond to one or more research disciplines which will have Honours projects that are most appropriate for you. **Note: this is only a guide and is by no means definitive! You may find yourself with the expertise/interest for multiple disciplines.**

Step 1. Select your Undergraduate course



Step 3. The research discipline that align with your 3rd-year subjects is where we suggest you focus on finding a Honours project.

Now you have a feel for the research discipline that is your best fit, it's time to look at the projects on offer. Every project page in this booklet will tell you:

- The name and contact details of the supervisor, so you can organise a meeting.
- How many project positions they have available, whether they start in February or July, and whether they are available for full-time or part-time study.
- The techniques that you will likely learn by doing Honours with them.
- Information about the lab/research theme and maybe some project specifics.

Find your Honours supervisor

Need help finding a project?

Finding a research project and supervisor is the most important part of the Honours application process.

First, contact the Honours coordinator who works in the discipline that you wish to conduct your Honours (you may wish to contact multiple discipline coordinators depending on your interests). The coordinators for each science discipline and their contact details are provided below. The discipline coordinators will guide you through the process of arranging a meeting with a supervisor and the Honours supervisor assignment process.

For general enquiries, or if you are totally stuck, contact the SABE Honours email: sabehonours@latrobe.edu.au.



Dr. Keith White

SABE Honours coordinator
k.white2@latrobe.edu.au

Contact for supervisors and projects in the following disciplines:

- Chemistry
- Cancer Medicine (ONJCRI)



Dr. Brooke Huuskes

Microbiology, Anatomy, Physiology and Pharmacology Honours coordinator
b.huuskes@latrobe.edu.au

Contact for supervisors and projects in the following disciplines:

- Microbiology
- Anatomy
- Physiology and Pharmacology



Dr. Emma Grant

Biochemistry and Cell Biology Honours coordinator
e.grant@latrobe.edu.au

Contact for supervisors and projects in the following disciplines:

- Biochemistry and Cell Biology
- Cancer Medicine (ONJCRI)



Dr. Tom Karagiannis

Cardiovascular Research (Baker Institute) Honours advisor
tom.karagiannis@baker.edu.au

Contact for supervisors and projects in the following disciplines:

- Cardiovascular Research (Baker institute)



Dr. Charles Feigin

Ecology & Evolutionary Biology Honours coordinator (Feb intake)
c.feigin@latrobe.edu.au

Contact for supervisors and projects in the following disciplines:

- Animal Health and Biology
- Plant and Soil Sciences
- Ecology and Evolutionary Biology



Dr. Aleicia Holland

Ecology & Evolutionary Biology Honours coordinator (July intake)
a.holland2@latrobe.edu.au

Contact for supervisors and projects in the following disciplines:

- Animal Health and Biology
- Plant and Soil Sciences
- Ecology and Evolutionary Biology

**Projects
Available in
2027**

SABE research disciplines

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Animal Biology & Health

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Prof. Travis Beddoe AgriBio



Bioinformatics



Infection & Immunity



Protein biochemistry



Proteomics



Protein purification



Field work



Animal models of disease



Molecular cloning



Molecular modelling



E-mail: t.beddoe@latrobe.edu.au

Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

The Agriculture Bio-Solutions Lab has access to state-of-the-art facilities for studying host-pathogen interactions in livestock.

Due to industrialized farming, there has been an increase in endemic disease that has resulted in multi-million-dollar losses to the farming industry per annum due to poor productivity, failure to thrive and death. The use of antimicrobials to treat these diseases has led to an increase in drug-resistant strains of pathogens. Pathogen control programs based solely on the use of anti-microbial drugs are no longer considered sustainable because of an increased prevalence of bacterial resistance, high costs and concerns regarding residues in the food and environment. To provide improved sustainable health and welfare outcomes in livestock production, the Agriculture Bio-solutions lab has developed a complete "Bench to Barn" research program focusing on 1) field-deployable diagnostics, and 2) molecular understanding of disease pathogenesis 3) sustainable treatment solutions (vaccines and breeding).

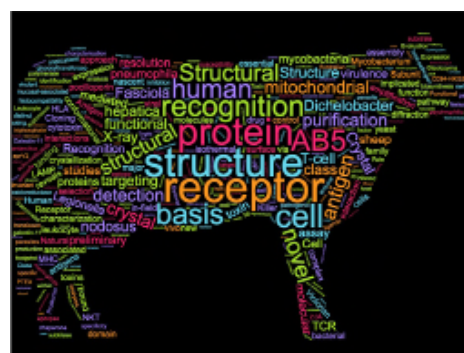
Project 1. Pathogen signals driving transgenerational immune priming in honey bees. Transgenerational immune priming (TGIP) occurs when parental exposure to a pathogen or pathogen-derived molecule enhances immunity in offspring. In honey bees (*Apis mellifera*), this process may strengthen colony resilience against infectious disease, but the pathogen-associated molecular patterns (PAMPs) that initiate TGIP in queens remain poorly defined. This project will investigate whether PAMPs from major honey bee pathogens can activate queen immune responses and promote immune protection in the next generation.

Candidate PAMPs will be compared using molecular assays that measure immune activation in queens, alongside functional assays that assess offspring immune responses and disease resistance.

By identifying the signals that drive maternal immune priming, the project will provide new insight into how honey bees transfer pathogen-specific immune information across generations. The outcomes may inform novel approaches to improving honey bee health, reducing colony losses and enhancing resistance to key pathogens.



Project 2. Identification of novel vaccine antigens from the Asian longhorned tick using reverse vaccinology. The Asian longhorned tick (*Haemaphysalis longicornis*) is an invasive, economically important ectoparasite that affects livestock and can transmit multiple pathogens. Control currently relies heavily on acaricides, which can drive resistance and raise environmental concerns, creating a need for sustainable alternatives such as anti-tick vaccines. This project will use reverse vaccinology to identify and prioritise novel vaccine antigens from *H. longicornis*. Genomic, transcriptomic and protein sequence datasets will be analysed with bioinformatic tools to find proteins with desirable vaccine features, including exposure to host antibodies, conservation, predicted antigenicity and likely roles in tick feeding, survival or reproduction. High-priority candidates will then be selected for recombinant expression and experimental testing of recognition by host antibodies. The project will provide training in bioinformatics, molecular biology and immunology while contributing to the development of next-generation vaccines for sustainable tick control in livestock systems.



Dr. Lucille Chapuis Bundoora



Bioacoustics analysis



AI



Field work



Data analysis



E-mail: l.chapuis@latrobe.edu.au

Website: [click here](#)

Number of projects: **1**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

Our lab explores how marine animals sense and respond to the underwater world of sound. The ocean is a noisy place, filled with natural sounds from animals and the environment, as well as increasing amounts of human made noise. We study how marine organisms (inc. fish and invertebrates), hear and use sound, how their ear anatomy has evolved, and how human activities might affect them. To answer these questions, we use a wide mix of tools, from anatomy and neuroscience to behaviour, bioimaging, and even artificial intelligence. Ultimately, our goal is to understand how animals experience their acoustic environment.

Project 1. The soundscape of bryozoan biogenic reef systems in Western Port. This project will explore how underwater soundscapes can be used to measure biodiversity in bryozoan reef habitats found in Western Port. Students deploy hydrophones in WP and work with the recordings, applying and testing emerging AI tools for sound analysis to better understand how reef "acoustic signatures" reflect ecological diversity in these poorly known ecosystems.



Prof. Shaun Collin Bundoora



Whole organism
bioimaging (CT)



Microscopy - Electron, light



Animal handling



Histology



E-mail: s.collin@latrobe.edu.au

Website: [click here](#)

Number of projects: **1**

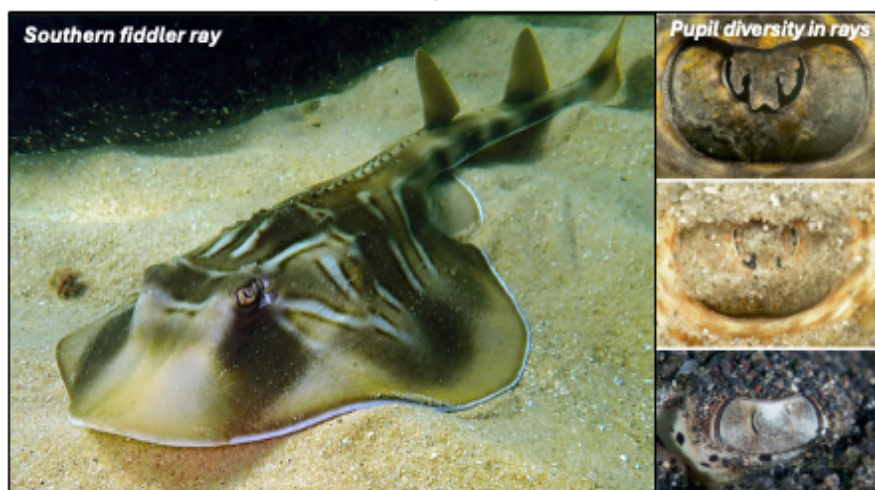
Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**

The Neuroecology Group studies how animals use their senses to survive in their environment. Marine animals rely on vision, smell, taste, hearing, the lateral line, and electroreception to find food and mates, avoid predators, and migrate over long distances. We investigate the importance of each of these senses by studying the peripheral sense organs and the brain, and their capacity to adapt to a changing environment. Our research not only deepens our understanding of marine biology but also helps inform conservation and management by identifying which species are most vulnerable to human impacts. Projects are co-supervised by academics such as Lucille Chapuis, Travis Dutka, Caroline Kerr, and Amanda Franklin.

Project 1. Visual adaptations in fiddler rays. Fiddler rays are bottom-dwelling cartilaginous fishes that live in bright light conditions and rely on their eyes to survey a panoramic visual environment to identify food, avoid predators and seek out conspecifics. This project investigates how their eyes are adapted for life on the sandy seafloor. Investigations could focus on various parts of the visual pathway including corneal filters, the distribution of retinal receptors and visual input to the brain. Using a range of techniques (light and electron microscopy, bioimaging (microCT), spectroradiometry and underwater photography of live and preserved specimens, you will explore how fiddler rays see their world. The project will provide training in sensory biology and neuroecology, giving insights into how early marine vertebrates process visual information and how they may cope with future environmental change.



Dr. Kerry Fanson Bundoora



Immunoassays



Microscopy



Animal handling



Animal behaviour studies



Field work



E-mail: k.fanson@latrobe.edu.au

Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

The Wildlife Endocrinology Lab studies the complex interactions between stress and reproductive physiology with the aim of improving animal conservation and welfare. A major focus in our lab is understanding how changes in the environment impact animal physiology. We rely primarily on non-invasive hormone monitoring to conduct longitudinal investigations on the physiology of wildlife species, but often integrate a range of other techniques depending on the project.

Project 1. Untangling the interactions between stress and reproduction. Glucocorticoids (cortisol and corticosterone) are often referred to as “stress hormones” and are assumed to inhibit reproduction. However, there is growing evidence that glucocorticoids promote healthy reproduction under certain circumstances. Our lab employs a range of techniques (non-invasive hormone monitoring, histology, PCR) to tease apart the complexity of this relationship between glucocorticoids and reproductive success.



Project 2. Novel indicators of stress. Stress is one of the most widely studied topics in biology, but unfortunately there are no good bioindicators of how “stressed” an animal is. Our lab is exploring different techniques to develop novel indicators of animal condition, or stress. Potential methods include metabolomics, steroid profiling, IgA, and longitudinal hormone monitoring.

Project 3. Zoo animal welfare. The Wildlife Endocrinology Lab works closely with Zoos Victoria to monitor the health and reproductive status of their animals. The exact project will depend on the current requests from Zoos Victoria. Examples of previous projects include: how zoo visitors affect animal well-being, characterising the reproductive endocrinology of mountain pygmy-possums to improve captive breeding success, and using detection dogs to identify oestrous in Tasmanian devils.



A/Prof. Kylie Robert Bundoora



Animal handling



Animal behaviour studies



Field work



Animal or plant identification



Ecological assays

Research in the Robert Lab is broadly focused on **reproductive ecology and conservation biology**. Current reproductive research examines parental effects on offspring phenotypes, sex allocation and the physiological and endocrinological basis for the variation in life history. While our conservation research address questions on endangered species, anthropogenic disturbance, captive breeding and reintroduction biology. The group uses a multidiscipline approach to question oriented research using a diverse range of taxa, including but not limited to reptiles, birds, bats and mammals. Other La Trobe researchers we collaborate with include but are not limited to; Dr Richard Peters (reptiles & behaviour), Dr James Van Dyke (reptiles & energetics), Dr Kerry Fanson (endocrinology), Dr Katherine Harrison/Dr Nick Murphy/Dr Susan Hoebee (genetics), Dr Jen Wood (microbiology), Dr Robert Ross (engineering), Dr John Lesku (animal physiology).

Project 1. Ecological impacts of artificial lighting on wildlife
Artificial lighting has fundamentally changed the earth's night-time environment, with a wide range of biological effects on animals. Over billions of years organisms have evolved to respond to natural light cues to control or modulate behaviour, activity, reproductive timing and physiological function. Our research has focused on the impact of artificial light on different species (inc. bats, marsupials, & insects) and testing different wavelength lights to mitigate the negative effects of light at night.



E-mail: k.robert@latrobe.edu.au

Website: [click here](#)

Number of projects: **2**

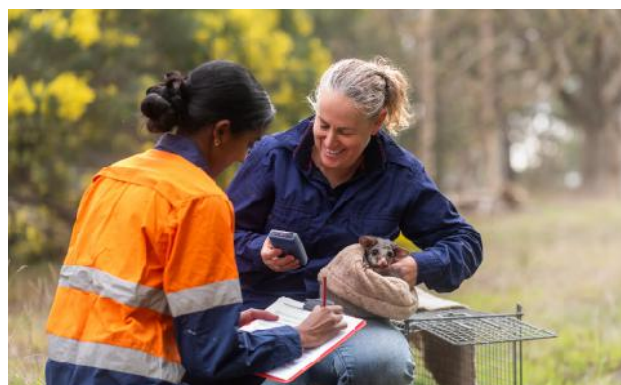
Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**

Project 2. Climate change and physiological impacts of extreme weather events. Current climate change scenarios for southern Australia predict mean temperatures to rise 2.7 – 4.2°C by 2090. Increased maximum temperatures, higher frequency of hot days and longer duration of heat waves are already being observed/ Despite this, the consequences of climate warming are poorly understood for many organisms. Our work in this field includes the energetic costs of thermoregulation, the thermal biology of artificial roosts for hollow dependant fauna, and the impact of thermal extremes during gestation in viviparous reptiles.

Project 3. Captive breeding and reintroduction biology. Captive breeding is one aspect of threatened species conservation, however attempting to breed and raise species in captivity presents many challenges for recovery programs. Captivity results in various environmental modifications that can lead to behavioural, morphological and physiological changes that result in potentially detrimental effects upon reintroduction. Some of our research has focussed on maternal mate choice to improve both conception rates and offspring fitness in captive breeding programs. While other research is assessing host-associated microbiota, predator recognition and behavioural traits linked to survival success post release.





Plant & Soil Science

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Dr. Ali Bajwa

AgriBio



Microscopy - Light



Plant phenotyping



Glasshouse work



Bioinformatics



Gene expression analyses



Metabolomics



Analytical skills



Industry experience



E-mail: a.bajwa@latrobe.edu.au

Website: [click here](#)

Number of projects: **3**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

We deal with the 'bad guys' of the plant world. Weeds and invasive plant species, often labelled as 'unwanted plants', have far-reaching impacts on food security and environmental protection. These noxious plants cost the Australian economy over \$4 billion per annum through reduced food production and expensive weed control practices. Our research is focused on understanding weed biology and evolution to develop sustainable weed management strategies.

Project 1. Seed germination ecology of important weeds in Australian horticultural systems. This project aims to investigate the seed germination ecology of important problematic weed species influencing horticultural systems in Australia. Firstly, seeds of selected weed species (we have many) will be collected from the horticulture field. Then seed morphology of the collected seeds will be carried out. The effects of key environmental factors, such as light, temperature, pH, drought, salinity and burial depth on seed germination will be studied under controlled laboratory conditions. The knowledge gained will help predict the key germination triggers to develop a timely and effective management program for weed species in horticulture production systems. The student will gain a dynamic experience from seed collection, conducting laboratory experiments and data analysis. This project is well-suited for students with an interest in weed ecology, seed biology and plant science.



Project 2. Metabolic profiling and toxicity bioassays of important weeds in leafy vegetables. This project will investigate the metabolic and toxic profiling of three to four important weed species collected from leafy vegetable production systems. The aim is to understand which weeds can be toxic to humans and therefore, should be prioritised for eradication from the fields. We will perform metabolomic profiling using LC-MS technique to identify bioactive compounds present in these species and then do toxicity bioassays in the laboratory to assess the toxic potential of these weeds. Finally, comparative analysis will be carried out which will reveal the chemical differences and toxic potential among the weed species. Student will have the opportunity to learn bioassay methods, metabolite extraction

and data analysis. This project would suit to a molecular biology or biochemistry student interested to learn about the fascinating world of naughty plants (weeds), while help improve health and nutrition by identifying key toxic weeds in important salad crops.

Project 3. What's turning the beauty into a beast? Studying soil microbial interactions of weedy Gazania species. In this project, you would be working with arguably Australia's most beautiful weed, gazania. Two weedy species of genus Gazania (Gazania linearis and G. rigens), both introduced from South Africa as ornamental garden plants, have become widespread invasive weeds in southern and western Australia. They have significant negative ecological, environmental, agricultural and socio-economic impacts. We hypothesise that gazanias manipulate soil microbiome to favour their establishment and proliferation in natural and agro-ecosystems. We will collect soil samples from a range of contrasting environments with and without gazania infestations to assess the composition and function of microbial networks. Better understanding of their soil microbial interactions will help understand their overall invasion ecology and pathways. This knowledge can be used to predict and manage future invasions. You will learn and/or improve your skills in weed and soil ecology as well as bioinformatics. The project would suit a molecular biology student with a learning attitude to unravel the basis of invasion success of an interesting wild plant.



A/Prof. Berin Boughton AgriBio



**Mass Spectrometry
Imaging**



Histology



Bioinformatics



Microscopy - Light



**Proteomics &
Metabolomics**



Data analysis



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Number of projects: **2**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

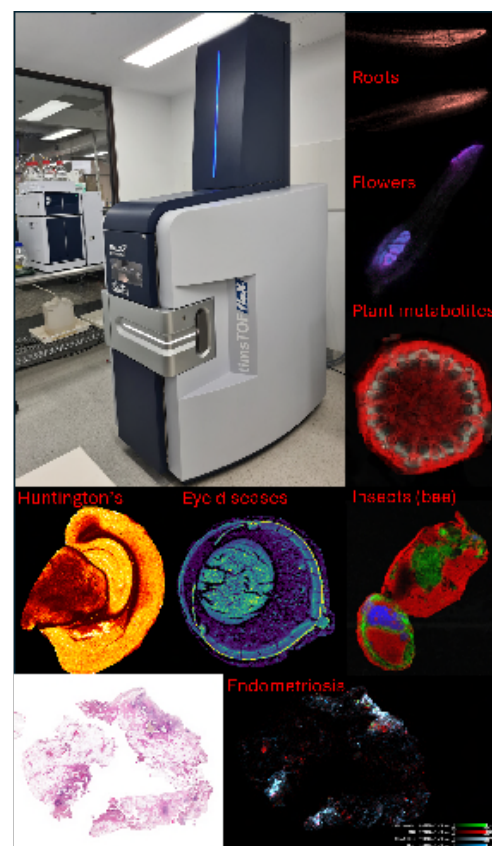
Masters conversion: **Yes**

Spatial mapping of biomolecules using Mass Spectrometry Imaging (MSI) is a powerful technique that can provide unique insights into their functional roles in higher organisms. Animals and plants are exquisitely compartmentalized into specific tissues and cells performing specialized processes. Understanding the spatial distribution and expression of biomolecules, including metabolites, proteins and glycans is fundamental to advancing our understandings in physiology, medicine and biology. Based in the La Trobe Institute for Sustainable Agriculture and Food, my research dissects plant, animal and human biology using mass spectrometry and bioinformatic approaches.

Project 1. Spatial mapping of cold acclimation proteins in barley using MALDI-MSI. Frost causes more than \$360 million in annual losses to the Australian grains industry, yet the cellular and tissue-level protein changes that distinguish frost-tolerant from frost-sensitive barley varieties remain poorly resolved. While proteomics approaches have identified cold-responsive proteins in bulk tissue extracts, the spatial distribution of these changes across specific cell types and tissues has never been mapped. This project will adapt and optimise on-tissue tryptic digestion and MALDI mass spectrometry imaging (MALDI-MSI) workflows – well-established in mammalian systems – for application in plant tissues, mapping protein changes at cellular resolution across barley sections collected before and after cold acclimation. The skills developed will span sample preparation, on-tissue enzyme chemistry, ion-mobility MSI data acquisition and bioinformatic analysis, providing a strong foundation in spatial proteomics with direct applications in agricultural and biological research.

Project 2. Endometriosis – Linking biomolecules to endometriotic lesions using MSI. Endometriosis is a common disease affecting >11% of women in Australia, with a range of symptoms that include chronic pelvic pain, dysmenorrhea and infertility. Diagnosis is often by expensive, invasive surgery, which contributes to lengthy diagnostic delays. Endometriosis remains poorly understood but patients, clinicians and researchers all agree new non-surgical therapies are urgently needed to reduce the severity of symptoms. Identification of non-invasive endometriosis biomarker/s – a measurable factor correlating with disease presence or activity – has therefore become a priority. Little is known about the localised metabolomic and proteomic microenvironment associated with lesions. We believe that profiling and identification of metabolites and proteins directly associated with lesions and peritoneal fluid will unveil important new information on endometriosis biology and allow us to identify potential diagnostic biomarkers. new insights into the pathophysiology of neurodegenerative conditions.

Techniques used in these projects: Mass Spectrometry and Mass Spectrometry Imaging, Microscopy, Spatial - Proteomics, Lipidomics, Metabolomics, Bioinformatics



Prof. Phil Brewer

AgriBio



Molecular cloning



PCR assays



Bioinformatics



Gene expression analyses



Genetic sequencing



Data analysis



Glasshouse work



Plant phenotyping



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Number of projects: **3**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

Our research explores how plant hormones shape growth, architecture, yield and defence, and how these pathways can support productive, resilient crops. We are particularly interested in strigolactones, hormone crosstalk, dwarfing, stress responses, reactive oxygen species and metabolism. Our work spans Arabidopsis, tomato and cereals including barley, maize and sorghum, using plant physiology, molecular biology, genetic modification and synthetic biology. It contributes to broader programs such as ARC CoE in Plants for Space and industry collaborations, including Bayer Crop Science. Projects are flexible and can be tailored to each student's interests, skills and emerging opportunities.

Project 1. Synthetic switches for simultaneous growth and defence. Design and test a synthetic gene switch that activates growth and defence responses together. Generate GM tomato plants and determine whether targeted activation can improve stress resilience while maintaining biomass, architecture and productivity.

Project 2. Strigolactones and the growth-defence trade-off during fungal infection. Determine how strigolactones influence the balance between growth and defence during Botrytis cinerea infection. Using hormone treatments, mutants, disease phenotyping and molecular analysis, test whether this pathway can improve resistance without a major growth penalty.

Project 3. Hormonal and synthetic control of dwarfing. Investigate how hormone crosstalk could be used to regulate dwarfing and plant architecture using a combination of different plant hormones and inhibitors. A synthetic gene switch could also be designed that represses plant height.

Project 4. Strigolactones, ROS and mitochondrial antioxidants. Investigate how strigolactone signalling affects mitochondrial function, reactive oxygen species and antioxidant defences under normal and stress conditions. Approaches may include isolated mitochondria, respiration measurements, biochemical assays, microscopy and gene expression analysis.

Project 5. Do other butenolides act like strigolactones? Compare strigolactones with other butenolide-containing compounds, including sesquiterpene lactones, to determine whether they produce similar growth, stress and antioxidant responses. Selected compounds will be tested in plant and zebrafish models through cross-disciplinary collaboration.

Project 6. Next-generation hormone-enhanced biostimulants. In an industry-linked project, evaluate commercial biostimulants for their effects on crop growth, yield, stress tolerance and quality. Promising products will be combined with selected plant hormones to develop and test new formulations with improved and more consistent performance.



Dr. Gary Clark AgriBio



Data analysis



Glasshouse work



Chemical analysis



Field work



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Number of projects: 1

Full-time or part-time: **Either**

Feb or July start: **Both**

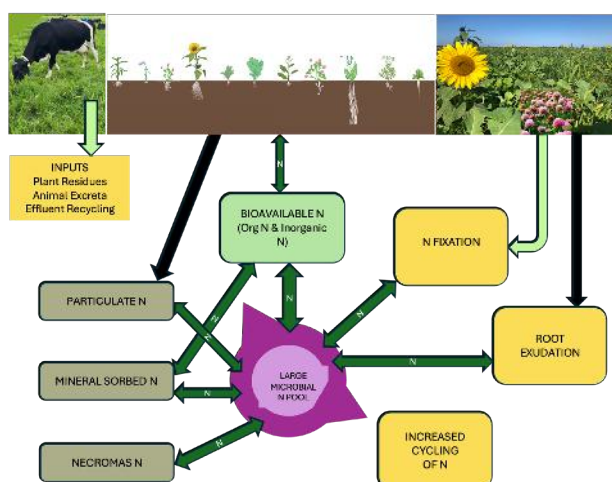
Masters conversion: **Yes**

Adoption of multispecies pastures (MSP) is based on the need for increasing home-grown forage availability in the context of increasingly variable climate. The concept is to introduce a diverse assemblage of plants to a conventional perennial ryegrass (PRG) pasture. Species, which are mostly annual, span the following functional groups of grasses and cereals, legumes, tall and short forbs/herbs, and brassicas. The establishment method varies from a complete re-sow of pasture with a mixture of PRG and MS mix to inter-sowing MS into existing PRG. We have been involved with three dairy farms who use the inter-sowing method of sowing a multispecies mixture, in autumn and spring, into an existing well-established PRG pasture. Twice yearly sowing allows selection of species suited to either the cool and wetter periods, or the hot and dry periods of the year. MSP is grazed 'regeneratively'. Increased rest periods between grazing allows for increased growth of above ground biomass, and likely increased root growth and root exudation. Multispecies tend to have greater exploration of the soil profile as shown by increased root depth of some of the species in comparison to perennial ryegrass. This results in greater access to water and nutrients, and decreased loss of nutrients, such as nitrate. Observations of MS pastures reveal improved drainage and resilience to pugging. This could be attributed to increased soil organic matter, particularly at depth. We have observed this on a West Gippsland beef farm.

Questions that arise - our three farmers grow their forage without any fertiliser. Hence, where do plants source their nitrogen?

Likely sources:

1. Increased cycling of C and N
2. Increased soil organic matter content
3. Increased microbial necromass.
4. Incorporation of 'green' residues at time of inter-sowing.



Project 1. Post grazing, residual plant material is incorporated into the soil at the time of inter-sowing the multispecies annual crops. The amount and quality (low C:N versus high C:N) of this material is likely to have differing effects on the cycling of the nutrients, particularly N in the decomposing plant material. This project will investigate the effects of incorporation of differing quality plant material on the soil nutrient cycling.

Project 2. What are the changes to soil when using inter-sowing Multispecies over time? This project will investigate changes to the soil over 10 years + and less than 5 years. Field and laboratory measurements will be used to build a 'picture' of these changes.

A/Prof. Marisa Collins AgriBio



Field work



Data analysis



Plant phenotyping



Agronomy



Glasshouse work



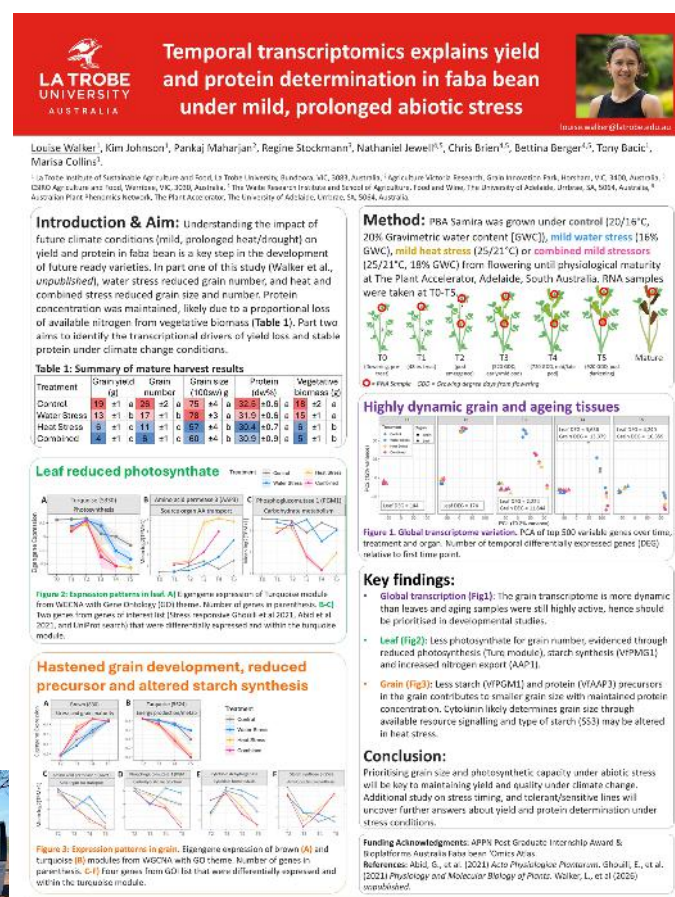
Crop physiology

Whole organism
bioimagingE-mail: marisa.collins@latrobe.edu.auWebsite: [click here](#)Number of projects: **2**Full-time or part-time: **Either**Feb or July start: **Both**Masters conversion: **Yes**

Climate change and resource limitations are reshaping the future of agriculture, and our research is focused on helping crops thrive in a hotter, drier, and more variable world. We work across a diverse range of agricultural systems, from legumes, canola, and pastures to broad-acre crops such as wheat, exploring how plants respond to drought, heat, nutrient limitations, and other environmental stresses. By uncovering the mechanisms that drive crop productivity, water-use efficiency, and nitrogen-use efficiency, particularly in legumes, we develop knowledge and tools that improve both yield and product quality.

Our lab specialises in translating discoveries from the laboratory and glasshouse into practical solutions for farmers. Through field-based research, we test how crops perform under real-world conditions and work to deliver outcomes that directly benefit growers and agricultural industries.

Students in our lab contribute to research with tangible impact, helping to build more productive, resilient, and sustainable farming systems for the future. Current Honours projects include improving pasture productivity under future climate scenarios, increasing nitrogen fixation in lentil and field pea crops, enhancing phosphorus uptake on highly phosphorus-fixing soils, and understanding how potassium nutrition can improve stress tolerance in crops such as lentil and faba bean.



A/Prof. Tony Gendall AgriBio



Bioinformatics



Genetic sequencing



Glasshouse work



Metabolomics



CRISPR-Cas9 gene editing of cells



X-ray crystallography



Data analysis

My lab using a wide range of tools, including genetics, molecular biology and bioinformatics to investigate aspects of plant biology, physiology and development in both model and non-model species, crops and horticultural plants.



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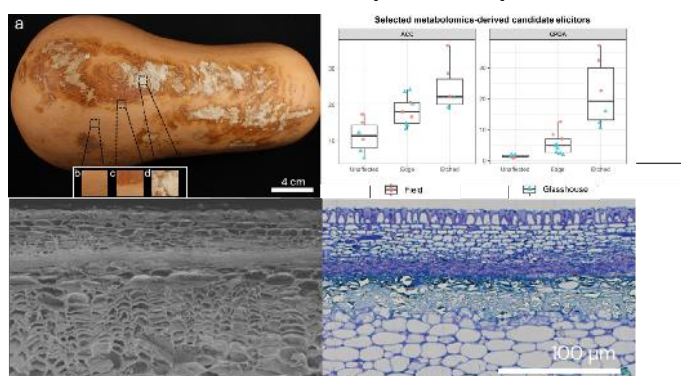
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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

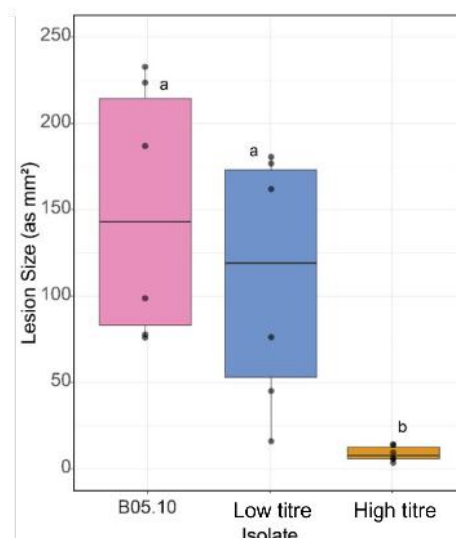
Masters conversion: **Yes**



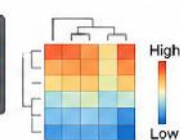
Project 1. Spatial metabolomics of brown etch disorder in pumpkin (with Berin Broughton and Matthew Welling). Brown etch is a poorly understood disorder of butternut pumpkin (*Cucurbita moschata*) that causes brown surface lesions and reduces marketable yield. This project will use matrix-assisted laser desorption/ionization (MALDI) imaging mass spectrometry to map the metabolic changes in situ across healthy, etched and lesion-boundary tissues. These 2D molecular maps will be used to identify spatial signatures associated with brown etch development, with a particular emphasis on metabolites involved in plant stress, defence and cell-wall modification.

Project 2. Gene-editing to improve seed quality in cowpea (with Penny Smith). This project will investigate the roles of peptide (UMAMIT) and sugar (SWEET) transporters in regulating seed development, maturation, and quality in cowpea (*Vigna unguiculata*). Bioinformatic approaches will be used to identify members of these transporter families that are expressed during seed development to prioritise candidate genes for functional analysis. Selected genes will then be investigated through the generation and characterisation of gene-edited mutant and overexpression lines. The effects of altered transporter activity on seed quality will be assessed by analysing key metabolites and seed protein profiles.

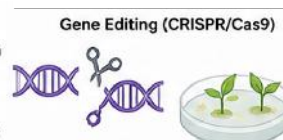
Project 3. Mycoviruses for biocontrol of plant pathogens. This project will investigate the potential use of viruses infecting the widespread plant pathogen *Botrytis cinerea* as biocontrol agents. We have demonstrated that most *Botrytis* isolates carry one or more viruses and that some of these viruses can reduce the pathogenicity of their fungal host during plant infection. This project will explore the diversity of these mycoviruses and their effects on their *Botrytis* hosts.



Genome-wide Identification



Expression Profiling During Seed Development

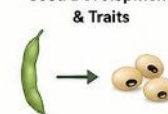


Gene Editing (CRISPR/Cas9)



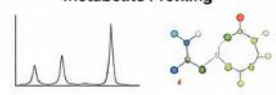
Overexpression

Seed Development & Traits



- Seed size
- Seed weight
- Seed number
- Maturation timing

Metabolite Profiling



Seed Protein Profiling



A/Prof. Kim Johnson

AgriBio



Gene expression analyses



Microscopy - Light, electron



Glasshouse work



Data analysis



Plant phenotyping



Mass spectrometry



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

The research aims of our group is to understand how plants alter their growth and development in response to stress. Stress can be experienced from developmental processes, such as cell growth or from the external environment. These stresses initiate responses to adapt the carbohydrate-rich cell wall that surrounds each cell and plays an incredibly important role regulating plant shape, strength and provides protection to the plant. Walls are our most renewable bioresource and they determine the quality and quantity of most plant-based products used in modern human societies such as food, fibre, fuel and biomaterials. The expected outcome of projects in our group is the ability to modulate wall composition and plant growth to improve Australian crops.

*Project 1. Investigating Pre-Harvest Stress Treatments to Improve Fruit Quality in Hydroponically Grown Cucumber and Strawberry. Cucumber (*Cucumis sativus* L.) and strawberry (*Fragaria × ananassa* Duch.) are high-value crops increasingly grown in hydroponic and protected-cropping systems. While these systems enable precise control of water and nutrients, production conditions that maximise yield do not always optimise fruit flavour, nutritional quality or post-harvest performance. This project will investigate whether controlled pre-harvest stress can improve fruit quality without causing unacceptable reductions in productivity. Hydroponically grown cucumber and strawberry plants will be exposed to selected treatments such as temporary nutrient limitation, mild salinity and short-term changes in light intensity. Plant responses will be assessed through measurements of biomass, flowering, fruit number, fruit size, marketable yield and nutrient status. Students will gain experience in hydroponics, plant stress physiology, fruit-quality analysis, experimental design, statistics and scientific communication.*



Project 2. Investigating soil compaction tolerance mechanisms of kangaroo grass. Australian native grass species are adapted to Australia's variable climate and reported to tolerate low nutrient, acid soils and water stress. Soil compaction is a major issue in Australia and along with a range of other soil constraints, reduces rooting depth of plants and their ability to access water and nutrients. Themeda triandra or kangaroo grass is an important grassland species adapted to a wide range of environments. This project will investigate the changes in root traits such as water barrier structure formation and mucilage secretion in response to compaction to attempt to uncover the mechanisms by which kangaroo grass tolerates challenging environments.

Project 3. Physiological and spatial responses to cold acclimation in barley. Frost is a major constraint to Australian grain production, yet the physiological mechanisms that enable some barley varieties to better tolerate low temperatures remain incompletely understood. Cold acclimation involves coordinated changes in plant water relations, membrane stability, metabolism and protective proteins, but how these responses differ between tolerant and sensitive genotypes is not well characterised at the tissue level. This project will investigate physiological and biochemical responses to cold acclimation in contrasting barley genotypes. Plants will be exposed to controlled cold treatments and assessed for physiological traits and freezing tolerance. Selected tissues will then be analysed using MALDI mass spectrometry imaging to explore the spatial distribution of metabolites and/or proteins linked with cold response and develop a spatial proteomics workflow. The project will provide training in plant stress physiology, controlled-environment experimentation, biochemical assays, imaging, mass spectrometry and data analysis, while contributing to a better understanding of cold tolerance mechanisms in barley.

Prof. Mathew Lewsey AgriBio



Gene expression analyses



PCR assays



Plant development analysis



Light microscopy



Bioinformatics

My lab studies how plants perceive the world around them and interact with their environments by regulation of their genomes. We apply this work with commercial partners who grow a range of agricultural crops including cannabis, opium poppies, barley, oats and peas. In a project co-supervised with senior postdoc Lim Chee Liew, you can study how gene expression contributes to the control of seed germination.

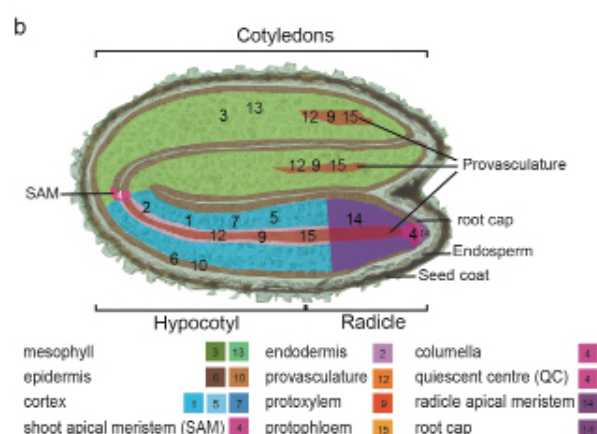
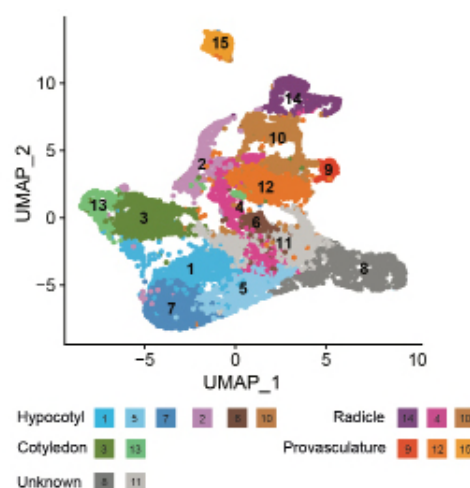
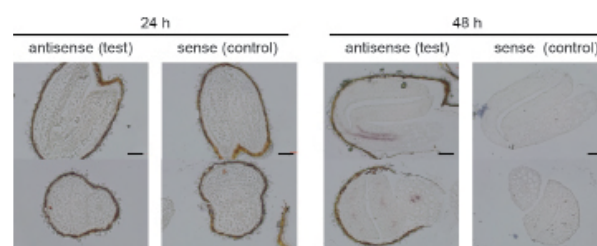
Seeds provide 70% of global food resources, being the most valuable output from plant production. They also play a critical role in agriculture because germination is the first step during a plant's lifecycle which involves extensive changes in gene expression. It is governed by nutrient resources, endogenous hormone levels and environmental stimuli, and these requirements vary between plant species. Despite the importance of germination, crucial information is missing in our current understanding of gene expression profiles during seed germination.

Changes of gene expression are regulated by transcription factors. Transcription factors are proteins that control gene expression by binding to the promoter regions of genes. This project aims to study transcription factors involved in seed germination by using T-DNA mutant lines of *Arabidopsis thaliana*, the model plant species for research in plant biology. First, we aim to obtain homozygous T-DNA lines by genotyping which involve basic molecular techniques including DNA extraction, polymerase chain reaction (PCR), and gel electrophoresis. After we obtain homozygous T-DNA line, we will confirm the gene knockout by examining the gene expression of the target gene. This will require RNA extract, cDNA synthesis, and qRT-PCR. Then, we can use the T-DNA knockout mutants to study the effect of mutation of transcription factors on seed germination by phenotyping. Several traits will be measured to evaluate seed germination such as germination rate, hypocotyl length, and cotyledon expansion.

By understanding the fundamental genome regulation network during seed germination, we can develop practical solution to ensure germination happen at the right time uniformly. Uniform germination enables growers to achieve optimal plant-spacing and harvesting time and germination at correct time increase the likelihood of successful plant growth.

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Number of projects: 2

Full-time or part-time: **Either**Feb or July start: **Both**Masters conversion: **Yes**

Dr. Dugald Reid

AgriBio



Bioinformatics



Plant phenotyping



CRISPR-Cas9 gene editing of cells



Gene expression analyses



Molecular cloning



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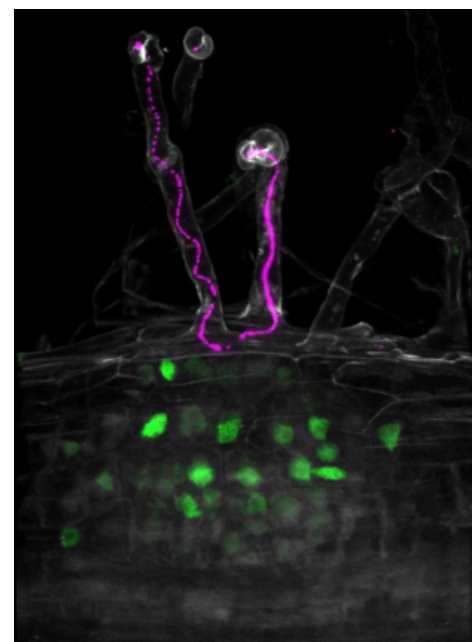
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Number of projects: **1**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**



Legumes provide a sustainable means of producing high value protein for human diets and animal feed. These characteristics of legumes arise due to their ability to engage in a symbiotic relationship with soil bacteria that provide nitrogen to support plant growth. This nitrogen-fixation occurs in specific organs that form on legume roots known as nodules. Despite this beneficial relationship, legumes have not realised their full potential in our predominantly cereal-based cropping systems. One of the major reasons that legumes fail to compete with cereal crops is their relatively poorer tolerance of environmental stresses. We use genetics, gene expression analysis and plant developmental studies to identify mechanisms of legume adaptation and resilience to the environment. These approaches aim to identify genes that can be manipulated to improve legume performance, ultimately increasing the productivity and profitability of legume agriculture.

Project 1. Tuning N-fixation to the environment. We have identified a master regulator of nitrogen fixation that controls the senescence (controlled breakdown) of legume nodules. This project aims to generate genetic variation in this key gene guided by our understanding of the protein structure and function. Novel genetic variants will be tested for their ability to enhance the tolerance of legume nodules to applied stresses.

Project 2. Root system responses to water stress. This project will investigate the variation in root system responses to water stress within a natural population of the model legume *Lotus japonicus*. This variation can be used to identify the genes underlying phenotypic variation using genome-wide association mapping. These genes will be further investigated to understand how they contribute to improving the resilience of legume root systems.

A/Prof. Penelope Smith

AgriBio



Plant phenotyping



Molecular cloning



PCR assays



Bioinformatics



CRISPR-Cas9 gene editing



Glasshouse work



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Number of projects: **1 Feb, 1 Jul**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

Legumes can form a symbiotic relationship with soil bacteria called rhizobia, which convert atmospheric nitrogen (N₂) into forms that plants can use. This process, known as symbiotic nitrogen fixation, provides nitrogen to support legume growth and can reduce the need for nitrogen fertiliser in subsequent non-legume crops. Symbiotic nitrogen fixation contributes an estimated \$3.5 billion in value to crop rotations in Australia.

Our research group uses genetic modification, gene editing, and genetic diversity panels to investigate how symbiotic nitrogen fixation can be improved. Our goal is to increase nitrogen availability for production of high-protein seeds and to improve the benefits that legumes provide in crop rotations. We work with lentil, pea, and faba bean, which are important legume crops in Victoria. We also work with cowpea and Lotus, which we use as model systems to investigate the molecular mechanisms that control legume–rhizobia symbiosis and nitrogen fixation.



Project 1 (with Dugald Reid). Gene editing of transporter genes in cowpea. The transport of a wide range of compounds between plant tissues and symbiotic rhizobia is essential for nitrogen fixation. Transport proteins help supply rhizobia with the nutrients needed to fix nitrogen and allow the products of nitrogen fixation to be transported and used by the plant. In this project, you will use CRISPR gene editing to investigate the roles of candidate transporter genes in cowpea and determine whether they are important for symbiotic nitrogen fixation. You will design and create a CRISPR construct targeting a candidate gene, introduce the construct into cowpea using Agrobacterium-mediated transformation, and generate transgenic plants. You will also analyse existing gene-edited plants and phenotype them to determine whether knocking out specific transporter genes affects symbiotic nitrogen fixation.

Prof. Caixian Tang

AgriBio



Soil analyses



Glasshouse work



Data analysis



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Number of projects: **2**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

Soils contribute \$63b annually to Australian economy through agricultural production. Soil degradation is widespread and limits sustainable food production under current climate change. Our interdisciplinary research focuses on management of soil constraints, contamination and nutrients, and impacts of climate change and farming practices on soil processes and carbon sequestration.

Project 1. Climate change is increasing the frequency and severity of drought, threatening the sustainability of Australian pasture systems. Organic amendments such as chicken manure may improve soil fertility, root growth, water retention, and soil carbon sequestration, thereby enhancing drought resilience. This project will investigate how organic amendments improve drought tolerance and soil carbon accumulation in mixed pastures by quantifying plant carbon inputs, soil carbon dynamics, plant growth and nutrient uptake, and changes in soil properties.

Project 2. Increasing levels of atmospheric CO₂ associated with global warming, stimulates the growth of many plant species. However, it is unknown how high CO₂ levels affects soil health and crop nutrient demands. This research aims to understand how elevated CO₂ affects carbon, nitrogen and phosphorus dynamics in major soils. It elucidates the interconnection between soil organic matter decomposition and nitrogen and phosphorus availability, and understand the microbiological contribution to carbon, nitrogen and phosphorus cycling under elevated CO₂.

Project 3. Phosphorus fertilizers are important in sustaining crop yields. Each year, Australian farmers use ~450,000 tonnes of P fertilizers. Only 10-30% is absorbed by crops, leaving unused P remaining in the soil. The project studies the impacts of crop species, soil type and farming practice on biochemistry at the soil-plant interface (rhizosphere) to understand how to enhance crop P-use efficiency and to reduce P-fertiliser use.



ARC Center of Excellence - Plants for Space (AgriBio)



Bioinformatics



Gene expression analyses
incl. PCR, qPCR



Chromosomal, nucleotide
extraction & PCR assays



Molecular cloning



Plant development analysis



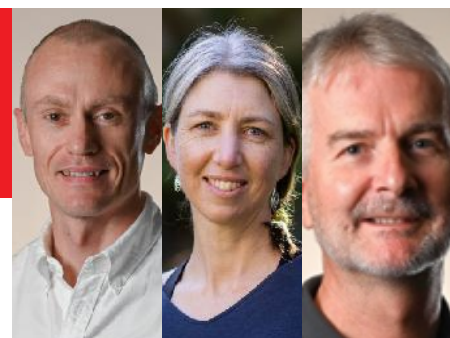
CRISPR-Cas9 gene editing



Plant tissue culture



Plant biotechnology



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Number of projects: **1 Feb, 1 Jul**
 Full-time or part-time: **Either**
 Feb or July start: **Both**
 Masters conversion: **Yes**

Long-term off-Earth habitation is on the horizon. By 2028, an established presence on the Moon will be a precursor to crewed Mars missions, but key challenges still exist. P4S is a major research initiative for Australia that aims to create a legacy of global leadership in engineering on-demand, zero-waste, highly compact and efficient plants and products to support a bold new future in space exploration.

Project 1. Mechanosensing of Space environments in tomato. In low-gravity environments, plants display altered growth and produce less cell wall material. Reduced mechanical stress and mechanosensing pathways are proposed to contribute to these phenotypes. This project will generate mutants in a key mechanosensor protein in tomato using synthetic biology approaches and investigate resulting effects on growth, stress resilience, and yield.



Project 2. Integrating growth and defence through hormones and synthetic biology. Plant hormone crosstalk coordinates growth and stress responses, but it remains unclear whether strong defence can be maintained without reducing biomass and productivity. This project will use hormone treatments and abiotic and biotic stresses to investigate growth-defence trade-offs in tomato. It may also involve generating GM plants to activate growth and defence pathways together.

Project 3. Hormonal and synthetic control of dwarfing. Compact crops are valuable for controlled-environment and space agriculture. This project will investigate how combinations of plant hormones and inhibitors regulate tomato height and architecture. It may also explore a synthetic gene switch that represses plant height while maintaining overall performance.

Project 4. Mitochondria, ROS and antioxidant responses. Mitochondria are central to plant energy metabolism and stress responses, including reactive oxygen species production and regulation. This project will investigate how hormone signalling influences mitochondrial function and antioxidant defences under normal and stress conditions. Approaches may include isolated mitochondria, respiration measurements, biochemical assays, and gene expression analysis.

Project 5. Environmental regulation of MAP kinase signalling. Mitogen-activated protein (MAP) kinases are central regulators of plant development and stress responses, integrating signals from multiple hormone pathways. This project will dissect the promoters of key MAP kinase genes to understand how their expression is regulated by environmental cues (terrestrial and beyond). This knowledge could help optimise growth-defence trade-offs for more resilient crops. The project will involve molecular cloning, plant transformation, plate-reader assays and microscopy.



Project 6. Hormonal regulation of nutrient-use efficiency in hydroponic systems. Plant hormones regulate root development and nutrient transport, but their influence on nutrient-use efficiency in industrial hydroponic systems is not fully understood. This project will investigate how hormone treatments affect nutrient uptake, allocation and utilisation in hydroponically grown plants. Approaches will include nutrient-solution analysis, plant ionomics, root and shoot measurements, physiochemical assessments, and fruit quality analysis.

ARC Research Hub for Protected Cropping (AgriBio)



Microscopy



Gene expression analyses



Molecular cloning, CRISPR-Cas9 gene editing of cells



Glasshouse work



Plant phenotyping



Bioinformatics

The ARC Research Hub for Protected Cropping (PC Hub) is driving a transformation in Australia's horticultural and medicinal agriculture industries by advancing protected cropping (PC) and improving sustainability, crop quality, yield, and reliability. Through innovative research, PC Hub aims to help growers produce higher-quality crops, develop new food and plant-based products, and create more sustainable and efficient production systems. Based within the **La Trobe Institute for Sustainable Agriculture and Food (LISAF)**, the PC Hub offers Honours students the opportunity to work alongside researchers and industry partners on applied research with real-world impact.

Project 1. Investigating the Influence of LED Lighting and Hydroponic Growing Conditions on Basil Growth and Quality. Basil (*Ocimum basilicum* L.) is a high-value culinary and medicinal herb widely grown in protected cropping and indoor farming systems. Hydroponic production offers improved water and nutrient efficiency and greater control over growing conditions, but basil growth, yield and quality are strongly influenced by light and nutrient availability. This project will investigate how LED lighting and hydroponic nutrient management affect basil growth and quality. Treatments will include different proportions of red, blue and broad-spectrum LED light combined with variations in nutrient formulation. Plant responses will be assessed using measurements of growth, chlorophyll content, fresh and dry biomass, and RGB and multispectral imaging. Quality will be evaluated through leaf colour, texture, aroma, antioxidant activity and phenolic concentration using biochemical and metabolomic approaches. Environmental and hydroponic parameters, including temperature, humidity, light intensity, nutrient solution temperature, pH and electrical conductivity, will also be monitored. The project will identify growing conditions that improve basil productivity and marketable and nutritional quality, supporting more efficient and sustainable indoor production. The student will gain experience in hydroponics, controlled-environment experimentation, imaging, laboratory analysis, statistics and scientific communication.

Project 2. Photoperiod sensitivity in wax flowers. Australian waxflower (*Chamelauicum* spp.) is an important native ornamental crop valued for its attractive flowers, long vase life and suitability for domestic and export markets. However, commercial production is strongly seasonal, with flowering concentrated within a relatively narrow period of the year. This limits continuity of supply and reduces opportunities to meet market demand outside the traditional harvest season. This project will investigate the photoperiod sensitivity of selected Australian waxflower cultivars to determine how day length influences vegetative growth, floral initiation and flowering time. Plants will be grown under controlled conditions and exposed to a range of photoperiod treatments using supplementary LED lighting and/or blackout treatments. Responses will be assessed through measurements of plant growth, time to floral initiation, flower number, stem length, flowering duration and overall marketable quality. The project will identify whether specific photoperiod treatments can be used to manipulate flowering and extend production beyond the normal seasonal window. The findings will improve understanding of flowering physiology in waxflower and support the development of year-round or extended-season production systems. Outcomes may provide practical recommendations for commercial growers seeking to improve crop scheduling, consistency of supply and access to higher-value market periods.

Project 3. Using plant biotechnology tools for precision breeding (in partnership with the Plant Synbio – La Trobe University node). Modern plant biotechnology tools have enabled the identification and modification of specific genes associated with important agronomic traits at a much faster pace than conventional breeding. Tools such as CRISPR-Cas gene editing allow targeted changes to be made in crop genomes, while marker-assisted selection, genomic selection and speed breeding accelerate the identification and development of superior plants. In crops such as barley and tomato, these approaches are being used to improve traits including disease resistance, plant architecture, yield, stress tolerance, fruit quality and grain composition, providing greater precision and speed than conventional breeding alone. Transient expression is a fast, cost-effective method for testing candidate genes linked to agronomic traits. This project will develop and optimise transient expression systems for cereals and/or horticulture crops to enable rapid gene screening and synthetic biology applications, e.g. therapeutics, novel agrichemicals or functional food ingredients. It may also involve designing new plant gene circuits for stable transformation. The student will gain hands-on experience in plant biotechnology, including transformation and CRISPR) as well as genetics, molecular biology (cloning, PCR), biochemistry (assays), and cell biology (microscopy).



ARC Research Hub for Protected Cropping

Website: [click here](https://pchub@latrobe.edu.au)

pchub@latrobe.edu.au

Number of projects: 3

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**





Ecology & Evolutionary Biology

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Prof. Nick Bond Albury-Wodonga



Field work



Ecological assays



Animal handling



Animal behaviour studies



Ecological modelling (GIS)



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Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

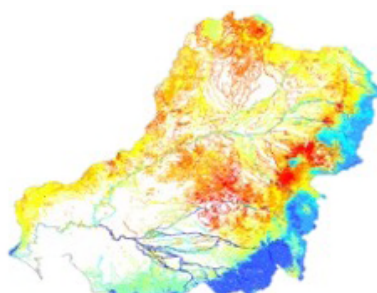
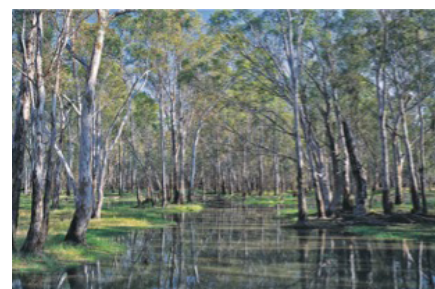
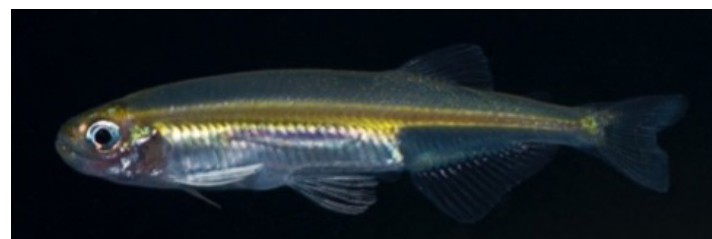
Masters conversion: **Yes**

My research focusses on understanding the influence of biotic and abiotic drivers on the structure and function of aquatic ecosystems. A major focus for this work is understanding the effects of climate and hydrologic variability on population dynamics and on ecosystem processes, including ecosystem productivity and food web dynamics. My research combines both field and desktop analysis, including the use of GIS and spatial datasets to explore hypotheses at large spatial scales. I am also particularly interested in applying research to help tackle important water and catchment management issues.

Project 1. The effects of climate-variability and change on species distributions. Australia is the driest inhabited continent and experiences extreme patterns of interannual climate variability and frequent drought. Water stress, particularly during drought, is a major driver of species distributions in aquatic ecosystems, and climate change will strengthen this effect. Projects in this area involve using a range of field and modelling approaches to relate species occurrence patterns to the effects of climate, hydrology, fire and other physiographic variables, and then used these models to predict potential future shifts in species range, abundance and occupancy of particular habitats. These predictions are also being combined with conservation planning models to prioritise areas for protection and targeted management interventions.

Project 2. Ecohydrology of intermittent stream networks. In many regions of the world up to 80% of the river network undergoes regular drying. During these dry periods surface water habitats can contract to isolated waterholes dotted along the river channel, which become critical refuges for aquatic biota. Project opportunities exist to study processes occurring within individual waterholes, such as the water quality and food-web structure, through to the role of catchment hydrology in determining waterhole persistence across entire riverscapes, and the way in which this influences metapopulation structure and dynamics.

Project 3. Quantifying productivity and fish growth rates across different habitats. Many fish species have a short critical period after hatching when sufficient food must be available to allow survival. This project will investigate zooplankton production and associated fish growth across a range of floodplain habitat types, including river channels, perennial wetlands and intermittent wetlands.



Dr. David Deane Bundoora



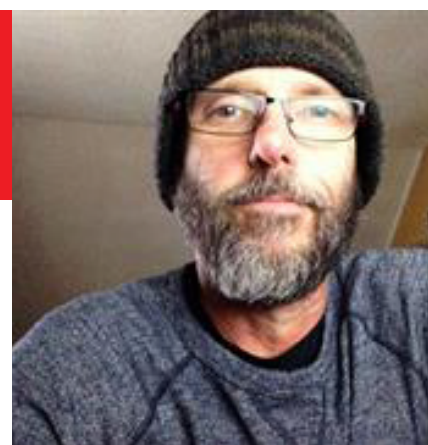
Field work

Statistical or spatial
modelling

Glasshouse work



Data analysis

E-mail: d.deane@latrobe.edu.auWebsite: [click here](#)

Number of projects: 1

Full-time or part-time: **Full-time**Feb or July start: **Feb only**Masters conversion: **Yes**

My research interests lie in making, testing and improving predictions about patterns of biodiversity. I come at these questions from two main directions. 1. scale dependence: how the biodiversity we see (e.g., the number of species) depends on the lens through which we look (e.g., the size of the sampling unit). The scaling laws that determine how this occurs are super interesting and important for prediction. 2. Community assembly: the reasons we see what we see where we see it depends on variations in abiotic conditions (e.g., gradients in moisture, pH, etc), biotic interactions (e.g., competition, facilitation) and dispersal (in space and time).

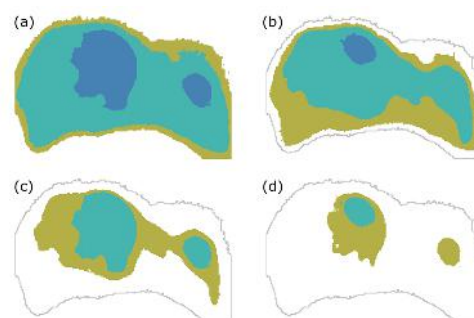
My favourite study system is wetland plant communities. Wetlands are being lost at a rate three times that of forests and, pound-for-pound, freshwater ecosystems harbour more biodiversity and provide more critical ecosystem services than pretty much anything else on the planet. If you want to work on issues relating to addressing global change, you could do worse than consider wetlands.



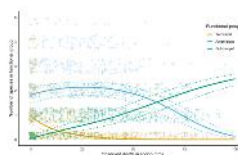
My wetland research tries to understand how water availability affects the biodiversity we see. As a study system, I like wetland plant communities for three reasons: first, they tend to hang around

in landscapes after everything else is cleared, so they are often the last remnants of native habitat to be found. Second, plants don't move around (much) and because water is strongly influential on community composition, it makes them (relatively!) easy to model. Third, we have some nice theory on how to group wetland plant species to model things like zonation as a function of changing water level (i.e., trait-environment relationships).

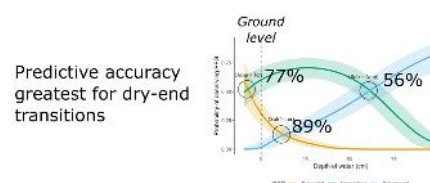
In terms of potential projects, depending on whether you prefer the idea of field or experimental (glasshouse) work, we can tailor an Honours project to suit. Field work could involve either re-visit surveys of historical sites (with questions around climate-driven changes in composition or non-native species incursion) or spatial modelling to identify optimal locations for restoration of a keystone species at a managed wetland. Experimental work could focus on questions around how water availability or root architecture plasticity influences competitive outcomes between native and non-native species.



Scenario	Wetland area (ha)	Total species (mean [sd])	Zone area (ha)		
			F	A	S
(a) Base	6.6	40.6 [2.7]	1.1	4.2	1.3
(b) -0.25 m	5.3	38.8 [2.3]	2.1	3.1	0.2
(c) -0.50 m	3.0	25.3 [3.3]	1.7	1.3	0.0
(d) -0.75 m	1.0	13.4 [2.4]	0.8	0.2	0.0



Explained variation in response >70%



Predictive accuracy greatest for dry-end transitions

Take homes

Below-ground saturation will determine dry end hydro-niche transitions in wetland plants

Simple correlative models have potential to predict drying impacts on wetland plants

Dr. Charles Feigin Bundoora



Animal handling



Genetic sequencing



Bioinformatics



Light microscopy



Chromosomal and/or
nucleotide extraction
assays



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Number of projects: **1**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

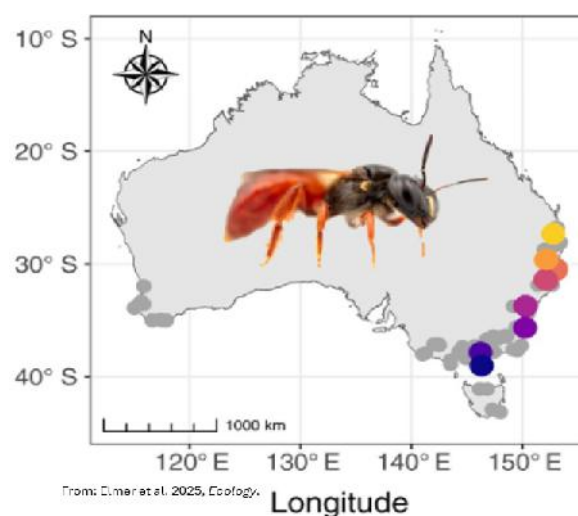
Masters conversion: **Yes**

My lab aims to better understand the consequences of genetic variation for adaptive evolution and genetic health. The 'endless forms' among animal species have arisen through evolutionary forces like natural selection that change the information encoded in their genomic DNA. However, changes in the DNA are linked to changes in organismal traits through complex, multi-layered molecular mechanisms that remain poorly understood. Importantly, many of these same mechanisms underpin inherited developmental disorders and shape risk factors for inbreeding depression. My group makes extensive use of comparative, population and functional genomic approaches, with a special emphasis on non-traditional model organisms. Key areas of research include studies on the evolutionary and mechanistic basis of complex traits in animals, the role of epigenetic mechanisms in predicting health and application of whole genome sequencing data for threatened species management. Within these areas, potential projects include:

Project 1. What makes a "living fossil"? The Red Queen Hypothesis argues that you can't stay the same in a changing environment. Predators become better at catching prey, so prey must get better at avoiding predators. Pathogens improve their ability to infect, so species' immune systems must adapt. Thus, its argued that constant evolution is required for species to avoid extinction. Yet, some taxa seem to defy this rule. "Living fossils" often show incredible stasis in key traits that hardly change even over hundreds of millions of years. This project will use whole genome sequencing of tadpole shrimp (Family Triopsidae) and comparative genomics with other Branchiopod crustaceans to explore just how "fossilised" these species really are.

Project 2. Can genome-wide variation predict adaptive potential and genetic health of native bees? The limits of a species' geographic range and the long-term stability of its populations are heavily dependent on genetic variation. This variation determines a species' ability to adapt to environmental conditions but also creates a burden of harmful mutations that quietly reduces survival and reproduction. Both leave traces in DNA that can be valuable for predicting resilience in the face of climate change. For essential pollinators like Australian native

bees, little is known about their standing genetic variation or how it varies with population size, locality or history. This project, conducted in collaboration with the Kellermann Lab, will use whole genome sequencing data to assess how much diversity each population holds, estimate its mutational burden, and identify genetic variation associated with climate and habitat.



Dr. Amanda Franklin Bundoora



Field work



Biomechanics



Animal handling



Animal behaviour studies



Data analysis

We are fascinated by how animals sense, move through, and respond to their environment. How do animals perceive the world around them? How do they function within that environment? How do environmental conditions shape both perception and performance? Much of our current work centres on animal sensory systems and colouration – how animals see, and why they look the way they do. Sensory systems are critical for navigating the environment and completing essential tasks such as locating food, selecting mates, or finding shelter, and colouration often plays a key role in these same processes, from mate choice to warning signals to camouflage. We're interested in how these traits interact to shape behaviour and ecology across species. More broadly, our lab is united by an interest in the functional biology of animals – how physical and sensory traits are shaped by, and adapted to, the environments animals live in. This extends beyond vision and colouration to questions of biomechanics and physiology: how organisms move, how their structures perform under real-world conditions, and how these functional traits influence survival and behaviour. To investigate these questions, we draw on techniques from diverse fields including ecology, evolutionary biology, behavioural ecology, physiology, bioengineering, and biomechanics. We work with a wide range of animal groups depending on the research question, including insects, arachnids, crustaceans, molluscs, fish, and birds. Currently, we have several ongoing projects suitable for an Honours student, spanning sensory ecology, colouration, and biomechanics.

Project 1. How do animals use iridescence and gloss? Iridescence and gloss are characterised by a changeable appearance – iridescent effects shift in colour and glossy effects produce bright flashes. We have shown that this changeability is a key property that influences behaviour of conspecifics and predators. This project further interrogates our initial findings to understand how environmental properties, animal behaviour and context influences these functions.

Project 2. How do prey avoid predators? And how do predators overcome these strategies? Prey have all sorts of strategies to avoid predation – camouflage, erratic movement, toxic chemicals. This project investigates what strategies prey have evolved to evade predators – such as colours or patterns that disrupt localisation of moving prey, or ultrafast movements to rapidly escape.



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Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**



Project 3. How do environmental conditions impact predator-prey strategies? Predators rely on sensory cues to localise and target prey. But human impacts on the environment can disrupt these cues – such as light pollution or noise pollution. This is an early stage project to investigate how anthropogenic changes impact behaviour and if animals can adapt.



Dr. Susan Hoebee Bundoora



Field work



Bioinformatics



Plant breeding



Glasshouse work



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Number of projects: **2-3**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

My research mainly focuses on the conservation of native plant species where I am interested in understanding plant reproduction, population genomics, and evolution.

Students under my supervision use a range of approaches, from field-based ecological studies and investigations of floral traits related to different pollinator groups, to genetic studies of mate choice and large-scale next-generation sequencing.

Project 1. Threatened Grevillea genomics (Feb 2027 or Jul 2027). *Grevillea* is Australia's 3rd largest genus and contains many threatened species. These projects will apply genomic studies to inform conservation management. Projects could conceivably be single or multiple species studies where there are various questions around species disjunction and connectivity, and/or diversity in pre- and post-fire stands.

- *G. patulifolia* (pre- & potentially post fire)
- *G. montis-cole* (with Dr Steve Sinclair, ARI and Dr Gareth Holmes, RBGV – disjunction distribution, as well as pre- & post fire)
- *G. steiglitziana* (with Ryan Phillips)
- *G. floripendula* (with Ryan Phillips, disjunction distribution)
- *G. rosmarinifolia* Lara Form (with Geelong Botanic Gardens and Friend Groups)

Project 2. Gentiana genomics and floral visitation (Feb 2027). This project will generate vital biological knowledge of the endangered and cryptic *Gentiana baeuerlenii* at Wilsons Promontory, the only known extant population in Australia, and will specifically assess genomic diversity and floral visitor interactions.

Project 3. Breeding System, Seed Biology and Translocation Ecology of *Ballantinia antipoda* (co-supervisor: Dr Stan Wawrzyczek, TSC) (Jul 2027). This project will investigate key aspects of *B. antipoda*'s breeding system, as well as pollen and seed biology, following controlled pollination in a seed orchard maintained at NTWS. During the project there will be scope for the honours student to join TSC staff to evaluate the success of recent translocation efforts (time and availability dependent) and assist with collection of wild seeds from extant populations at Mt Alexander.

Project 4. *Ptilotus* pollination ecology and breeding systems (with Dr John Morgan) (Jul 2027). This project will investigate the pollination ecology and breeding systems of three co-occurring species of *Ptilotus* (*P. macrocephalus*, *P. erubescens* and *P. spathulatus*) from native temperate grasslands in western Victoria, yet little is known about how they coexist. A key question is, do they partition pollinators through differences in flowering phenology, floral visitation, or reproductive strategy?

Project 5. Pollination and genomic studies on threatened Gariwerd peas: *Daviesia laevis* Crisp and *Swainsona brachycarpa* Benth. (with Dr Noushka Reiter, RBGV) (Jul 2027). This project will use existing ex situ collections and in situ field observations in Gariwerd National Park to identify the pollinators and determine the mating systems of *D. laevis* and *S. brachycarpa*. For *S. brachycarpa*, this project will also characterise the genetic diversity of wild populations to inform future seed collections, maximise the capture of genetic diversity in ex situ collections, and guide translocations.

Project 6. Sex allocation in *Pimelea spinescens* subsp. *spinescens* (with Dr Steve Sinclair, ARI) (Jul 2027). Flowers of *P. spinescens* are bisexual exhibiting both hermaphroditism and dioecy but maleness appears 'leaky'. This project will examine whether this 'leakiness' varies with environmental gradients.



Dr. Aleicia Holland Albury-Wodonga



Field work



Animal handling



Ecological assays

Animal or plant
identification

Ecotoxicology

E-mail: a.holland2@latrobe.edu.auWebsite: [click here](#)Number of projects: **1 Feb, 1 Jul**Full-time or part-time: **Either**Feb or July start: **Both**Masters conversion: **Yes**

Aquatic ecosystems: freshwater and marine are at increasing risk from climate change and anthropogenic pressures. Our research investigates the effects of abiotic factors on aquatic systems, communities and biota using a range of field and laboratory techniques. Our field sites span tropical, temperate, marine and alpine environments including streams, rivers, lakes and wetlands, where we explore interactions of aquatic biota with their environment such as the influence of dissolved organic matter (DOM) on aquatic communities and food webs, fish/microbe interactions, and direct effects of contaminants and environmental stressors on ecosystem function and biota.

We also use controlled laboratory experiments to understand chemical processes, interactions of biota with their chemical environment, and the bioavailability and toxicity of contaminants.

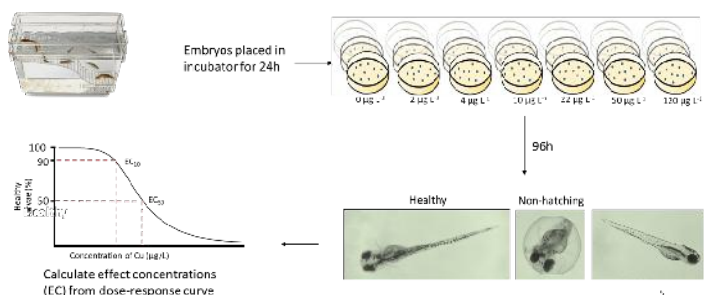
I currently have interest in recruiting students for the following topics:

Project 1. Microbiomes of Flathead and Fiddler ray and response to contaminants in Port Phillip Bay.

Project 2. Effect of fire on alpine peatland streams.

Project 3. Mechanisms behind toxicity of metals to aquatic biota.

Project 4. Biota of naturally acidic streams.



Dr. Vanessa Kellermann Bundoora



Field work



Ecological assays



Animal handling



Drosophila melongaster
models



PCR assays



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Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

My research aims to understand how abiotic and biotic factors shape the distribution of insect species and, in doing so, make predictions about how species will respond to climate change. Because insects are ectothermic and do not regulate their body temperature, a species' capacity to tolerate hot/dry/cold environments often dictates where they live. I am interested in studying the evolution of these traits (heat/desiccation/cold tolerance) and the extent to which these traits can shift via genetics and plasticity. To answer these questions, I work on two systems I work on two systems: the highly tractable (lab-based) *Drosophila* system and (field-based) native bees.

Project 1. Exploring trade-offs between cold tolerance and phenotypic plasticity in Drosophila. Phenotypic plasticity is the capacity for individuals to modify their phenotypes in response to the environment. Understanding species' capacity to respond to plasticity is important, given that plasticity is expected to shape how species respond to climate change. Theory predicts that the capacity to respond via phenotypic plasticity stress/tolerance traits trades off with innate resistance. That is, you can't be highly tolerant to stress (cold) and highly plastic. In this project, you will examine whether phenotypic plasticity in cold resistance varies across species adapted to different environments and whether high cold tolerance trades off with plasticity.



Project 2. How does temperature shape competitive outcomes in Drosophila. Temperature is often considered the most important variable shaping the distribution of insect species. But species rarely live in isolation, and competition between other species can influence species' capacity to adapt to different environments. In this project, you will examine how competition between *Drosophila* species affects fitness traits (fecundity/viability) across a range of temperatures to determine how competition and temperature interact to shape *Drosophila* distributions.

Project 3. Flying thermal limits and endothermy in bees. Native bees offer crucial pollination services to natural and agricultural environments, yet how temperature shapes their foraging decisions is poorly understood. In this project, you will sample native bees from natural environments across thermally variable days to determine the temperature range at which different species forage. You will examine how the body temperatures of bees match with ambient temperatures to examine whether bees are physiologically or behaviourally regulating their body temperatures.

A/Prof. John Morgan Bundoora



Field work



Data manipulation and analyses



Ecological assays



Glasshouse work



Plant identification



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Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

We focus on the factors that affect plant species distributions in nature, and the plant population dynamics that underpin changes over time. Understanding how plant species respond to ecosystem drivers (like fire, climate change, feral species) is fundamental to predict their future over coming decades. I have lots of project ideas as starting points for discussion with prospective students. I'm always interested in hearing from students who have their own ideas, particularly if they are variations on the themes listed here (or include topics such as extreme events, species distributions, historical ecology, floristic survey). As an example of projects available in 2027:

Project 1. Range shifts of mountain plants - I am seeking an Honours student to study why mountain plant species are failing to shift their ranges fast enough to track climate change. We have a particularly poor grasp of long-distance dispersal rates, and how propagule origin and biotic interactions constrain establishment beyond species' ranges. Focusing on mountain plants, this project aims to disentangle the importance of the species interactions and demographic processes governing shifts of plants' high-elevation range limits.

Project 2. Hydrological-niches as a basis for species richness in plant communities - I am seeking an Honours student to investigate how hydrological niches - plants growing along soil-moisture gradients - contribute to plant community structure in native grasslands. Hydrological niche theory would suggest that diversity is structured by segregation of species along niche axes of soil drying and soil aeration, but this has never been tested in native grasslands. This question is important since hydrology is expected to be altered by climate change and therefore, this information is of practical, predictive value.



Project 3. Long-term fire impacts on savanna trees - I am seeking an Honours student to quantify opposing tree demographic processes - i) seedling regeneration and ii) tree mortality - in tropical savanna in relation to fire. Using a long-term fire regime experiment ("Burning for Biodiversity", Territory Wildlife Park, Darwin) where the frequency of burning has been manipulated, we will assess how well tree seedlings survive fire in their first dry season after germination and how well (tagged) trees have survived over more than two decades of experimental fire. The aim is to better understand the mechanisms that underpin tree population dynamics where fire is very frequent.



A/Prof. Nick Murphy Bundoora



Phylogenetics



Ecological assays



Population genetics



Genetic sequencing



Field work



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Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

My lab uses genetic tools to better understand biodiversity. Techniques such as DNA sequencing, phylogenetic reconstruction, and population genetic analyses are used to understand why species are found where they are and how changes in environmental impact distributions occur. We also utilise state-of-the-art genetic techniques such as diet analysis, and eDNA to determine how species interact with their environments. I have three projects currently listed below.

Project 1. Evolution of invertebrates in SE rainforests. The rainforests of SE Australia exist as islands of wet habitats surrounded by seas of dry forest and are home to a group of extremely restricted forest floor arthropods, including amphipods, isopods, and millipedes. This project will choose one of these groups and undertake DNA sequencing studies, phylogenetics, and/or morphological analyses to understand the drivers of short-range endemism SE Australia. You are guaranteed to find a new species!

Project 2. Yellow crazy ants on Christmas Island. Yellow crazy ants (YCA) are a major issue on Christmas Island, where they kill the iconic red crabs. There are two options for this research project; 1) Utilising the insatiable appetite of yellow crazy ants for sugar and protein, this project will undertake genetic analysis of YCA diets and examine the interaction between ants, trees and honeydew producing scale insects, to help develop future biocontrol. Or 2) utilising the weird chimeric genomes of YCA, you will develop new genetic markers to assess the genetic relationships and invasion history of YCA on Christmas Island and investigate evolutionary signals relating to large scale ant baiting efforts.



Project 3. Understanding the relationship between habitat improvement and chytrid infection rate for Growling Grass Frogs in Nangak Tamboree Wildlife Sanctuary. The Wildlife

Sanctuary is investigating the establishment of growling grass frogs (GGF) with significant habitat improvement to create warm basking spots for frogs to fight the impacts of chytrid infection. This project will use genetic analyses to examine the relationships between habitat improvement, and chytrid infection loads in Nangak Tamboree, and will look at similar habitats across GGF populations to ensure the best chance for survival within the wildlife sanctuary.

Other projects. Please speak with me if you are interested in molecular ecology and evolution in general from an applied or theoretical perspective. Other possible projects include; deer dynamics on the urban fringe, eDNA for terrestrial vertebrate management, aquatic invertebrate evolution and ecology, invasive species diets, allopatric speciation and genome evolution and evolutionary signals of life in refugia.



Dr. Ryan Phillips

Bundoora



Ecological assays



Field work



Plant reintroduction



Animal behaviour studies



Animal or plant
identification



Data analysis



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Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

The study of plant-pollinator interactions is critical for understanding the evolution of the incredible morphological and taxonomic diversity of both flowering plants and nectar feeding animals. Further, in Australia there are many cases of specialised pollination systems, meaning that numerous plants are vulnerable to the loss of pollinators following anthropogenic modification of the landscape. We tackle both theoretical and applied questions, with a particular focus on orchids pollinated by sexual or food deception, and the rich diversity of Australian plants pollinated by birds or mammals.

Project 1. Using plant-pollinator networks to inform reintroductions of endangered plant species. Plant-pollinator networks have become a popular tool for attempting to understand the processes that enable co-existence of diverse communities of plants and pollinators. However, a potentially important application for the network approach is to understand the role of pollinators and co-occurring plant species for facilitating reproduction of endangered plant species. This project will investigate plant-pollinator networks for endangered Victorian plants with the aim of identifying key species for management, and suitable communities for plant reintroductions. I also co-supervise projects on this topic with Dr Noushka Reiter at the Royal Botanic Gardens Victoria, with a focus on orchids and flora of the Grampians and Little Desert region.

Project 2. Floral adaptations to specialised pollination strategies. Although having multiple pollinator species may provide greater reproductive assurance, many plants are specialized on one or few pollinator species. Specialized plants often evolve exaggerated floral traits as natural selection favours morphological and chemical refinement based on the preferences, behaviours and morphology of a specific pollinator. Thus, understanding the origins of specialized pollination systems is critical for understanding the diversity of floral traits exhibited by flowering plants. Potential topics include identifying the pollinators of morphologically unusual Australian plants, testing the role of various floral traits in achieving pollinator attraction, and exploring the ecological and conservation consequences of using specialized strategies.

Project 3. How do bird-pollinated plants shape bird communities? In Australia, bird pollinated plants vary from towering eucalypts to diminutive understory plants. They also vary in floral structure, ranging from generalist species that attract numerous honeyeaters and parrots, to species with tubular flowers that are likely specialised on long-beaked honeyeaters. Surprisingly, many understory species have received little attention in terms of which species pollinate them, and whether their flowering drives the composition of bird communities. We plan to investigate these issues in threatened Grevillea species (co-supervised with Susan Hoebee).



Dr. Michael Shackleton Albury-Wodonga



Field work



PCR assays & genetic sequencing



Ecological assays



Light microscopy



Animal behaviour studies



Metabolomics



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

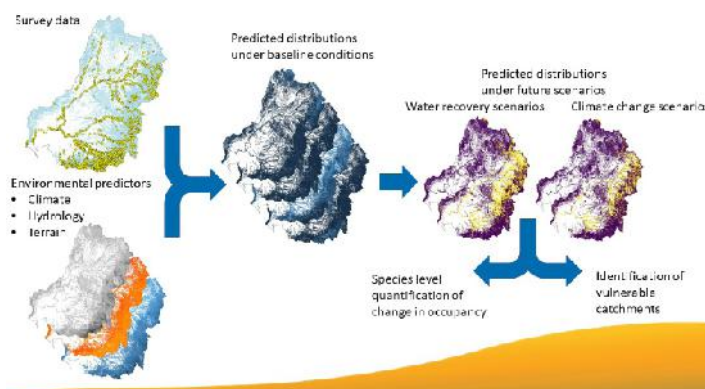
My lab is primarily interested in aquatic ecology, specifically around understanding species distributions and responses to environmental parameters - especially those impacted by climate change. I use traditional and molecular (i.e. metabarcoding) survey techniques to characterise communities and model their responses to various impacts. Projects in my lab generally involve some field and lab work, spatial analyses, and modelling. I am open to discussing project areas that potential honours, masters or PhD students are interested in. However, projects that I am particularly wanting to pursue over the next year include:

Project 1. Understanding the impact of temperature on invertebrates. Multiple research questions can be investigated here but will involve measuring invertebrate body mass and nutritional makeup and could involve rearing invertebrates at different temperatures or collecting invertebrates from various climates.

Project 2. Investigating the role of groundwater inflows in alpine streams as potential refugia for aquatic organisms. This project will investigate whether groundwater impacted zones support communities of aquatic macroinvertebrates that are distinct from other microhabitats.

Project 3. Understanding the phenology of insect emergences. This project will involve collecting insects over time and quantifying their abundances. It may involve using already collected specimens, collecting new specimens, or a mix of both, depending on the student's preference.

Project 4. Taxonomy of aquatic Trichoptera. There are heaps of insects yet to be discovered and some of them just need a bit more work to be described. I have a selection of Trichoptera waiting for someone to name. This project will involve working with preserved insects, visiting museums and collecting material.



A/Prof. James Van Dyke Albury-Wodonga



Animal handling



Ecological assays



Field work



Animal behaviour studies



Animal or plant
identification



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **July only**

Masters conversion: **Yes**

My lab studies a range of topics related to vertebrate ecology, reproduction, and conservation. Currently, I have funding available for projects focusing on the ecology and conservation of freshwater turtles, as well as citizen science initiatives (1 Million Turtles) aimed at engaging the public in turtle conservation. Most of this work takes place in the Murray-Darling basin, and I have contacts and collaborations from throughout the region. Our main aim is to develop, test, and implement new ways of protecting turtle nests from foxes, which destroy turtle nests. While doing this, we also conduct trapping surveys to compare and monitor turtle populations over time. I have three key projects available in 2026:

Project 1: Estimating juvenile turtle recruitment and survivorship rates to understand how much reproduction is needed to increase turtle populations. This project involves mark-recapture of hatchling turtles hatched out of artificial floating islands. Our aim is to understand how many hatchlings must be produced before we start re-capturing juvenile turtles in large numbers. This project will take place in Winton Wetlands near Benalla, VIC, and will involve extensive on-ground fieldwork.

Project 2: Developing conditioned taste aversion as a method to reduce fox predation on turtle nests. My collaborator, Dr Ligia Pizzatto, is leading this project, and aims to use a distasteful compound to train foxes to not eat turtle eggs. The project will involve extensive on-ground fieldwork in northern Victoria, near Wodonga and Wangaratta

Project 3: Estimating turtle population dynamics in the rivers of western NSW. Currently, data on turtle populations in the western Darling and Lachlan Rivers are limited. PhD student Wesley Smith is leading a project to estimate basic turtle population parameters and movement rates in this system, and many further projects could be developed to run alongside his.

I work with all prospective honours students to develop their own projects within these areas and based on their own interests and expertise. If any of these ideas sound interesting, please get in touch with me, because our summer field season is near and there are plenty of opportunities to get some hands-on experience with the work we do for a day or two, which may help you make a decision about a possible project. Our honours projects typically are extendable for MSc degrees as well.





Biochemistry & Cell Biology

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Dr. Pamali Fonseka

LIMS



Cell culture - eukaryotes
incl. primary & cell lines



Proteomics



Bioinformatics



Animal models of disease



Cell transfection



CRISPR-Cas9 gene editing
of cells



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Number of projects: 1

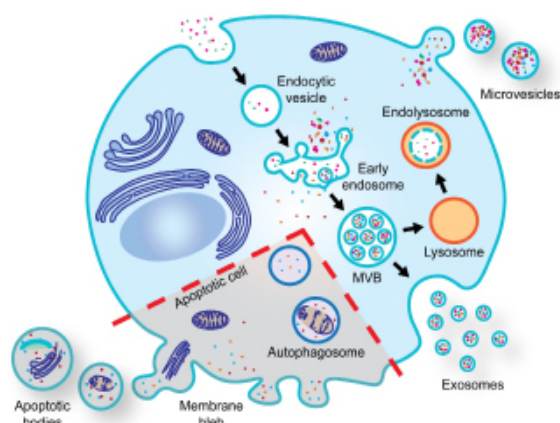
Full-time or part-time: **Full-time**

Feb or July start: **Both**

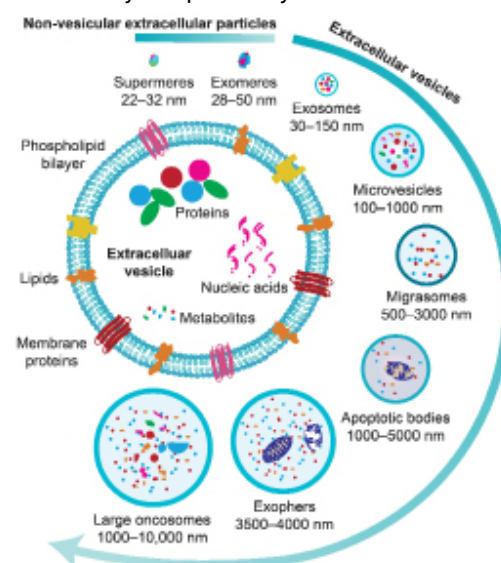
Masters conversion: **No**

The Fonseka Lab is dedicated to exploring how extracellular vesicles (EVs) are formed, released, and function in different biological systems. EVs are nanosized particles composed of a lipid membrane, and they are secreted by many types of cells—including mammalian (human and animal), bacterial, and fungal cells. These vesicles carry a wide variety of cargo inside them, such as DNA, RNA, proteins, fats (lipids), and small molecules called metabolites.

One of the most important features of EVs is their protective outer layer, which shields their cargo from damage in the outside environment. This allows EVs to safely deliver their contents to other cells. When EVs reach a recipient cell, they can trigger a series of biological signals, influencing how that cell behaves. This process is known as intercellular communication. EVs are involved in many important biological processes. For example, they help with tissue repair, support pregnancy and early foetal development, and play roles in aging and immune system regulation. They are also linked to how diseases progress, including cancer and infections. Because of their ability to carry and deliver specific molecules, scientists are now using EVs as tools for targeted drug delivery. This means EVs can be engineered to carry medicines, RNA interference molecules (RNAi), or inhibitors directly to diseased cells—offering exciting new possibilities for treatment.



The Fonseka Lab is currently investigating the role of adherens junction proteins in the biogenesis and secretion of extracellular vesicles (EVs). Adherens junctions are specialised structures found at the lateral surfaces of epithelial and endothelial cells, where they mediate cell-cell adhesion. These junctions are primarily composed of cadherins (such as E-cadherin) and catenins (like β -catenin and p120-catenin), which link the cadherin molecules to the actin cytoskeleton inside the cell. We hypothesise that adherens junction proteins may modulate EV formation by influencing membrane curvature, endocytic recycling, or cytoskeletal tension, thereby affecting the trafficking and release of EVs. Additionally, these proteins might play a role in cargo selection, determining which nucleic acids, proteins, or lipids are packaged into EVs. Understanding this connection could reveal new insights into how intercellular communication is regulated in tissues, especially during processes like development, wound healing, and tumor progression. It may also open up new avenues for therapeutic EV engineering, where manipulating junctional proteins could enhance the efficiency or specificity of EV-based drug delivery systems.



Prof. Stephanie Gras LIMS



X-ray crystallography



Bacterial over-expression of protein & purification



Cell transfection



Bioinformatics & molecular modelling



Flow cytometry & immunoassays



Protein biochemistry



Molecular cloning



Infection & immunity



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Number of projects: 5

Full-time or part-time: **Either**

Feb or July start: **Both**

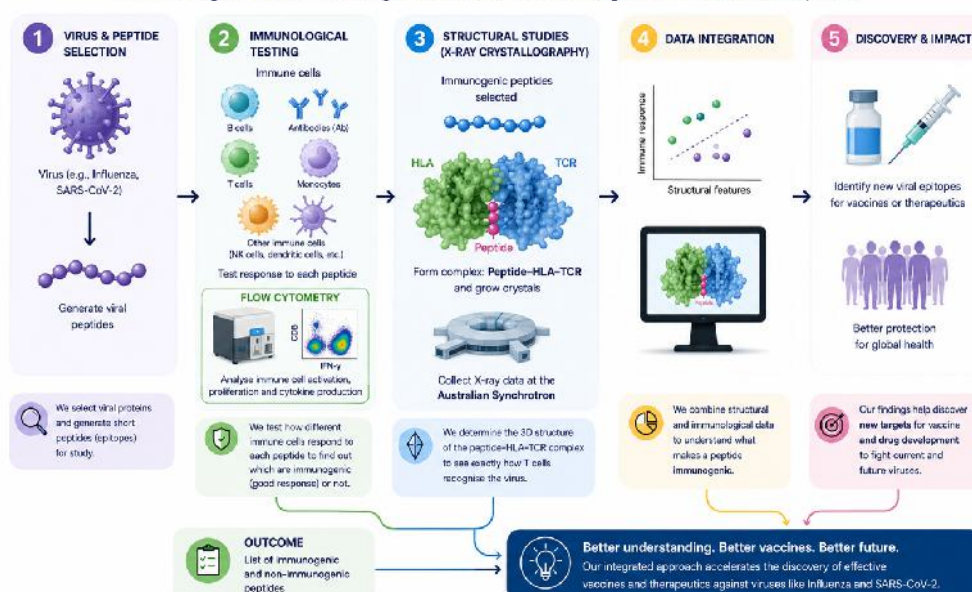
Masters conversion: **Yes**

Viruses and other pathogens are part of our everyday environment, and our immune system must constantly protect us from them. However, we still do not fully understand how the immune system detects, recognises, and eliminates viral infections. Viruses can also mutate, allowing them to escape immune surveillance and continue to infect our cells. To develop better vaccines and antiviral drugs, including effective vaccines against challenging viruses such as HIV, we first need to understand how the immune system recognises viruses and how viruses evade immune responses. Our lab investigates these questions using a range of techniques in biochemistry, structural biology, and cellular immunology (Figure below: from virus to vaccine: our workflow). Students can choose from projects that use these different approaches to explore how viruses interact with and escape the immune system.



From Virus to Vaccine: Our Workflow

Understanding how immune cells recognise viruses to discover new targets for vaccines and therapeutics



Prof. Stephanie Gras & Dr. Anurag Adhikari

LIMS



X-ray crystallography



Bacterial over-expression of protein & purification



Cell culture - eukaryotes, prokaryotes



Bioinformatics & molecular modelling



Flow cytometry & immunoassays



Protein biochemistry



Molecular cloning



Gene expression analyses & sequencing



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Number of projects: 1

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

Current HIV diagnostics begin with rapid antibody tests followed by costly, centralised nucleic acid-based confirmation requiring advanced lab infrastructure. These logistical and economic barriers, along with HIV-related stigma, limit access, especially for marginalised communities.

Project 1. Development of an Instrument-Free, Smartphone-Based Human Immunodeficiency Virus (HIV) RNA Detection Platform. This project aims to develop a low-cost, portable, smartphone-based device that enables HIV diagnosis without the need for laboratory instruments. The proposed device combines passive HIV lysis, RNA stabilisation, and aptamer-based selective RNA capture within a single, disposable unit (Figure 1A). It features a dual-channel design: one channel concentrates HIV-specific RNA for targeted detection, while the other elutes total RNA for benchmarking and broader molecular analyses. Detection of HIV RNA is achieved using a patented smartphone-based electrochemical sensing platform developed already at La Trobe University (Figure 1B).

This system repurposes the smartphone's audio interface to function as a potentiostat, enabling aptamer-based RNA detection. Test strips used in this system are embedded with a tethered DNA probe that binds to a segment of the aptamer-HIV RNA complex (Figure 1C). The probe includes a redox reporter that produces an electrical signal. When the test strip encounters a sample containing the aptamer-HIV RNA complex, the reporter's position shifts, resulting in a measurable change in electrical current that correlates with the concentration of the target RNA.

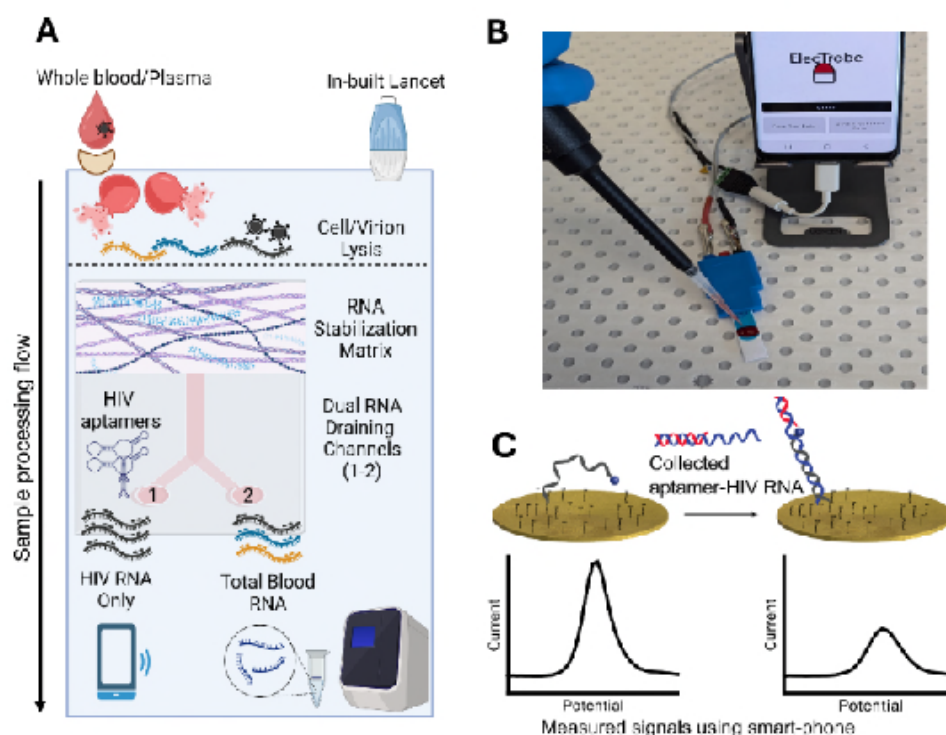


Figure 1: **A)** Prototype microfluidic device for RNA extraction/stabilization, detection, and storage. **B)** Image of patented, instrument-free, smartphone-based electrochemical detection using disposable test strips in fluids. **C)** Surface chemistry on test strip for detecting HIV RNA-aptamer material collected by the device.

Prof. Stephanie Gras & Dr. Dimitra Chatzileontiadou

LIMS



Flow cytometry



Blood processing



X-ray crystallography



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Viral infections can have lasting health consequences long after the initial infection has resolved, contributing to chronic inflammatory, immune, neurological and cardiovascular conditions. The mechanisms that drive this transition from acute infection to chronic disease remain poorly understood. Research into these processes is essential to identify people at risk, develop effective diagnostics and treatments, and ultimately prevent long term disease.

Number of projects: **1**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

Project 1. Understanding chronic disease such as AIDS, Long COVID, Multiple sclerosis (MS). HIV has an exceptionally high mutation rate, allowing the virus to rapidly change and escape recognition by the immune system. Although antiretroviral therapies have dramatically improved the lives of people living with HIV, HIV/AIDS remains a significant global health challenge, and an effective vaccine is still needed. In this project, we investigate a fascinating group of individuals known as HIV controllers, whose immune systems can naturally control HIV infection and/or delay disease progression. Understanding what makes their immune responses particularly effective could reveal important clues for developing new HIV vaccines and therapies.

Long COVID is a complex condition in which symptoms persist or develop months after SARS-CoV-2 infection, affecting multiple organs and significantly reducing quality of life. Although millions of people are affected worldwide, there are currently no definitive diagnostic tests or targeted treatments. In this project, we investigate the immune and biological mechanisms that drive Long COVID, particularly why women are disproportionately affected. Understanding these mechanisms could reveal new biomarkers and therapeutic targets, enabling earlier diagnosis and more effective, personalised treatments.

Multiple sclerosis (MS) is a chronic autoimmune disease in which the immune system mistakenly attacks the central nervous system, causing inflammation and damage to myelin and nerve fibres. Although current therapies can reduce disease activity and slow progression, there is still no cure, and treatment responses vary considerably between individuals. In this project, we investigate the immune mechanisms that drive MS and determine why some individuals develop more severe or progressive disease. Understanding these differences could reveal important clues for developing new biomarkers and more effective, personalised therapies.

Methods: T cell functionality, flow cytometry, blood processing, immune cells purification, T cell activation, intracellular cytokine staining. Students will use flow cytometry to investigate how immune cells recognise and respond to viruses (HIV, SARS-CoV-2, and EBC), including their activation and functional responses. The project can also incorporate X-ray crystallography to determine 3D structures of virus derived peptides presented to immune cells and examine, at the molecular level, how those interact.



Prof. Stephanie Gras & Dr. Emma Grant

LIMS



Immunoassays



Flow cytometry



Cell culture - Human T cells



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Number of projects: **1**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

Influenza viruses remain a significant global health threat, causing seasonal epidemics and occasional pandemics. Current vaccines primarily induce antibody responses against highly variable surface proteins and therefore require annual reformulation. There is an urgent need to develop universal influenza vaccines that provide broader and more durable protection. T cells are an attractive target for universal vaccine design because they recognise more conserved regions of the virus. CD8⁺ T cells recognise short viral peptides presented by HLA class I molecules, while CD4⁺ T cells recognise longer peptides presented by HLA class II molecules. Importantly, some longer CD4⁺ T cell epitopes can contain shorter CD8⁺ T cell epitopes within them, creating “nested” epitopes that have the potential to activate both arms of the cellular immune response.

Our group recently characterised a pair of “nested” CD4⁺ and CD8⁺ T cell epitopes and found that the “nesting” the CD8⁺ T cell epitope within the longer CD4⁺ T cell epitope affected the quality of the corresponding CD8⁺ T cell response. These findings suggest that nested epitopes may influence T cell immunity in ways that could be important to understand for vaccine design. This Honours project will build on these findings by investigating several other identified influenza-derived “nested” peptide pairs. Using human derived peripheral blood mononuclear cells (PBMCs), the student will generate T cell lines against the “nested” peptide pairs, or the shorter CD8⁺ T cell epitope alone. Then, using an intracellular cytokine staining (ICS) assay, the student will assess the quality and magnitude of the CD4⁺ and CD8⁺ T cell responses in both conditions. CD4⁺ and CD8⁺ T cell responses will be compared to determine whether the changes observed in the first nested epitope pair represent a broader phenomenon. This project will provide important insights into how nested influenza epitopes shape cellular immunity and whether they represent promising targets for next-generation universal influenza vaccines.

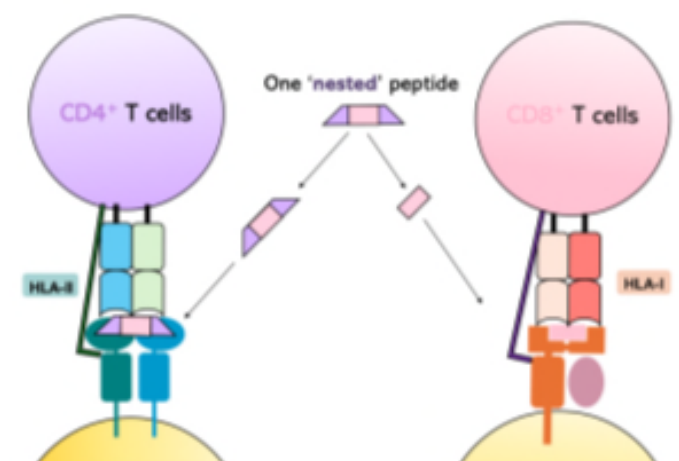


Figure 1. “Nested” influenza T cell epitopes. A shorter CD8⁺ T cell epitope (8-10 amino acids) is nested within a longer CD4⁺ T cell epitope (14-16 amino acids). The CD8⁺ T cell epitope is presented by HLA class I (HLA-I) molecules to activate CD8⁺ T cells, while the longer CD4⁺ T cell epitope is presented by HLA class II (HLA-II) molecules to activate CD4⁺ T cells.

Prof. Stephanie Gras & Dr. Janesha Maddumage

LIMS



X-ray crystallography



Protein expression in bacterial cells



Protein refold and purification



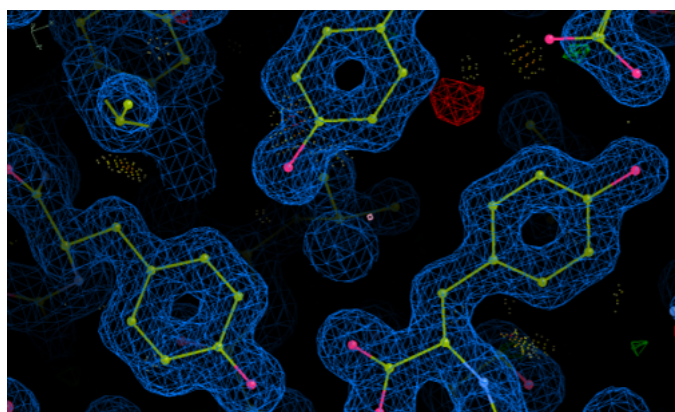
AI-based structure prediction

Human leukocyte antigen (HLA) molecules play a central role in immune surveillance by presenting peptides derived from viruses, cancer cells, and other diseased tissues to T cells. While HLA molecules are critical for protective immunity, many aspects of peptide presentation and T cell receptor (TCR) recognition remain poorly understood at the molecular level. In particular, HLA-C molecules are among the least studied HLA class I allotypes, despite their important roles in viral infections, cancer, autoimmune diseases and transplantation.

Project 1. Exploring the impact of viral mutation on antigen structure. This project will investigate the molecular basis of immune recognition using a combination of structural biology, biochemistry, and computational approaches. The student will study how peptides are presented by HLA molecules and how these complexes are recognised by T cells. A particular focus may involve understanding the structural features of understudied HLA-C molecules and their interactions with disease-relevant peptides and TCRs. In addition, the project may explore the concept of peptide promiscuity, whereby conserved viral peptides can bind multiple HLA molecules and elicit broad T cell responses. For example, conserved SARS-CoV-2-derived epitopes have been shown to be presented across several HLA class I allomorphs, providing a unique opportunity to understand the structural basis of broad immune recognition. Investigating how a single peptide is accommodated by different HLA molecules may reveal important principles that govern antiviral immunity, immune escape, and vaccine design.

During the project, the student will gain hands-on experience in recombinant protein expression, protein purification, peptide-HLA-TCR complex assembly, protein crystallisation, and X-ray crystallography to determine three-dimensional structures of peptide-HLA and TCR-peptide-HLA complexes. Computational modelling and AI-based structure prediction tools (AlphaFold, TFold) will be used alongside experimental approaches to investigate molecular interactions and generate new hypotheses regarding immune recognition.

Methods: protein expression in bacterial cells, protein refold and purification, crystallisation, X-ray crystallography, protein stability and affinity measurements, AI-based structure prediction, Synchrotron radiation at the Australian Synchrotron.



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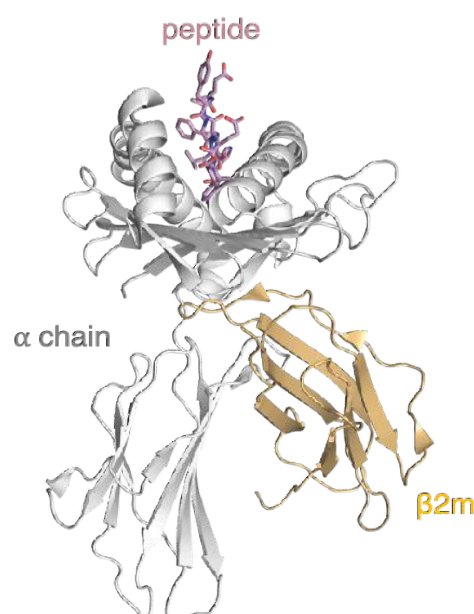
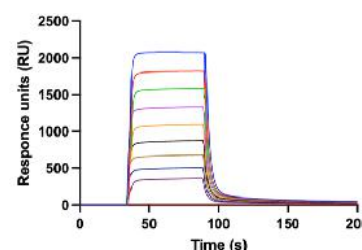
Website: [click here](#)

Number of projects: 1

Full-time or part-time: Full-time

Feb or July start: Feb only

Masters conversion: Yes



Prof. Stephanie Gras & Dr. Vivian Tran

LIMS



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More than 65 million people worldwide are living with Long COVID, making it one of the greatest emerging health challenges of our time. Many experience persistent fatigue, chest pain and reduced exercise capacity months or even years after infection, yet effective treatments remain elusive because the underlying biology is poorly understood. Women are twice as likely as men to develop these cardiovascular complications, but nobody knows why. It is an important unanswered question in Long COVID research and has the potential to transform how we understand and treat post-viral cardiovascular disease.

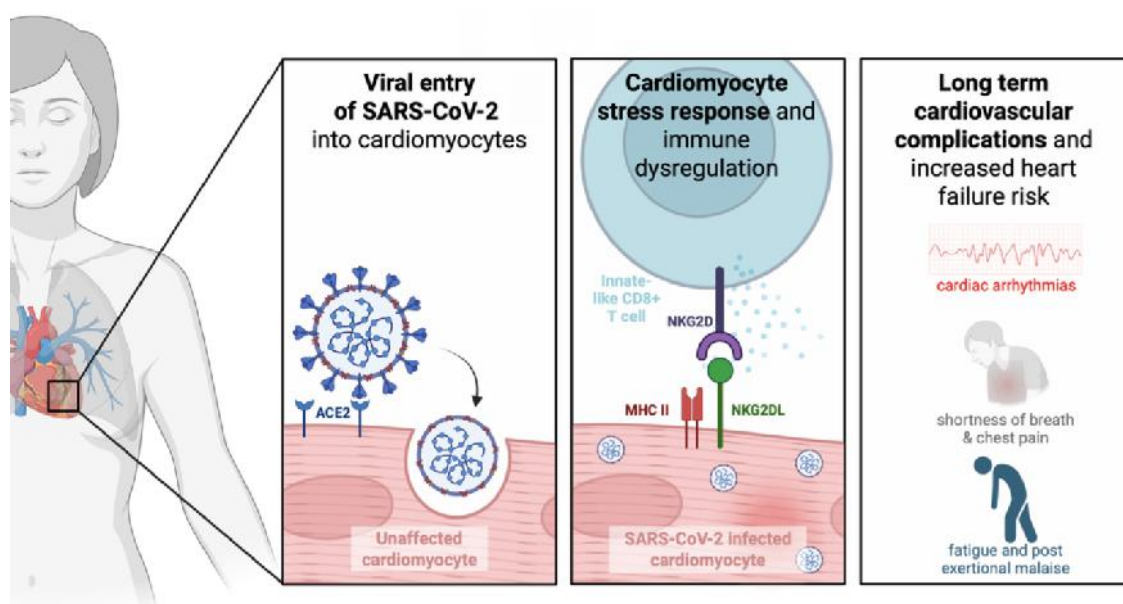
Project 1. Understanding why women are more susceptible to cardiovascular complications of Long COVID. This Honours project will combine a unique mouse model of Long COVID with clinically characterised patient samples to investigate how biological sex influences persistent cardiovascular injury following SARS-CoV-2 infection. The student will characterise heart and vascular pathology in Long COVID mice before determining whether circulating factors from patients can directly induce endothelial dysfunction. As part of the nationally collaborative NHMRC Centre for Research Excellence PAVING (<https://cre-paving.org/>), the student will contribute to research aimed at uncovering immune mechanisms driving cardiovascular complications of Long COVID and identify new therapeutic targets. You will receive hands-on training in cardiovascular phenotyping, immunofluorescence microscopy, cell culture and quantitative image analysis while contributing to research with the potential to improve the lives of millions of people living with Long COVID.

Number of projects: **1**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**



Dr. Carol Gubert

LIMS



Animal handling and
behaviour studies



Animal models of disease



Bioinformatics



Data analysis



Immunoassays



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Number of projects: 1

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

The Gubert Lab investigates how the gut microbiome shapes brain function, behaviour and disease. Our research explores how gut microbes, their metabolites, diet and the immune system communicate with the brain to influence neurological and psychiatric disorders, with a particular focus on Huntington's disease and schizophrenia. We aim to understand why these diseases affect not only the brain, but also the gut and other body systems, and how targeting the gut may improve brain health. Our research spans three interconnected themes. We investigate how microbiome-targeted interventions, including dietary strategies and microbial metabolites, can be developed as novel therapies for brain disorders. We study how alterations in the gut microbiome contribute to disease onset, progression and treatment response. Finally, we seek to uncover the biological mechanisms that connect the gut and brain, including neural, immune, metabolic and epigenetic pathways. Using multidisciplinary approaches that combine behavioural neuroscience, microbiome science, molecular biology and multi-omics technologies, our research bridges fundamental discovery with translational medicine. Students joining the Gubert Lab will work in a collaborative environment and gain experience in cutting-edge preclinical research, with opportunities to contribute to projects ranging from microbiome analysis and behavioural neuroscience to therapeutic development and gut-brain communication.



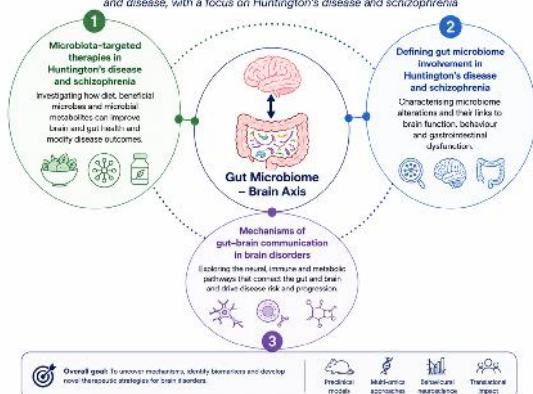
Project 1. Developing microbiome-targeted therapies for brain disorders. Can changing the gut microbiome improve brain health? This project investigates how dietary interventions, beneficial microbes and microbial metabolites influence behaviour, cognition and gut function in preclinical models of Huntington's disease, schizophrenia and related neurological disorders. The aim is to identify safe, microbiome-based therapies with potential for clinical translation.

Project 2. Understanding the role of the gut microbiome in brain disorders. This project explores how changes in the gut microbiome contribute to neurological and psychiatric disease. Students will investigate how microbial communities and their metabolites influence disease progression, cognition, gastrointestinal dysfunction and treatment response, helping to identify new biomarkers and therapeutic targets.

Project 3. Decoding gut-brain communication. How does the gut communicate with the brain? This project investigates the neural, immune, metabolic and epigenetic pathways that link the gut microbiome with brain function and behaviour. Students will explore the biological mechanisms underlying gut-brain communication and how they can be harnessed to improve brain health and resilience.

Core Research Focuses

Understanding how the gut microbiome influences brain health and disease, with a focus on Huntington's disease and schizophrenia



Prof. Begona Heras & Dr. Jason Paxman

LIMS



X-ray crystallography



Protease activity assays



Bacterial over-expression of protein



Molecular cloning



Biophysical characterisation of proteins (SAXS, CD, etc)



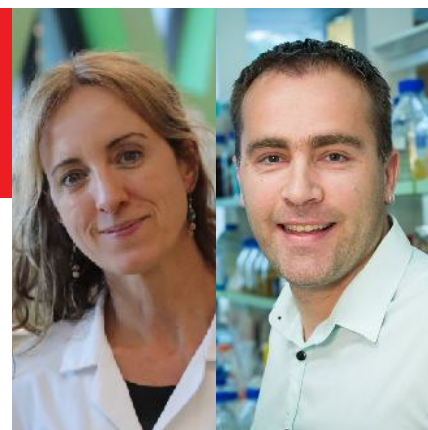
Protein biochemistry incl. immunoprecipitation



Microscopy - confocal, super resolution fluorescence



Cell culture - eukaryotes incl. primary & cell lines



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Number of projects: **2**

Full-time or part-time: **Either**

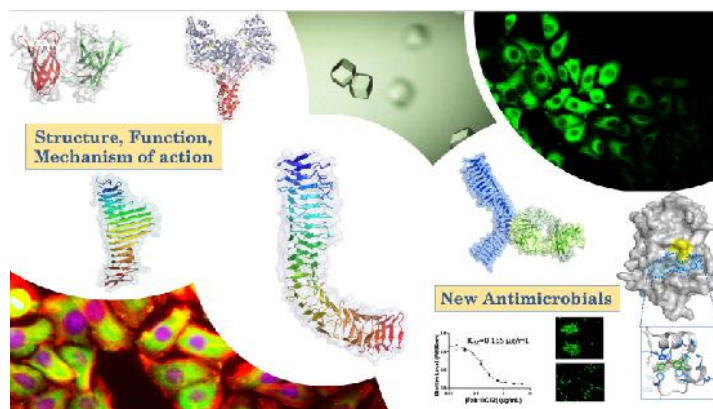
Feb or July start: **Both**

Masters conversion: **Yes**



Bacterial infections pose one of the most significant health threats of the 21st century. Antimicrobial-resistant superbugs are projected to cause over 10 million deaths annually by 2050, potentially becoming the leading cause of death in humans. With increasing bacterial resistance and a lack of new drugs entering the market, there is an urgent need to deepen our understanding of the mechanisms underlying bacterial pathogenesis to identify new therapeutic targets.

At the Heras/Paxman laboratory, we focus on investigating virulence mechanisms in Gram-negative bacteria to develop antibiotics that disarm rather than kill bacteria. Our research particularly targets critical high-priority pathogens listed by the World Health Organization (WHO), such as *Escherichia coli*, *Serratia*, *Salmonella*, and *Neisseria* species. Our ultimate goal is to develop "resistance-proof" antimicrobials.



Students working in the Heras/Paxman laboratory can engage in a variety of techniques applied to our key projects:

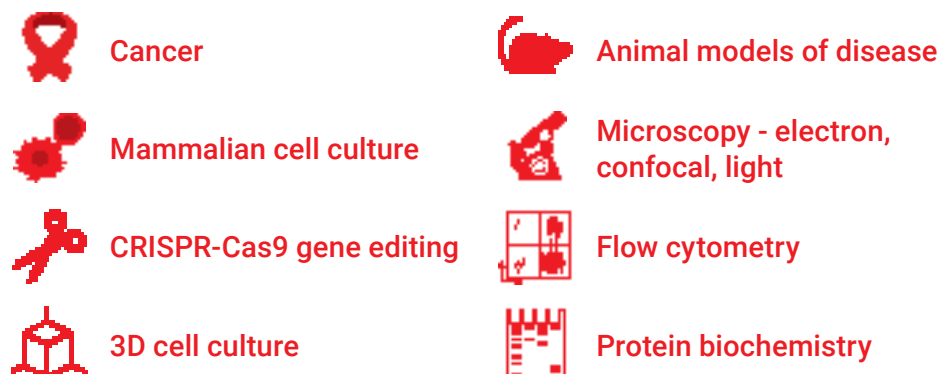
Project 1. Investigation of Bacterial Autotransporters. Autotransporters are the largest group of cell-surface proteins responsible for host colonization and biofilm formation. This project combines recombinant protein expression and purification, structural biology, molecular microbiology, and biophysics techniques such as Surface Plasmon Resonance (SPR), Circular Dichroism (CD), and Analytical Ultracentrifugation (AUC). The aim is to dissect the structure and function of these crucial bacterial proteins and develop molecules that block their function, thereby inhibiting biofilm formation and acting as new pathogenesis-blocking agents.

Project 2. Elucidating Mechanisms of Bacterial Resistance Development. This project focuses on understanding how bacteria develop resistance to antibiotics. Using X-ray crystallography in combination with biochemistry, molecular microbiology, and computational studies, we aim to uncover the mechanisms of resistance. The findings will be used to develop small, drug-like inhibitors that block these resistance processes, providing a new class of antibacterials.

With these projects, we aim to advance the field of antimicrobial research by identifying novel targets and developing innovative strategies to combat the growing threat of bacterial resistance. Our multidisciplinary approach will result in effective and sustainable treatments for bacterial infections.

Prof. Patrick Humbert

LIMS



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Number of projects: **1**

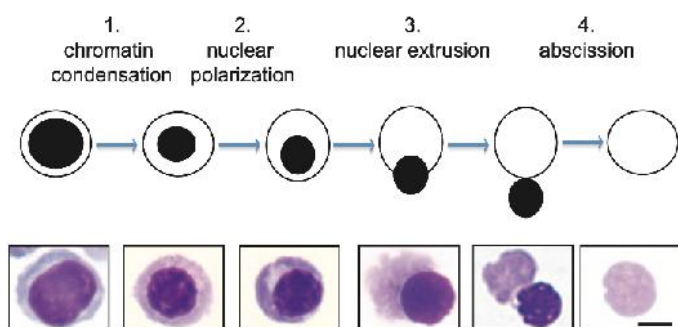
Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

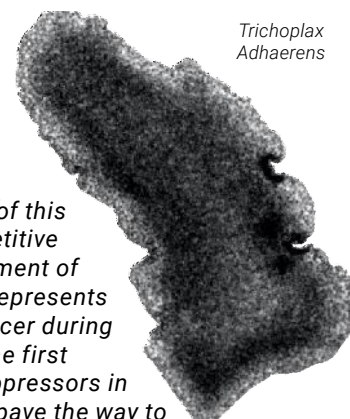
We are interested in the origins of cancer, both how cancer begins in humans but also when cancer first arose in multicellular organisms during evolution. One of the very first changes that drives cancer is a change in the organisation of cells in tissue, these are regulated by genes known as cell polarity genes and our lab focusses on how tissue organisation is regulated by these genes during tissue development, regeneration and at the outset of cancer. We examine this using 3D mini human organ cultures and by studying one of the simplest and most ancient animals on Earth, *Trichoplax Adhaerens*. These studies provide fundamental insights into the origins of cancer that pave the way to how we understand and prevent human cancer. A second area in the lab focusses on how our body generates red blood cells with the long-term aim to produce artificial bespoke blood for transplantation.

Project 1. How did the red blood cell lose its nucleus? Our lab has identified a number of new regulators of enucleation, the process by which red blood cells lose their nuclei. In this project you will identify how these new regulators control enucleation. This will help develop strategies to enhance the production of red blood cells in vitro for patient transplantation purposes.



Erythroid Enucleation

*Project 2. How did cancer begin? The evolution of the first animal from a single cell organism to one consisting of multiple cells required new mechanisms that allowed cooperation between cells. Breakdown of this cooperation by over-competitive 'cheating' cells to the detriment of the whole animal's health represents the first appearance of cancer during evolution. You will study the first oncogenes and tumour suppressors in *Trichoplax Adhaerens* and pave the way to how we understand human cancer.*



Trichoplax Adhaerens

*Project 3. How does gravity effect regeneration and cancer? Altered gravitational conditions (weightlessness) cause detrimental effects on stem cell function and wound healing. The impact of altered gravity on biology has become a critical consideration for the long-term stay of humans and animals in space as well as for space tissue engineering. You will work as part of an international collaboration with the German Aerospace Center (DLR), to test for the first time how altered gravity may affect the development of tissue organisation and regenerative programs in one of the simplest and most ancient multicellular animals on Earth, *Trichoplax Adhaerens*. Due to its size, regenerative properties and its reported ability to sense gravity, *Trichoplax* provides an ideal model system to decipher the effects of altered gravity on animal architecture and regeneration. We will initially use ground-based facilities to simulate weightlessness, then examine impact of real microgravity conditions (as well as Moon and Mars gravity) on tissue organisation and regeneration using parabolic flights. This will provide insights into molecular mechanisms impacting regeneration and cancer in space that will inform human health for long-term space flights.*

Dr. Ibrahim Javed

LIMS



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

 Immunoassays

 Protein biochemistry

 3D cell culture

 Confocal & super resolution fluorescence microscopy

 Proteomics

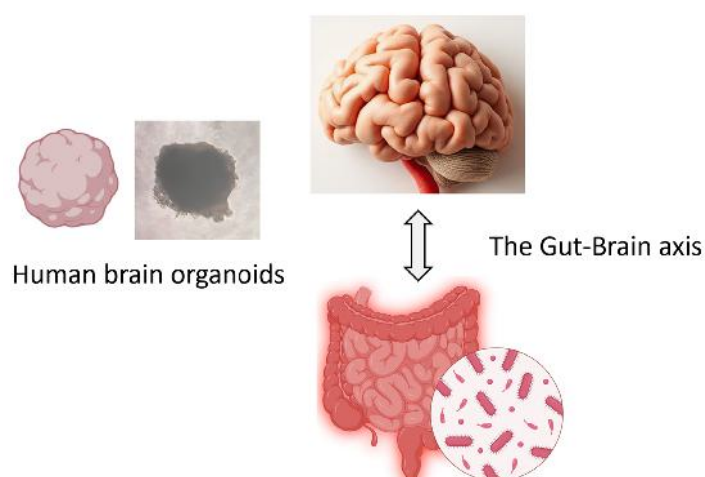
 Microscopy - Electron, light

Gut bacteria are now emerging as drivers of various human diseases and ageing. Our team is focused on understanding the impact of infectious gut microbes on brain ageing and brain diseases such as dementia. We have discovered that gut microbes use sticky proteins to form biofilms that adhere to the gut's inner lining. These biofilm-forming sticky proteins can leak out of the gut and reach the brain. Once in the brain, they can trigger or accelerate the underlying biochemistry of ageing and dementia. While discovering this, we ended up with more questions than answers: (1) How can these biofilm proteins access the brain from the gut? (2) How do they interact with human biochemistry of ageing and dementia and trigger brain diseases? (3) Can we model the gut-brain axis with relevance to the timescale of human ageing and complexity? and (4) Can we utilize the probiotic microbes in the gut to work alongside the medicine and provide therapeutic advantage?

To investigate these questions, students will be working on the following two projects:

Project 1. Develop a Gut-Brain Axis model to co-culture gut bacteria with human brain organoids. One of the major barriers in studying the role of the gut-brain axis in ageing and brain diseases is the lack of human-relevant model systems. In this project, you will use cutting-edge stem-cell technology to develop human brain organoids and culture them together with bacteria that are commonly found in the human gut. In this project, you will expose the organoids to gut bacteria in a controlled environment and study the biological impact on the brain organoids. In specific, you will be developing a human-relevant but in-vitro model system that can be used to study the impact of infectious and probiotic gut microbes on brain ageing and Dementia.

Project 2. How are proteins trafficked across the gut-brain axis in health and disease? Gut-Brain axis communication is bidirectional communication. In this project, you will study the proteins secreted by gut microbes and their hitchhiking across the gut-brain axis. We are specifically looking into the biofilm-forming sticky proteins which are secreted by gut bacteria. These proteins have the potential to access the brain and you will study the role of the enteric nervous system in the trafficking of these proteins from the gut to the brain.



A/Prof. Travis Johnson

LIMS



Drosophila melanogaster models



Protein biochemistry (SDS-PAGE, western blotting)



Confocal & super resolution fluorescence microscopy



Therapeutic screening



Animal models of disease



Metabolomics

The Johnson Laboratory uses the fruit fly (*Drosophila melanogaster*) to understand the genetic and molecular basis of rare inherited diseases and to develop new treatment strategies. Our research focuses particularly on inherited metabolic diseases, including severe childhood disorders that can lead to progressive neurological decline and dementia. Many of these conditions have few, if any, effective treatments, creating an urgent need for new therapeutic approaches. We investigate how precisely tailored diets (precision nutrition / nutrigenomics) can improve health in genetic disease models and perform drug screens to identify clinically approved compounds that could be rapidly repurposed for patients. This combination of genetics, nutrition and pharmacology allows us to move from understanding disease mechanisms towards discovering practical treatments. Students joining the laboratory gain experience in: *Drosophila* genetics, CRISPR/Cas9 genome engineering, advanced microscopy, molecular and cell biology, protein biochemistry, and genomic and other 'omics technologies. Projects also involve quantitative analysis of survival, behaviour, development and tissue morphology, providing opportunities to develop strong experimental design, data analysis and scientific communication skills.

Project 1. Using Precision Nutrition to Treat Rare Metabolic Diseases. Many inherited metabolic diseases result from an inability to process specific nutrients. This project will investigate whether carefully designed diets can improve health in a *Drosophila* model of a rare metabolic disorder. The project will involve fly genetics, tissue dissection and microscopy, and the measurement of disease traits including survival, developmental timing and behaviour across a range of chemically defined diets. Students will gain experience in genetics, experimental design, quantitative phenotyping and nutritional biology.



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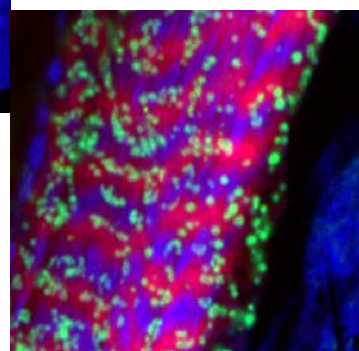
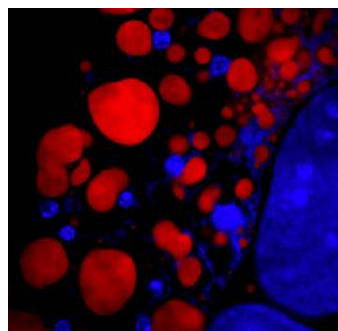
Website: [click here](#)

Number of projects: **1 Feb, 1 Jul**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**



Project 2. Screening Clinically Approved Drugs for Rare Disease Therapies. Developing entirely new medicines is slow and expensive. An alternative strategy is to identify existing approved drugs that can be repurposed for rare diseases. In this project, students will screen a library of clinically approved compounds using a *Drosophila* model of inherited metabolic disease to identify drugs that improve survival or reduce disease severity. The project involves fly genetics, high-throughput experimental screening, quantitative data analysis, and follow-up studies to investigate how promising compounds exert their beneficial effects.

Project 3. Determining Whether Genetic Variants Cause Disease. Modern DNA sequencing identifies thousands of genetic variants, but determining which variants are truly disease-causing remains a major challenge. In this project, patient-derived genetic variants will be introduced into *Drosophila* to assess their effects on gene function and development. Students will use fly genetics and quantitative phenotypic analysis to determine whether individual variants disrupt normal biological processes, helping improve the diagnosis of rare genetic disorders.

Dr. Ella Johnston LIMS



Flow cytometry



Data analysis



Microscopy - Electron, light



Cell culture - eukaryotes



Extracellular vesicle
isolation, characterisation,
and quantification



Western immunoblot



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Number of projects: 1

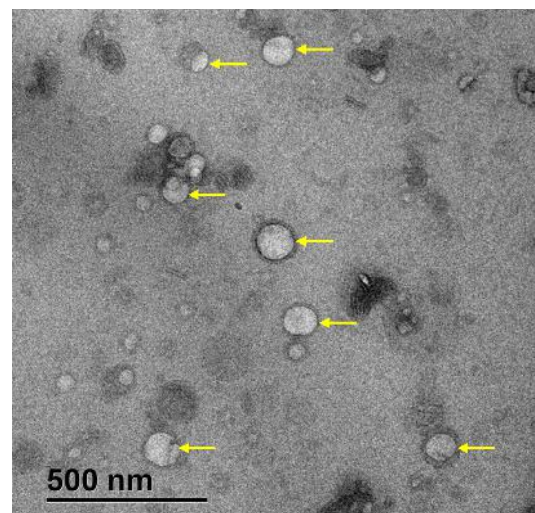
Full-time or part-time: **Full-time**

Feb or July start: **Both**

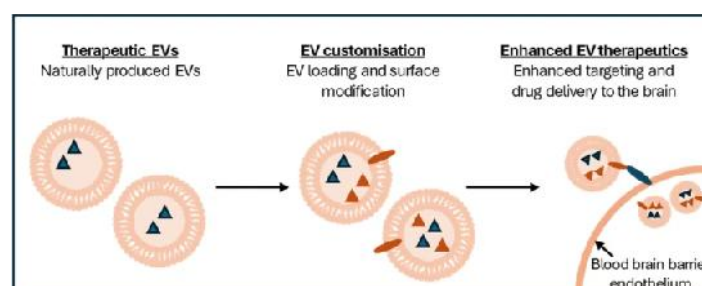
Masters conversion: **Yes**

Extracellular vesicles (EVs) are tiny nanoparticles, usually around 100 nanometres in size, that contain an outer lipid bilayer. EVs are rich in functional biomolecules, like proteins, DNA, and RNA. EVs are produced by all forms of life, from bacteria to human cells. They have many functional roles, notably their ability to deliver messages and molecules to recipient cells whilst avoiding detection by the immune system. EVs can also be customised. Their surface can be modified to enhance targeting, and they can be loaded with drugs to treat specific diseases. Due to their ability to package functional molecules and to target and deliver their cargo to recipient cells, EVs have the potential to be used as therapeutic drug delivery vehicles.

Industry Collaboration – VivaZome Therapeutics Pty Ltd: My research focuses on the development of new methods to analyse EVs, and the standardisation of these methods. Many methods are currently used to analyse EVs, including nanoparticle tracking analysis, nanoparticle flow cytometry, and Western immunoblot, but there are no standards in place to apply these methods in a therapeutic setting. For this research, I am working with VivaZome Therapeutics, a Melbourne-based company in EV therapeutics, on the standardisation of analytical methods for manufactured EVs. In addition to the standardisation of methods for analysing EVs, I am also developing methods for loading EVs with drugs in collaboration with VivaZome Therapeutics. The objective of this project is to develop novel EV therapies to treat neuroinflammatory conditions, including dementia and post-traumatic epilepsy.



In addition to working with industry on several EV projects, my research also focuses on developing “reporter” EVs that can be used to help the standardisation of EV analytics. This project involves molecular cloning methods to make customised EVs with unique biochemical signatures that can be used in various applications, including nanoparticle tracking analysis (NTA), flow cytometry, microscopy, in vitro cell uptake assays, and in vivo in animal models to monitor EV distribution using different administration methods. We are also interested in further understanding the storage conditions that help to maintain EV integrity, and different buffers and molecules that could help to stabilise EVs.



Prof. Erinna Lee

LIMS



Cell culture - prokaryotes



Bioinformatics



Protein biochemistry (SDS-PAGE, western blotting)



Data analysis



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Number of projects: 1

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

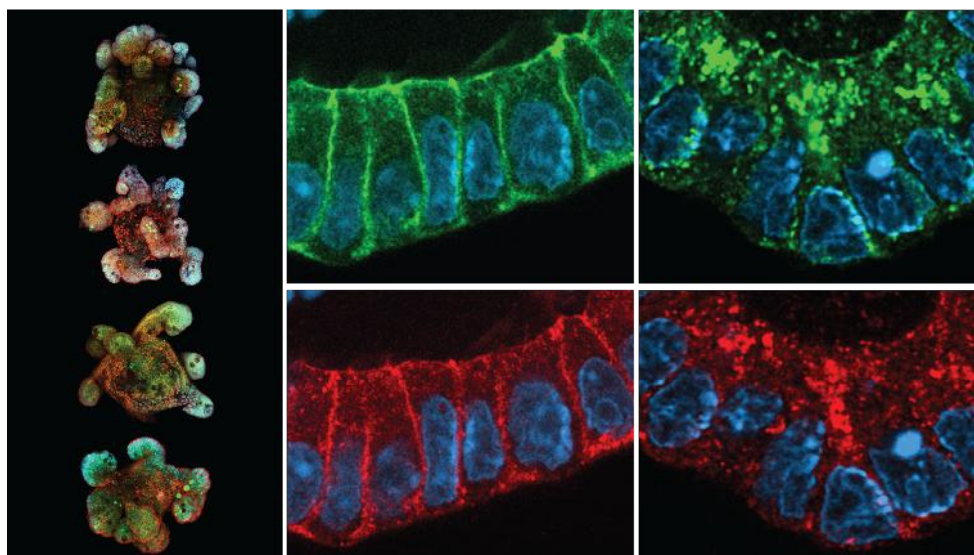
Masters conversion: **Yes**

The Gut Biology and Disease Signalling Lab explores how the gut influences health throughout the body. We investigate the processes that keep the gut lining healthy, allow damaged cells to be repaired or removed, and maintain a balanced relationship with gut microbes. When these safeguards break down, the consequences can extend beyond the intestine - contributing to chronic inflammation, inflammatory bowel disease, cancer, and changes in brain health. By combining laboratory models of the gut with genetics, molecular biology and large-scale analysis of genes and proteins, we aim to uncover the underlying causes of disease rather than simply treat its symptoms. A particular focus is how ageing and menopause affect communication between the gut, immune system and brain, and whether targeting the gut could help reduce longer-term risks such as cognitive decline and cardiovascular disease.

Project 1. Can gut bacteria influence health during menopause?

Co-supervisors: Dr. Carolina Gubert, Assoc. Prof. Anthony Vinh, Prof. Samuel Forster (Hudson Institute).

Menopause causes a major fall in oestrogen, but hormone levels may also be influenced by the trillions of microorganisms living in our gut. Some gut bacteria contain genes that allow them to reactivate oestrogens and other steroid hormones that the body has prepared for removal. This collection of hormone-modifying bacterial genes is known as the estrobolome. In this project, you will investigate whether the estrobolome changes during menopause and whether these changes could contribute to broader health risks. You will use computer-based genome analysis to search a unique collection of human gut bacteria for genes predicted to modify steroid hormones. Promising human bacterial isolates will then be grown in the laboratory and tested to determine whether they can break down hormone-related compounds. You will also examine samples from established laboratory models that mimic different aspects of menopause, investigating which microbial genes are present or actively being used. This project offers hands-on experience across microbiology, genomics and hormone biology. It is ideal for a student interested in women's health, the gut microbiome, ageing, or the rapidly developing field of personalised medicine.



Dr. Kazuhide Shaun Okuda

LIMS



CRISPR-Cas9 gene editing of cells



Animal models of disease



Gene expression analyses



Confocal & super resolution fluorescence microscopy



Zebrafish models



mRNA therapeutics



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Number of projects: 1

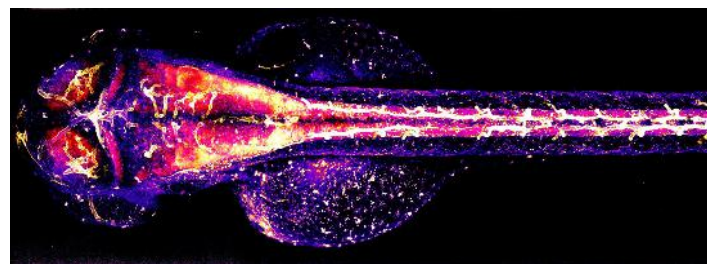
Full-time or part-time: **Full-time**

Feb or July start: **Both**

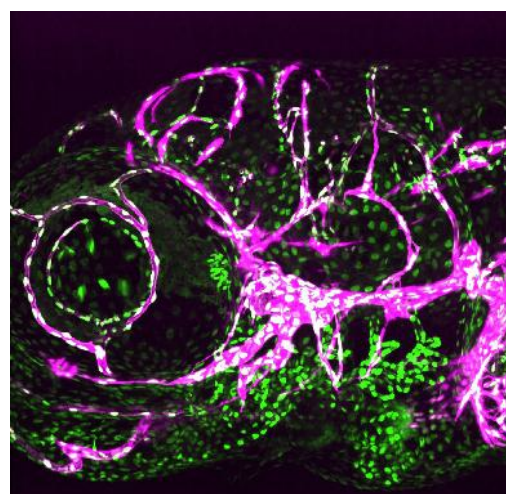
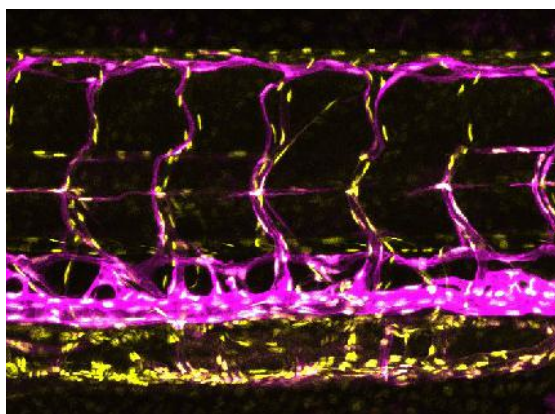
Masters conversion: **Yes**

Blood and lymphatic vessels play important physiological functions in our body and are dysregulated in various human diseases. Excessive blood or lymphatic vessel growth leads to vascular anomaly including lymphatic malformations and increases the risk of cancer metastasis by providing pathways for cancer cells to disseminate. Inversely, lack of lymphatic vessel growth/ regeneration results in primary or secondary lymphoedema, a major burden for post- cancer surgical/radiation therapy patients. Our group uses the optically transparent zebrafish model to identify vascular modulatory therapeutics that could be used to treat these diseases. We also characterize dynamic signaling mechanisms that drive vascular maintenance, regeneration and pathologies using various biosensor zebrafish transgenics and zebrafish disease models to decipher targetable therapeutic targets for these diseases.

Project 1. Identify pro-lymphangiogenic therapeutics. Lymphoedema is a disease associated with excessive tissue swelling. When left untreated lymphoedema symptoms can worsen, leading to decreased mobility, chronic pain and increased risk of potentially lethal infection. Primary lymphoedema (caused by genetic mutation) is currently incurable, and treatment options available only alleviate the symptoms. Using cutting-edge methodologies in zebrafish, we seek to understand the mechanisms that drive/ inhibit lymphatic regeneration to reveal therapeutic targets for stimulating lymphatic regeneration. We are also using various in vivo (zebrafish) screening approaches to identify pro-lymphangiogenic therapies that will be tested on our zebrafish lymphoedema models.



Project 2. Understanding dynamic signaling activity in blood and lymphatic vessels. The optical transparency of zebrafish embryos/larvae allows live-imaging of developing/ functional/regenerative/ pathological blood and lymphatic vessels at unprecedented resolution. We have developed zebrafish biosensor transgenic lines that enable real-time visualization of important signaling activities in blood and/ or lymphatic endothelial cells such as ribosome biogenesis and Erk signaling. We are developing new biosensor zebrafish transgenics that enable visualization/ quantification of various signalling activities in endothelial cells. We will use these biosensor transgenics to elucidate dynamic mechanisms that drive vascular development, maintenance, and regeneration.



Dr. Kha Phan

LIMS



Cell culture - eukaryotes



Animal models of disease



Histology (incl. immunohistochemistry)



Flow cytometry & immunoassays



Protein biochemistry (SDS-PAGE, western blotting)



Infection & immunity



PCR assays



CRISPR-Cas9 gene editing of cells



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Number of projects: **1 Feb, 1 Jul**

Full-time or part-time: **Full-time**

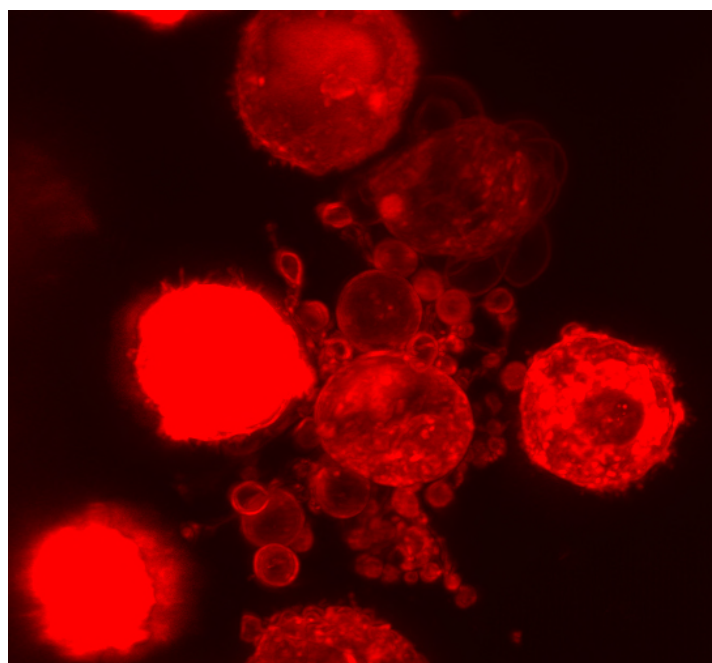
Feb or July start: **Both**

Masters conversion: **Yes**

Billions of cells die every day in our bodies as part of normal development, homeostasis and diseases. Dying cells often actively attract and engage scavenging phagocytes to promote the clearance of their cell corpses (a process known as 'efferocytosis'). Defective efferocytosis have been linked linked to chronic inflammation and autoimmunity due to subsequent cell lysis as well as exposure of autoantigens. Notably, upon efferocytosis, cell corpses elicit various cellular responses in the engulfing phagocytes depending on packaged cargoes, including immune modulation, cell survival, division and differentiation as well as pathogenesis. For example, we have recently shown that SARS-CoV-2 infection-derived ApoBDs can facilitate viral entry, independently of the canonical ACE-2 receptor (Phan et al. 2026, Nature Communications). into macrophages, triggering exacerbated

inflammation that is consistent to severe COVID-19. Despite the pivotal (patho) physiological roles and promising therapeutic potential, the molecular mechanisms underlying apoptotic cell clearance by efferocytosis remains largely underexplored.

In this project, you will identify novel regulators for this efferocytosis using a genome-wide CRISPR/Cas9 screening. You will also functionally characterise the identified leads and elucidate novel mechanism(s). This project will not only provide further insights into efferocytosis but also open a new avenue for therapeutic designs for infection and chronic inflammatory diseases.



Prof. Ivan Poon

LIMS



Infection & immunity



Cell culture - eukaryotes, incl. primary & cell lines



Flow cytometry



Animal handling



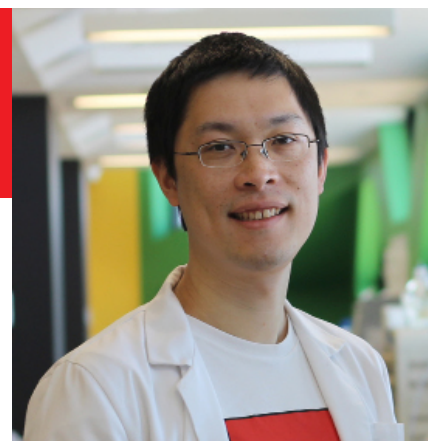
Microscopy - electron, confocal, light



CRISPR-Cas9 gene editing of cells



Cell transfection



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Number of projects: **1**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**

Billions of cells die daily as part of normal turnover in various organs. It is vital that dying cells are rapidly removed as their accumulation has been linked to inflammation, autoimmunity, cancer and infection. To aid efficient removal of dead cells, dying cells often disassemble into smaller fragments for neighbouring cells to engulf. Certain cellular components can be packaged selectively into these fragments to regulate tissue repair and immunity. We aim to understand the machinery that controls how dying cells can disassemble into smaller pieces, the importance of cell disassembly in disease settings (e.g. influenza A infection), and identify new drugs to control this process.

Project 1. Develop zebrafish models to visualise the cell clearance and disassembly. Apoptosis (programmed cell death) occurs in all tissues as part of development homeostasis, and pathogenic processes including infection and cardiovascular disorders. Apoptotic cells often disassemble into smaller membrane-bound extracellular vesicles called apoptotic bodies (ApoBDs). We have demonstrated that the formation of ApoBDs is a highly regulated process in T lymphocytes and monocytes. We discovered a new type of membrane protrusion (coined "apoptopodia") that facilitates the separation of membrane blebs during apoptosis to generate individual ApoBDs. In this project, you will develop new animal models to visualise this process in vivo. In particular, you will establish new transgenic zebrafish lines to monitor how dying cells disassemble and their interaction with neighbouring cells.

Project 2. Role of dying cell disassembly in viral trafficking. Extracellular vesicles including apoptotic bodies (ApoBDs) have been implicated to regulate physiological and pathological processes via the molecules they carry inside or exposed on their surface. The importance of generating ApoBDs during apoptosis in pathophysiological settings is poorly understood. In particular, we study the role of apoptotic cell disassembly in the context of viral infection. During certain viral infection, infected cells can undergo apoptosis to shutdown cellular machinery as a defence mechanism to limit viral replication. Notably, we

discovered recently that phagocytic removal of ApoBDs generated from influenza A virus or SARS-CoV-2 infected cells may also facilitate the spread of infection, and the phagocyte could become infected following the engulfment of ApoBDs containing viral particles. Utilising influenza A virus infection as a model, this project will explore the molecular mechanisms underpinning this novel route of viral entry into host cells. This include identifying the engulfment receptors involved in ApoBD uptake as well as elucidating the downstream mechanisms of viral entry.

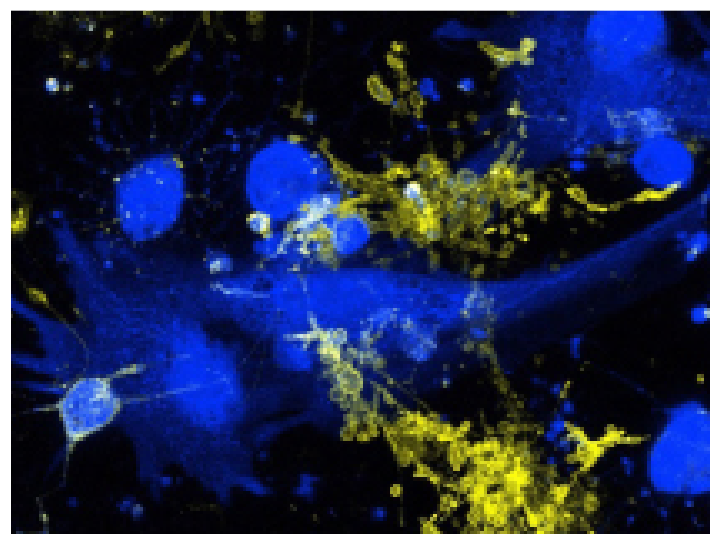
Further reading:

Apoptotic cell clearance and disassembly:

- <https://www.nature.com/articles/nri3607>
- <https://www.nature.com/articles/ncomms8439>

ApoBDs in viral infection:

- <https://www.nature.com/articles/s42003-020-0955-8>
- <https://www.biorxiv.org/content/10.1101/2023.11.03.565419v1.abstract>



Dr. Lakshmi Wijeyewickrema

LIMS



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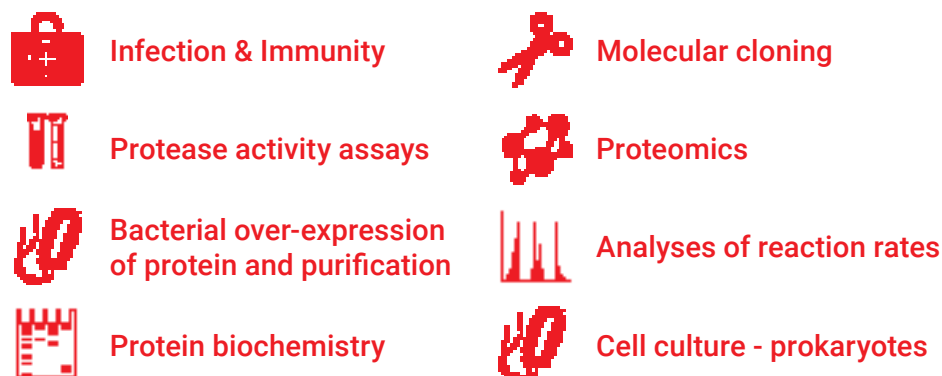
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Number of projects: 2

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

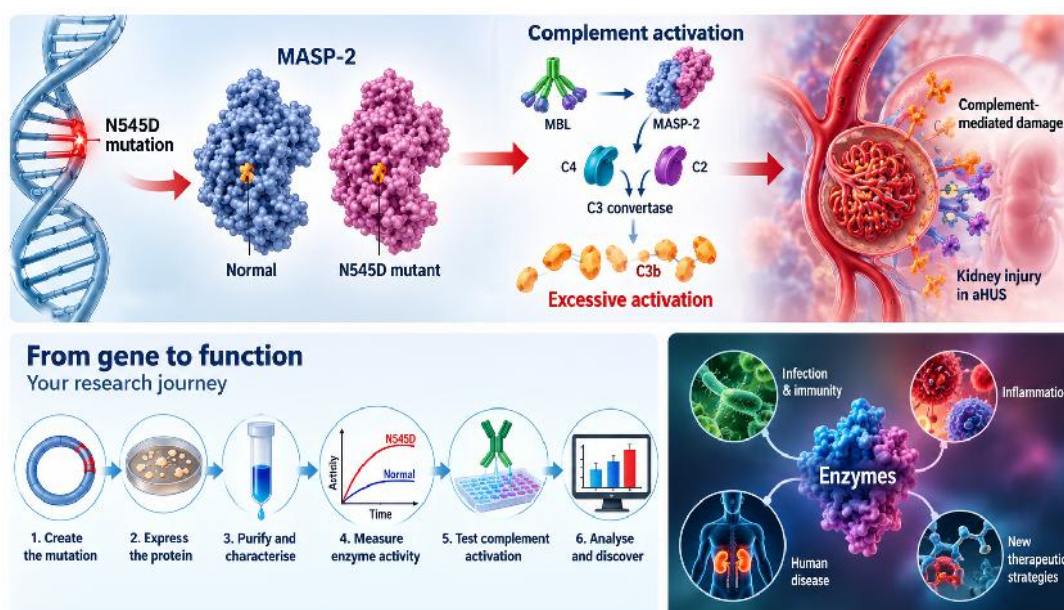


Our lab is interested in understanding how enzymes—tiny molecular machines in our cells—control the immune system, and what happens when this control goes wrong. Enzymes help protect us from infection and regulate inflammation, but changes in their activity can also contribute to disease. We use molecular biology, protein biochemistry and immune-based assays to investigate these processes and uncover how disease develops at the molecular level. Ultimately, our research aims to identify new ways of understanding, preventing and treating inflammatory and immune-related diseases.

Our Honours projects are highly hands-on and are ideal for students who are curious about how molecules cause disease and would like to experience what it is really like to work in biomedical research.

Project 1. When the immune system turns against us: How can a single mutation cause disease? Atypical Haemolytic Uremic Syndrome (aHUS) is a rare but serious disease in which part of our immune system, called the complement system, becomes overactive and damages the body's own cells, particularly in the kidneys. This project will investigate a genetic change in an immune enzyme called MASP-2 that has been identified in patients with aHUS. We want to discover whether this small change alters how the enzyme works and causes excessive activation of the immune system. You will create and study the altered protein and compare it with the normal version, gaining hands-on experience in molecular cloning, protein production and purification, enzyme assays, immunology and data analysis. This project is particularly suited to students interested in immunology, molecular biology, biochemistry, human disease or biotechnology, and to anyone considering a future career in biomedical research.

The big question: How can one tiny change in a protein have such a big effect on human health?





Chemistry

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A/Prof. Peter Barnard

LIMS



Chemical synthesis - organic & inorganic



Nuclear magnetic resonance



Light microscopy



Mass spectrometry



X-ray crystallography

The main focus of the Barnard research lab is the synthesis and development of organic ligands and coordination complexes for medicinal and biological imaging applications. Organic and inorganic synthetic chemistry in combination with a wide range of analytical techniques are used for the generation and characterisation of new compounds.

Project 1. Synthesis and Studies of Luminescent Gold, Ruthenium, Iridium and Lanthanide Complexes. We are interested in the synthesis of new luminescent coordination compounds of gold, ruthenium, iridium and the lanthanide metals. Current efforts are being directed at tuning the luminescent properties of the d-block complexes and the synthesis of d-f heterobimetallic arrays for sensor applications.

Project 2. Radiopharmaceutical Imaging Agents for Cancer Diagnosis. This is a collaborative project with the Australian Nuclear Science and Technology Organisation (ANSTO) involving the development of new radiopharmaceutical imaging agents for disease diagnosis. A range of ligand systems are being used in combination with metallic radionuclides such as Tc-99m, Cu-64 and Zr-89. Technetium-99m is the most widely used radionuclide in medical imaging and a wide array of 99mTc labelled compounds are currently used to image different organs and a number of diseases. As all isotopes of Tc are radioactive, we develop new chemistry using Re and we have prepared a series of Re(I) complexes of NHC ligands. Recently we have also labelled these NHC ligands with 99mTc. See: *Chemical Communications* 53 (15), 2311-2314, 2017 and *Inorganic chemistry* 53 (20), 10862-10873, 2014.

Project 3. Synthesis and coordination chemistry of amide containing molecules. The amide or peptide functional group is critical to life as it provide the linkage between adjacent amino acid residues in proteins. Amides also display interesting coordination chemistry. We are working on the synthesis of new ligands incorporating amide groups. An example of a triamidetriamine macrobicyclic cage ligand designed to form highly stable metal complexes is shown. See: *Inorganic Chemistry* 53 (1), 468-477, 2014.

Project 4. Silver and gold-based antibacterial compounds. We are interested in the development of gold and silver-based complexes of N-heterocyclic carbene ligands as new antibacterial agents. Some of the compounds prepared show excellent activity against multi-drug resistant bacterial strains and importantly no antibacterial resistance developed against these metal containing complexes, whilst resistance was developed against the widely used broad-spectrum antibiotic ciprofloxacin in the same bacterial strains. This project will aim to prepare targeted gold and silver metallodrugs and potential new antibiotics.



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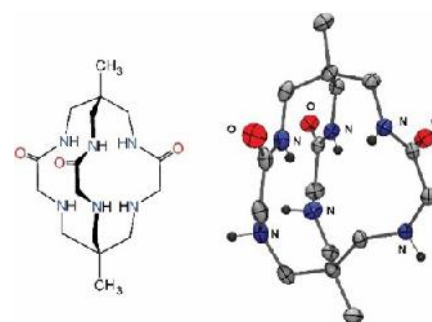
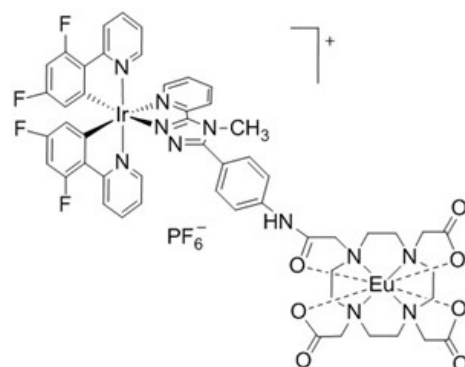
Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**



Prof. Jason Dutton

LIMS



Chemical synthesis -
organic & inorganic



Mass spectrometry



Nuclear magnetic
resonance



X-ray crystallography



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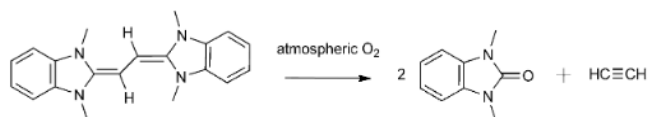
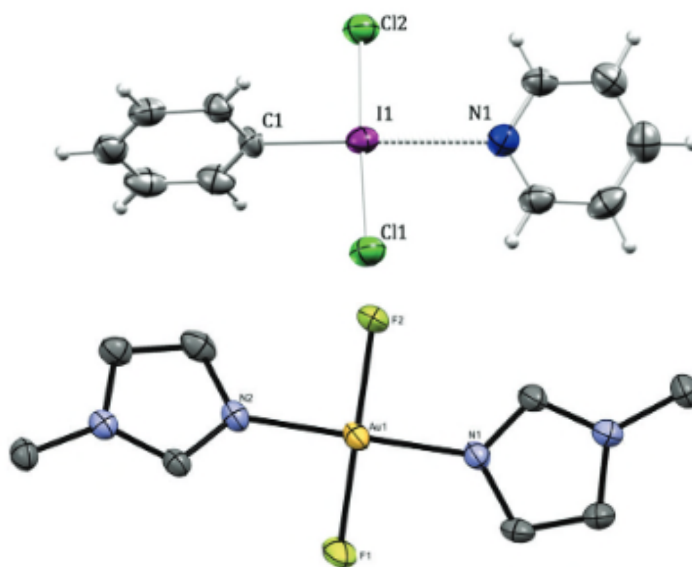
Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

The Dutton lab invents new chemistry across both inorganic and organic chemistry, covering the breadth of the periodic table. We do this with a general tact of making molecules uncomfortable by providing them with either too many or too few electrons, which normally leads to a reactive situation and the uncovering of interesting new classes of molecules or chemical transformations. We have for example in the past few years discovered the weakest known C=C double bond by giving a molecule too many electrons that is the only alkene known to react with atmospheric O₂, and the most positive metal-fluorine bond by giving a molecule too few electrons. Often the transformations we discover are found simply by serendipity.



Specific projects that are on offer next year include in organic chemistry the generation of halogenation reagents (ie brominating reagents) that are stronger and faster than Br₂ itself, yet much easier and safer to handle. For the inorganically inclined, we are looking at methods of making metal-fluorine bonds more reactive for the purpose of direct transformations of cheap C-H bonds into value added C-F bonds. A student joining the Dutton lab can expect to learn a variety of synthetic chemistry techniques, a whole lot of NMR and mass spec and some X-ray crystallography. Interested students can also potentially learn how to analyze their systems with theoretical chemistry techniques. Most of all students in the Dutton lab learn that chance favours the prepared mind!

Prof. Conor Hogan

LIMS



Cyclic voltammetry



Electrochemiluminescence



Spectroelectrochemistry



Electrochemical impedance spectroscopy



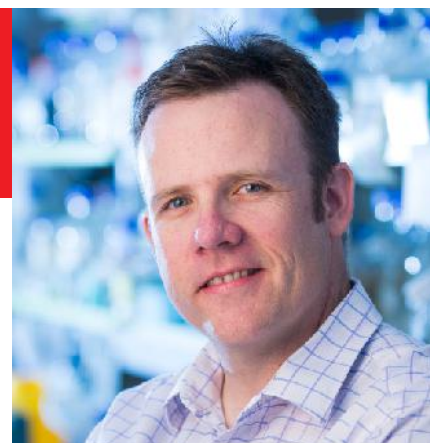
Materials inkjet printing



Time-correlated single photon counting



Photoluminescence spectroscopy



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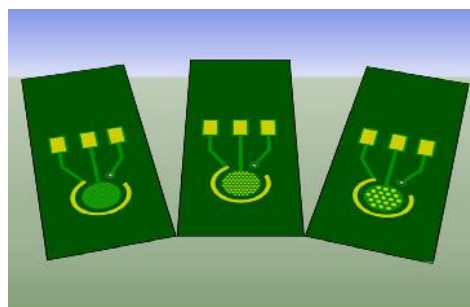
Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**



Our group conducts fundamental research to expand the bounds of analytical science, with a focus on **electrochemistry and electrochemiluminescence (ECL)**; and we translate these findings using a multidisciplinary approach into low-cost, miniaturised sensors and devices for health, the environment, and food and beverages.

We are leaders in mobile-phone based sensing, including developing and using Android voltammetry to measure analytes of interest to industry. We are producing our own sensors using materials printing, and laser cutting and engraving.

We also pioneer new approaches to detection science using ECL, which combines electrochemistry and photochemistry. Our work includes developing and characterising new ECL materials to enable sensing in whole blood, and of multiple analytes at the same time; optimising conditions so that we can detect exquisitely low analyte concentrations within and outside of laboratory settings; and exploring a new approach to detecting analytes through an emerging technique known as bipolar ECL.

Building on our fundamental science, we seek to develop novel sensing technologies and miniaturised instruments for use at point-of-need. The development of simple, inexpensive (yet quantitative) sensors has the potential make (bio) chemical analysis widely available. Such technology would be transformational for health, agriculture, industry and the environment.



Prof. Yuning Hong

LIMS



Chemical synthesis - organic



Flow cytometry



Cell culture - eukaryotes incl. primary & cell lines



Confocal & super resolution fluorescence microscopy



Protein biochemistry (SDS-PAGE, western blotting)



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Number of projects: **1 Feb, 1 Jul**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

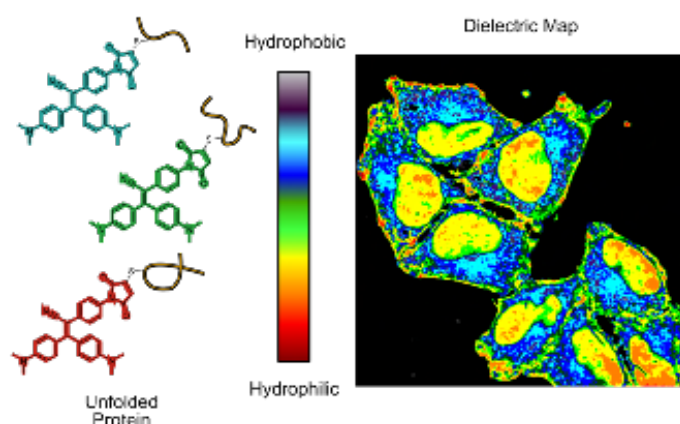
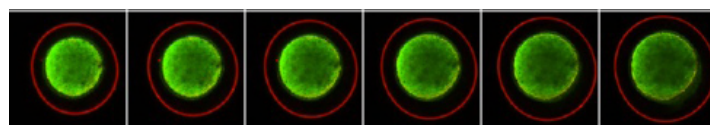
Our Group develops novel chemical compounds, usually with interesting fluorescent behaviors, to study how proteins changes in live cells under drug treatment and in cell models of Parkinson's, Huntington's and Motor Neuron Diseases. The molecules we create can selectively turn on their fluorescence or change their colors in response to subtle changes such as protein misfolding, modifications and degradation. Some of them can also allow us to enrich proteins that undergo abnormal changes from the entire proteome and serve as biomarkers for disease diagnosis and potentially targets for disease treatment.

If you love both chemistry and biology and couldn't decide which discipline you want to go, come and join us. In our group, you can design and synthesize your own fluorescent dyes and use them in live cells and even in zebrafish models to reveal hidden molecular level mechanisms related to protein quality control, stress response and cell survival.

Project 1. Develop novel autophagy sensors (two projects with different focuses). Autophagy ("self-eating") is a cellular housekeeping process in which unwanted components are identified, degraded, and recycled. As autophagy is a multi-step, dynamic process, current tools based on transfecting fluorescent proteins have many disadvantages. In this project, chemical probes that can selectively target autophagy marker proteins will be developed (synthesis). Their interaction with model marker proteins will be investigated (potentially protein expression, purification, and biophysics). Next, we will use these probes to visualize and quantify different stages of autophagy (cell culture, confocal microscopy and flow cytometry). Further to that will be the applications in neurodegenerative disease models in collaboration with Dr Sarah Annesley and Prof Paul Fisher in MAPP, and in zebrafish models with Dr Seb Dworkin in MAPP.



Project 2. Synthesis of orthogonal targeting chemical probes for misfolded proteins. Proteostasis is a housekeeping process cells undertake to maintain the proper folding and functions of proteins. Collapse of proteostasis capacity has been linked to many neurodegenerative diseases such as Huntington's, Alzheimer's and Motor Neuron Diseases. To monitor the effectiveness of the proteostasis machinery in cells, our strategy is to measure the change of certain amino acid exposure or modifications using novel fluorescent probes (synthesis). Their selectivity towards folded, misfolded, and aggregated proteins will be tested (photophysics, biophysics), followed by testing them in the complex cellular environment (cell culture, confocal microscopy and flow cytometry. Further to that will be in conjunction with mass spectrometry proteomics to identify proteins labelled by collaborating with A/Prof David Greening in Baker/LIMS.



Dr. Wenyi Li

LIMS



Chemical synthesis - organic



Biophysical characterisation of materials



Cell culture - eukaryotes



Bioinformatics



Cell culture - prokaryotes



Protein biochemistry



Mass spectrometry

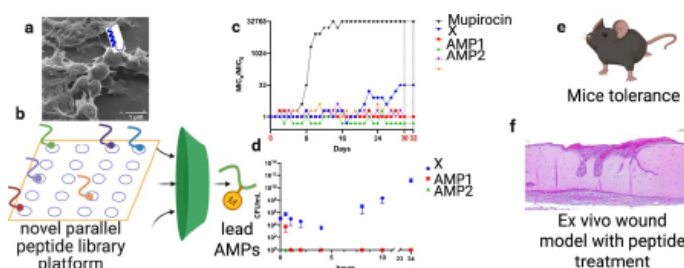


Protein purification

The healthcare costs of antimicrobial resistance (AMR) in Australia are estimated at over \$1 billion a year. Globally, the World Health Organisation predicts that AMR will cost the world up to 100 trillion USD in 2050. Given the emergence and spread of AMR, alternatives to antibiotic drugs are urgently needed. Antimicrobial peptides (AMPs), which form part of a native host defence system, could be a promising solution to this problem. They can have potent and broad-spectrum antimicrobial activity with a reduced tendency to induce resistance. To develop novel alternative antibiotics, our group's research focuses on chemical modifications to enhance their effectiveness and result in significant conformational changes, such as multimerization, bioconjugation and lipidation.

Project 1: Antimicrobial peptide-antibiotic conjugates. One solution for contending with multi-drug resistant (MDR) bacteria is the use of combinations of conventional antibiotics. The use of antimicrobial peptides (AMPs) in combination with, or covalently conjugated to, inexpensive antibiotics such as cephalosporin, may provide important specific antibiotics. However, this approach has met with little success due to the difficulties associated with chemically linking dissimilar compounds, particularly the small molecule antibiotics which have limited non-active site availability of functional groups for anchoring. Covalent conjugation of a conventional antibiotic or small molecules to a peptide can be achieved by either total solid phase synthesis using suitably protected and derivatized antibiotic or in solution via a variety of bimolecular reactions. Therefore, in this project, we aim to apply different linker and conjugation approaches to enhance the bioactivity of AMPs and investigate their mode of action.

Project 2: AI Mining Insect Proline-Rich Antimicrobial Peptides. The rise of antimicrobial resistance has created an urgent need for new antibiotics with novel mechanisms of action. Proline-rich antimicrobial peptides (PrAMPs) represent a promising class of antimicrobials that inhibit protein synthesis by binding to ribosomes. Insects have been a rich source of PrAMPs, with many potent examples discovered in various insect species. However, the vast sequence space and the computational challenge of annotating small open reading frames (smORFs) have hindered the systematic exploration of this resource. This study aims to develop a robust computational discovery pipeline to mine insect genomes and transcriptome databases for novel PrAMPs, leveraging machine learning models and sequence-based predictors.



Project 3: Dual-function molecules. Chronic wound infections are major complications of Diabetes mellitus and are responsible for significant morbidity and mortality. Over 50% of diabetes patients with Diabetic foot ulcers (DFUs) are estimated to develop diabetic foot infections by a polymicrobial community of microorganisms with wound chronicity. The increasing resistance of pathogens to antibiotics causes a huge clinical burden that places great demands on academic researchers and the pharmaceutical industry for resolution. Previously, we identified two leading AMPs that possess effective antibacterial activity against bacteria, including *Escherichia coli* and *S. aureus*. More recently, our recent study showed that the chemical modification enhanced their antibacterial activity against pathogens, but also increased their cytotoxicity. In this project, we will develop novel potent AMPs against DFI pathogens with wound healing properties on innovative chronic wound models.



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Number of projects: **1 Feb, 1 Jul**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**

Prof. Adam Mechler

LIMS



Atomic force microscopy



Chemical synthesis - organic



Biophysical characterisation of materials



Circular dichroism



Quartz crystal microbalance



Electronics

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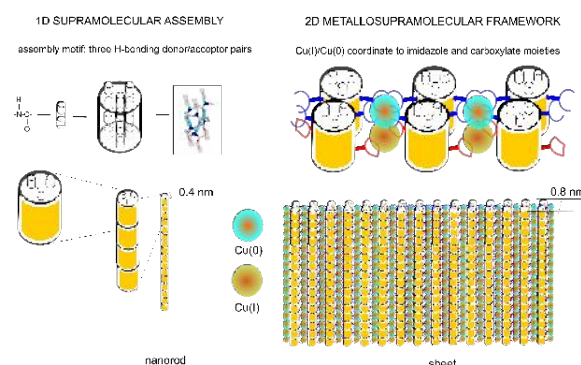
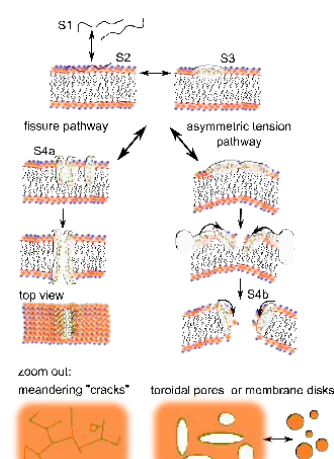
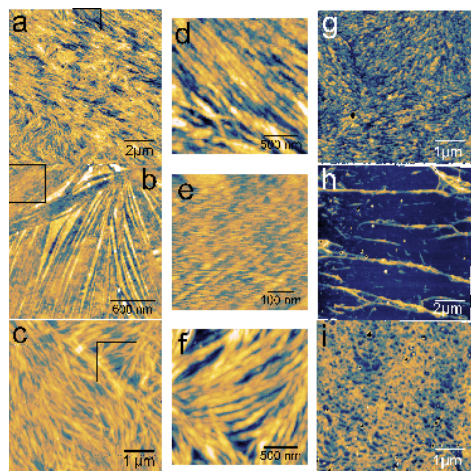
Number of projects: 2

Full-time or part-time: **Either**Feb or July start: **Both**Masters conversion: **Yes**

We study the interactions between molecules that lead to a range of phenomena from the simple, such as aggregation of small particles in a solvent, to the highly complex, such as the formation of cell membranes, stability of colloidal systems and the self-assembly of (bio)molecular machines. The spontaneous assembly of complex nano-to-microstructures from small molecule precursors opens up new horizons in designing and controlling molecular processes, leading to e.g. pharmacological strategies that target bacteria and viruses with molecular “smart bullets”, or self-assembling molecular electronics. The future of nanobiotechnology is underpinned by this research. Projects include:

Project 1. Save the salmon (on the menu). Lab scale optimization and testing of a unique low cost water purification method suitable for treating multiple problematic waste water streams, including fish pen effluents and commercial kitchen waste, to recover oils for biodiesel production, organics for composting and grey water for irrigation. The project has commercial backing and potential applications in the Tasmanian salmon industry. A large part of the project involves building and tinkering with prototype devices.

Project 2. Playing with the molecular LEGO. We have designed a unique self-assembling system based on small unnatural peptides that remain helical under all circumstances and snap together head-to-tail just like LEGO bricks. We build nanostructures using these materials, aiming for complex morphologies, conductive patterns for molecular electronics, and capturing small molecules for sensing. A range of projects are possible, using an exciting array of instruments.



Project 3. Towards the future of peptide drugs. We have studied membrane disrupting antimicrobial peptides for two decades, and the accumulated knowledge now lets us design peptides to target different pathogens. We explore ways to switch activity from antibacterial to antiviral and antifungal action, to create a new platform technology for a new generation of peptide drugs. We also work on improving metabolic and chemical stability by including unnatural amino acids in the peptide sequences.

Project 4. Pharmacological formulations: We also work on different ways of improving pharmacokinetic properties of existing drugs, by using co-crystallization, encapsulation and matrix assembly. These projects also have direct commercial relevance.

Project 5. Thinking outside of the box: we can embark on a range of blue sky projects focusing on the role of intermolecular interactions in new phenomena as well as practical applications, from the theory of surfactant self-assembly to organic piezoelectrics and sensors.

A/Prof. Evan Robertson

LIMS



IR spectroscopy



Molecular modelling



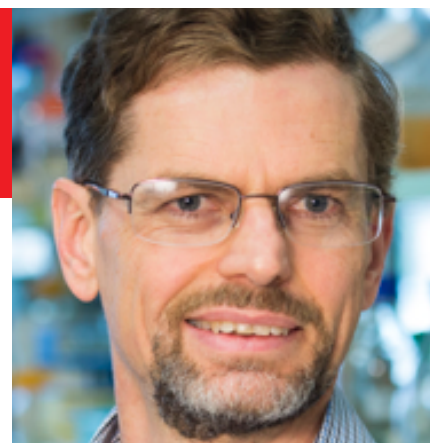
Raman spectroscopy



Pulsed ns lasers



Electronics



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Number of projects: **2**

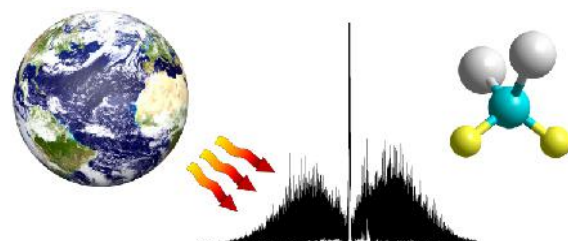
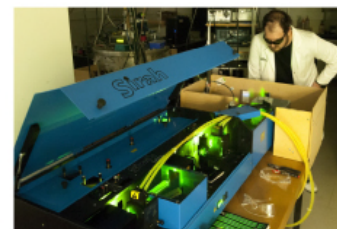
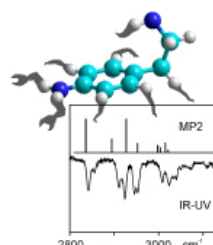
Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

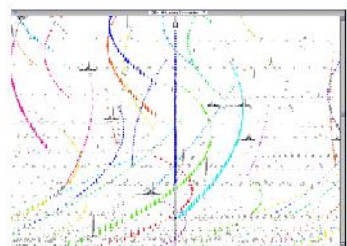
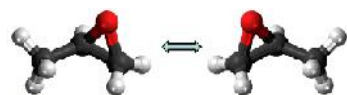
We exploit powerful light sources such as infrared, visible and ultraviolet lasers, or the Australian Synchrotron's infrared beamline to study molecules relevant to pharmaceuticals, atmospheres and astrochemistry. Life on earth is intrinsically chiral. In the building block molecules such as proteins and sugars, "left-handed" or "right-handed" forms are possible, but only one type is found and the reason for this choice remains unclear. Astrochemistry may well play a role and yet amongst the 200 molecules detected in the interstellar medium outside our solar system to date, propylene oxide is the only one that is chiral. We are undertaking work to increase understanding of its' spectral properties in the crucial microwave region used for detection. Other work is aimed at finding other chiral molecules in space and identifying the molecules responsible for thousands of unidentified absorption lines measured by radioastronomy.

The absorption of infrared radiation by greenhouse gases in the atmosphere is at the heart of human induced climate change. Some of our research into fluorocarbons has revealed the fine details that may be used to efficiently model the complex pattern of IR absorption within the atmospheric greenhouse window.



Aerosols also play a key role in our atmosphere, affecting the climate both directly through absorption and reflection of light, and indirectly by hosting chemical reactions and influencing cloud formation. A specialised cooling cell with unique capabilities at the Australian synchrotron's IR beamline enabled us to measure the first far IR spectra of water ice nanoparticles.

The conformational shape of biological molecules, and their interactions with the surrounding environment including water molecules are critical to their functioning. Laser-based gas phase spectroscopy combined with appropriate computer modelling generates precise structural information on molecules such as neurotransmitters that provide a rigorous platform for understanding their behaviour and ultimately, rationalizing drug design. The resonant two photon ionisation technique allows electronic and IR spectra to be measured for molecules cooled to a few Kelvin. This results in beautiful, simplified spectra that can be interpreted to reveal the preferred shapes of molecules and how strongly they interact via hydrogen bonding with water.



Dr. Saimon M. Silva

LIMS



Analytical chemistry



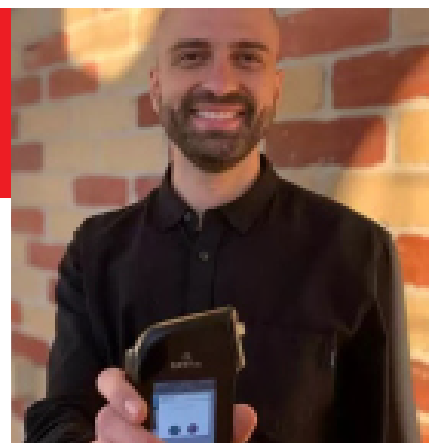
Electrochemical sensing



Sensors & Biosensors



Point-of-care diagnostics



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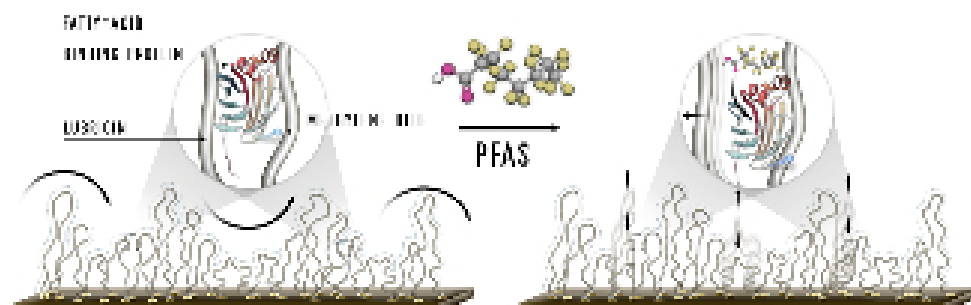
Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**



Our research group is highly interdisciplinary and strongly focuses on translational research. We build new smart materials and interfaces for application in sensors and biosensors to detect molecules of biological, medical, and environmental interest. Our main areas of expertise are electrochemistry, analytical chemistry, surface modification, and synthesis of nanomaterials and biomaterials.

Project 1. Point-of-care sensors for cancer diagnostics and monitoring. Blood-based cancer biomarkers represent a range of promising diagnostic analytes for the early detection and surveillance of cancer. Current detection approaches involving serology protein-based assays and circulating tumour DNA tests rely upon an intravenous blood draw, sample processing, and testing requiring a specialised laboratory setting. This project aims to advance the development of next-generation cancer biomarker detection for on-spot detection of cancer analytes using rapid and inexpensive portable electrochemical biosensors. This is expected to provide significant benefits for cancer patients, especially in remote locations, where surveillance methods can be limited and expensive for early detection of cancer and monitoring of disease recurrence during treatment.



Project 2. Chemical contaminated water: biosensors for rapid, on-the-spot detection. This project aims to develop a versatile biosensor system for rapid on-site detection and monitoring of toxic per- and poly-fluoroalkyl substances (PFAS) in contaminated waterways. PFAS are also known as the 'forever chemicals' and have become a major environmental pollutant that threatens human and ecological health; in Australia PFAS contamination is prevalent in both urban and rural areas, and all Australians are expected to have detectable levels of toxic PFAS in their blood. Current conventional PFAS detection methods rely on sample collection and transport to a centralized laboratory, which is expensive and time-consuming. Thus, there is a need for low-cost portable sensors for the on-spot monitoring of PFAS. In order to achieve specific molecular recognition for PFAS detection, this project will employ protein-based surface chemistries, where fatty-acid binding proteins will be used as the PFAS recognition elements. The produced electrode surfaces will be fully characterized and analytically challenged in 'real-world' contaminated water samples.

Dr. Keith White

LIMS



X-ray crystallography



Nuclear magnetic resonance



Thermogravimetric analysis

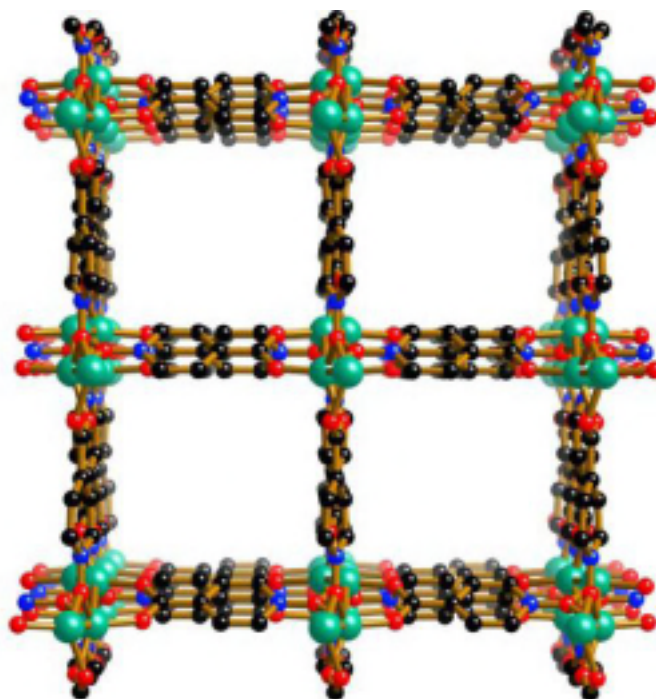


Chemical synthesis - organic & inorganic

My research involves the synthesis of crystalline metal-ligand network materials with open spaces. By carefully selecting the building blocks of the network, the nature of the open spaces may be tuned to capture and store a specific guest of interest, including: H₂ as a fuel, environmentally harmful substances like CO₂, or chemically useful compounds like ethene. In this chemistry, we get to make pretty crystals, shoot X-rays at the crystals to determine their structure and then dose them with interesting volatile substances.

Typical research tasks:

- Synthesis of crystalline materials
- Crystal X-ray diffraction analysis
- Thermogravimetric analysis
- Gas sorption
- UV absorption and emission analysis
- NMR



A metal-ligand network with square shaped open spaces



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Number of projects: 2

Full-time or part-time: **Either**

Feb or July start: **Feb only**

Masters conversion: **Yes**

Prof. David Wilson

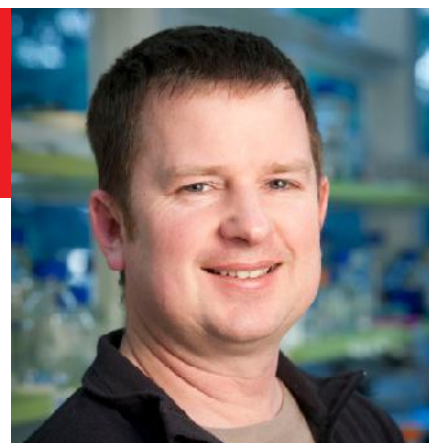
LIMS



Computational chemistry



Molecular modelling
(computational incl. AI)



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

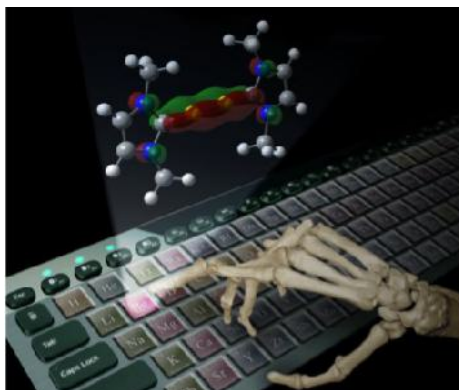
Masters conversion: **Yes**

Our group “does chemistry by computer” to understand the structures and properties of molecules and how they react. We focus on the chemistry of important molecules, molecules with unusual bonding environments, and the prediction of new and novel chemistry.

Project 1. Predicting new chemistry and probing novel bonding environments. Our group has a track record of proposing seminal main-group molecules that are inherently unstable but can be stabilized by ligands. We also proposed new covalent metal-metal bonds such as Be-Be and Be-Mg, which have subsequently been reported in Science and elsewhere. These metal-metal bonds are fascinating – they have properties of both covalent and metallic bonds. There are current projects focused on (i) beryllium chemistry and novel metal-metal bonding, (ii) designing new and novel carbene ligands, and (iii) coordination compounds, including using carbon as a ligand.

Project 2. Modelling reaction mechanisms to understand critical reactivity. There are several projects, such as the involvement of PhICl_2 in catalysing organic reactions or reactions of borole rings with unsaturated molecules.

Project 3. Making new tools for modelling chemistry. We develop new basis sets for use in molecular modelling, to ensure people can accurately model the entire periodic table!

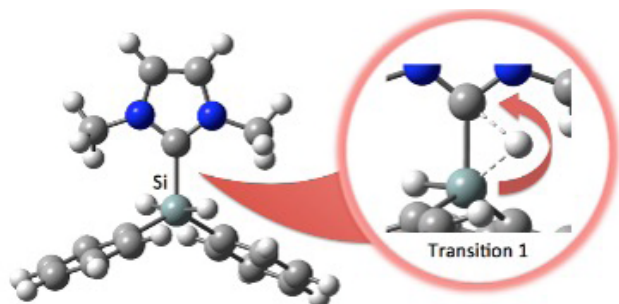
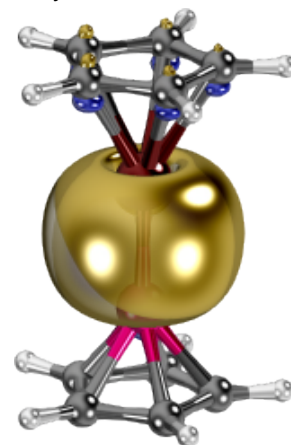


Project 4. Luminescent materials. The development of light-emitting diodes (LEDs) and sensors is a hot topic, for which metal-based (eg. iridium, ruthenium) materials and boron-doped PAHs are ideal targets. These are purely computational projects that are sometimes in collaboration with experimentalists including Prof Gilliard (MIT), Prof Francis (Deakin), Prof Hogan, and A/Prof Barnard. We model luminescence, in addition to UV-Vis spectra, MOs, and redox properties. Boron-doped systems often have unique radical character that is fascinating to model.

Project 5. High-accuracy energetics and properties. Focused on accurate energies and properties where we can push the limits of computational chemistry methods and supercomputers. We can produce results as good as, and sometimes better than experiment! We recently demonstrated how to calculate the shielding of H_2 to within 0.001 ppm of experiment, and extended the ^{19}F scale by 800 ppm! Projects include (i) NMR shielding including ^{19}F , ^9Be , and ^{15}N , (iii) development and/or testing of new basis sets, and (iv) assessing the anharmonicity of N-F bonds and its impact on molecular properties.

Project 6. Using machine learning in chemistry. This is a new field that is rapidly developing – using computer fitting to speed up analysis in areas such as drug design and materials design. For a student with python experience, this would represent a challenging yet rewarding project.

All students develop an advanced understanding of chemical structure and reactivity, develop enhanced analysis, and problem-solving skills.





Microbiology

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Dr. Sarah Annesley Bundoora



Live-cell metabolism assays



Cell culture - eukaryotes, incl. primary & cell lines



Cell culture - prokaryotes



Immunoassays



Gene expression analyses & sequencing



Molecular cloning



Protein biochemistry (SDS-PAGE, western blotting)



Metabolomics



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Number of projects: 2

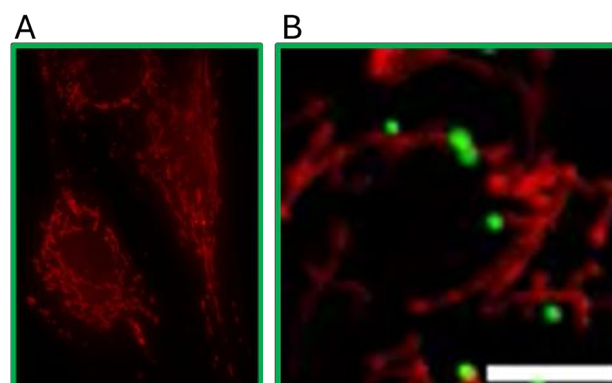
Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

My laboratory investigates diseases that affect the central nervous system with a particular focus on three main disorders, Parkinson's Disease, Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS) and Long COVID. Our aim is to characterise these disorders, investigating the mechanisms of the disease process at the cellular and molecular level. We aim to discover how these mechanisms can be manipulated for treatment and to identify biomarkers which can be developed into world-first diagnostic tests.

Project 1. Parkinson's Disease (PD). PD is the second most common neurodegenerative disorder worldwide. Most cases of PD are sporadic with no known genetic cause but a small percentage of patients (5-10%) are due to inherited genetic mutations. We use human cell lines (immortalised blood and skin cells called lymphoblasts and fibroblasts respectively) derived from patients with sporadic and genetic forms of PD. Our main objectives are to increase our understanding of the underlying disease mechanisms and pathways, identify biomarkers of the disease, identify patients early in the disease process prior to clinical diagnosis and test the effectiveness of various substances. We do this via analysing mitochondrial and lysosomal function, activity levels of proteins, measurement of calcium responses and analysis of gene expression changes. The substances we test for therapeutic potential are plant bioactives.



Project 2. Myalgic Encephalomyelitis/Chronic Fatigue Syndrome (ME/CFS). ME/CFS is a debilitating chronic condition characterised by a disabling fatigue and a post-exertional malaise which is a worsening of symptoms after a mental or physical exertion. The disease is triggered by a range of bodily insults, most commonly a viral infection. Currently there is no cure and no clear treatments or diagnostic tests are available. Using lymphoblasts generated from ME/CFS patients we have identified clear defects in energy production and in the activities and expression levels of key proteins involved in energy production. Using patient lymphocytes, lymphoblasts and fibroblasts we are now working to further characterise these defects, understand disease mechanisms, identify disease biomarkers and develop a diagnostic test.

Project 3. Long COVID. Beyond the immediate acute effects of the virus responsible for the COVID-19 pandemic a large number of people are experiencing ongoing symptoms many weeks and months beyond the original infection. The illness afflicting these patients is termed Long COVID and it shares many similarities with ME/CFS. Our laboratory investigates the similarities and differences between the two disease cohorts, and aims to identify biomarkers of Long COVID and increase our understanding of how this disease develops.

Prof. Ashley Franks Bundoora



Cell culture - prokaryotes



Field work



Genetic sequencing



Data analysis



Bioinformatics



Ecological assays



PCR assays



Animal models of disease



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

Microorganisms underpin the health and productivity of all ecosystems, yet most microbial interactions remain poorly understood. Our research focuses on understanding how bacteria interact with plants, soils, and each other, and how these interactions can be harnessed to improve agricultural productivity, environmental sustainability, and ecosystem resilience. We combine molecular biology, microbiome sequencing, microbial ecology, bioinformatics, and field-based studies to investigate microbial communities across agricultural and natural environments. Our research seeks to understand how beneficial microbes enhance plant nutrition and stress tolerance, how microbial communities influence soil health, and how specialised microorganisms transfer electrons and generate electrical currents. These discoveries have applications ranging from sustainable agriculture and carbon farming to environmental monitoring and bioenergy production. Students joining our group will gain experience in modern microbiome science while working on projects that address major global challenges including food security, climate resilience, and sustainable resource management.



Project 1. Understanding Soil Bacterial Networks that Support Plant Health. Healthy soils contain complex networks of bacteria that help plants acquire nutrients, resist disease, and tolerate environmental stress. However, we still know relatively little about which bacterial interactions are most important for maintaining productive soils. This project will investigate bacterial communities associated with agricultural soils and plant roots using culturing and community analysis techniques. The student will compare healthy and degraded soils to identify microbial interactions linked to improved soil function and plant growth. Outcomes may help develop strategies to restore soil health and reduce reliance on synthetic fertilisers.



Project 2. Human Microbiome and Health. The human microbiome plays an important role in digestion, immunity, metabolism, and overall health. Changes in microbial communities have been linked to conditions including obesity, diabetes, inflammatory bowel disease, and cardiovascular disease. This project will use investigate links between microbial communities and health outcomes. Students will analyse individual microbes, microbiome datasets and techniques to engineer the microbiome to identify microbial signatures associated with health and disease while gaining skills in microbiome science, data analysis, and translational health research.

Project 3. Electric Bacteria: Harnessing Microbial Electron Transfer. Some bacteria have the remarkable ability to transfer electrons outside their cells, effectively generating electrical currents. These "electric bacteria" play important roles in nutrient cycling, soil processes, and emerging bioelectrical technologies. This project will investigate the diversity and activity of electroactive bacterial communities in soils, wetlands, and bioelectrochemical systems. Students will combine microbiology, molecular techniques, and environmental measurements to understand how these bacteria function and how their unique properties can be applied in environmental monitoring, pollutant remediation, and renewable bioenergy production.

Dr. Shannon Hedtke Bundoora



Genetic sequencing



Molecular modelling



Bioinformatics



PCR assays



Light microscopy



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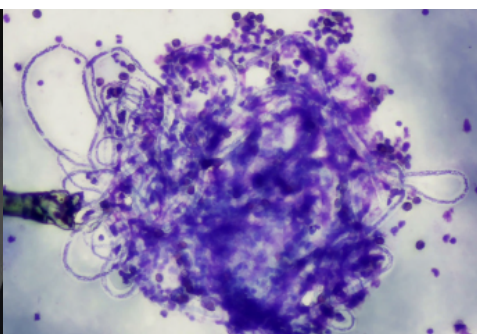
Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**



The vision of our group is to aid the elimination of parasitic diseases worldwide using genomics and ecological modelling.

In communities plagued by parasites, drugs are distributed to everyone to stop people from getting new infections. However, infection persists in many areas of Africa and the South Pacific despite using multiple drugs. Elimination of these diseases is possible only if the reasons for continuing infection are identified: are parasites evolving drug resistance or are new infections coming from outside the community? We work hand-in-hand with government and non-government organisations to ensure that our work has a real-world impact on public health policy.

Project 1. Elimination of lymphatic filariasis (LF) in the South Pacific. Globally, LF is the leading cause of long-term physical disability. Disease symptoms are caused by adult parasites that block lymph nodes and can lead to elephantiasis. The microscopic larvae are found in the blood of infected people and in the mosquitoes that transmit the disease. This project involves whole genome sequencing of these microscopic larvae to determine why the disease persists in the tropical islands of Samoa and Fiji.

Project 2. Elimination of river blindness in Africa. This parasite (Onchocerca volvulus) is transmitted by the bites of blackflies. Disease symptoms are caused by microscopic larvae that move through the skin and eyes of the person. Adult females are ~80cm long and are found coiled up in skin nodules. This project involves sequencing genomes of the parasite and blackflies to determine why infection continues. We are also examining the microbiomes of these blackflies to determine whether they might be transmitting other diseases.

Project 3. Ecological modelling of parasites. We are interested in using computational models to predict where infection might occur based on the ecology of parasites, and to figure out where parasites are being moved by people or insects. How will a changing climate affect disease risk?

Prof. Karla Helbig Bundoora



Cell culture - eukaryotes
incl. primary & cell lines



Cell transfection



Animal models of disease



Microscopy - confocal &
super resolution



Infection & immunity



Protein purification



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

Can We Build Better Defences Against the Next Pandemic?

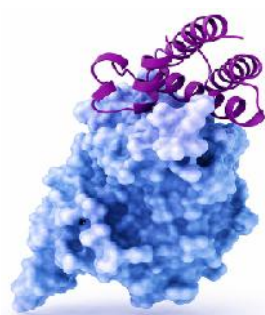
What if we could develop an antiviral treatment that works against many different viruses, helping save lives during the next pandemic while vaccines are still being developed? This is one of the big challenges driving research in the Helbig Lab. Viruses infect humans, animals and aquaculture species, causing major impacts on health, food security and the economy. Our laboratory studies how the innate immune system, the body's first line of defence, responds to viral infection. We are particularly interested in lipids and lipid droplets, tiny structures found within cells that were once thought to simply store fat. Our research has shown that lipid droplets rapidly increase following viral infection and play important roles in antiviral immunity. By understanding how natural antiviral defence pathways work, and combining this knowledge with AI-driven discovery, cell biology and protein engineering, we are developing broad-spectrum, or "pan-antiviral", treatments that could be effective against many different viruses. Honours students can contribute to projects across two major research themes.

Theme 1. Lipids, Lipid Droplets and Antiviral Immunity. How do our cells naturally fight viruses, and can we make these responses stronger? Students will investigate how lipid droplets interact with innate immune pathways to control viral infection. By using cell culture models, organoids or animal models, projects will explore how cells detect infection and activate antiviral responses. We use viruses such as influenza, dengue and Zika virus and students will gain experience in cellular and molecular biology, biochemistry, microscopy and genomic approaches while contributing to research aimed at developing future antiviral therapies.

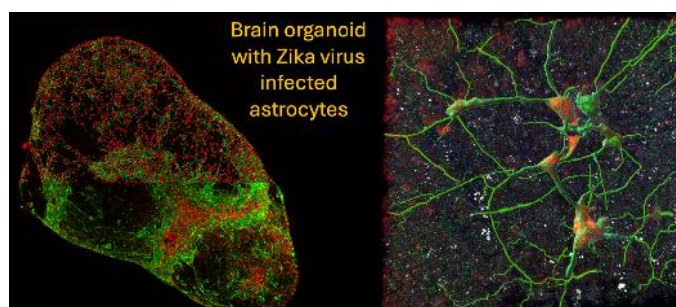


Theme 2. Protecting Australian Abalone from Viral Disease. Can we improve the health and survival of farmed abalone? Abalone herpesvirus threatens Australia's valuable abalone industry. Working with industry partners, students will investigate how abalone detect and fight viral infections, helping develop new approaches to improve disease resilience. These studies also reveal how antiviral defence pathways have evolved across species, providing insights that may contribute to the development of next-generation antiviral treatments for both animals and humans.

Through these projects, students will contribute to research with real-world impacts while developing valuable skills in virology, immunology, biochemistry and biomedical research.



AI-engineered
Pan-antiviral
target engagement



Brain organoid
with Zika virus
infected
astrocytes

A/Prof. Ashley Mansell Bundoora



Animal models of disease



Cell culture - eukaryotes, incl. primary & cell lines



Cell transfection



3D cell culture



Histology & Immunoassays



Live-cell metabolism assays



Microscopy - electron, confocal & super resolution



Protein biochemistry (SDS-PAGE, western blotting)



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Number of projects: 2

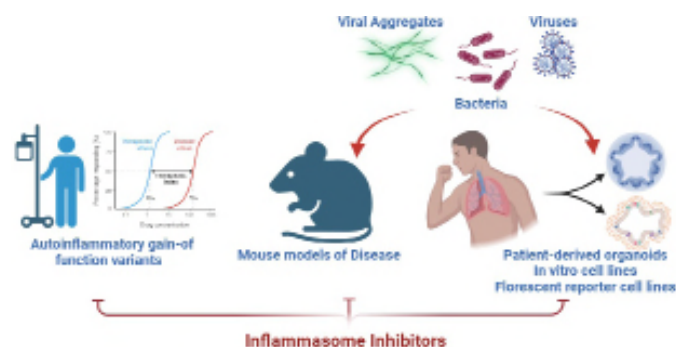
Full-time or part-time: **Full-time**

Feb or July start: **Either**

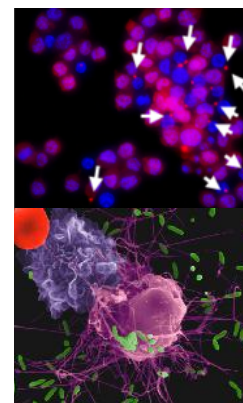
Masters conversion: **Yes**

Have you ever wondered why seasonal influenza usually only makes us mildly sick, while avian influenza has a mortality rate exceeding 40%? Or why SARS-CoV-2 caused severe lung pathology, while previous coronaviruses typically resulted in mild colds? The key to these questions lies in the body's innate immune response and the role of inflammasomes in driving disease severity.

Innate immunity is the body's first line of defense against infections and injuries, providing an immediate response to pathogens and stress. A key component of innate immunity is the inflammasome, a multiprotein complex that detects pathogenic microorganisms and stress signals. Excessive or dysregulated inflammasome activation is associated with infections, pulmonary, neurodegenerative, cardiovascular, metabolic, and gastrointestinal diseases. Our team uses novel animal and in vitro infection models, advanced imaging, and cellular and molecular biology techniques to understand the mechanisms of innate immunity and inflammasome activation. Based on these discoveries, we are also developing new therapies for infectious diseases, autoimmune disorders, and chronic inflammatory conditions, highlighting their fundamental role in maintaining health and combating disease.



Theme 1: Viral Aggregates Activate Inflammasome Complexes and Drive Disease Severity. Recent research has identified that certain viruses, such as pathogenic influenza strains, SARS-CoV-2, and Hendra virus, produce aggregated viral proteins when they infect human cells. These viral aggregates activate the NLRP3 inflammasome, a critical component of the innate immune system. The activation of the NLRP3 inflammasome leads to the production of excessive inflammatory cytokines, which drive the severity of the disease. This project aims to examine and characterize viral aggregates and their role in activating the inflammasome complex, molecular mapping these aggregates to identify emerging pathogenic viral strains and target the inflammasome to identify novel therapies.



Theme 2: The Role of the NLRP1 Inflammasome in Innate Immunity. The role of NLRP1 in human disease has only recently become clearer due to a lack of identified agonists, limited expression and activation in immune cells, and poor conservation between humans and rodents. This theme will characterise recently identified patient-derived human variants of NLRP1, investigate the role of NLRP1 in responding to infections by Dengue, Zika, Herpes, and influenza viruses, and characterize the world's first "humanised" NLRP1 mouse. Additionally, it will explore targeting NLRP1-induced inflammation with the world's only NLRP1 inhibitor, and to develop anti-NLRP1 therapeutic strategies.

Theme 3: Innate Immune Immunometabolism. Immunometabolism describes the interplay between immunological and metabolic processes, which are critical to the immediate innate immune response to infection. We have previously identified a critical role for the immune modulator STAT3 in regulating the immunometabolic programming of macrophage mitochondria. This theme will expand on these earlier studies to understand the mechanisms of action of mitochondrial STAT3 and its regulation of mitochondrial respiration.

Dr. Ebony Monson Bundoora



Cell culture - eukaryotes
incl. primary & cell lines



Infection & immunity



Molecular cloning



Microscopy - confocal, super
resolution fluorescence



Protein biochemistry (SDS-
PAGE, western blotting)



Gene expression analyses



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Number of projects: 2

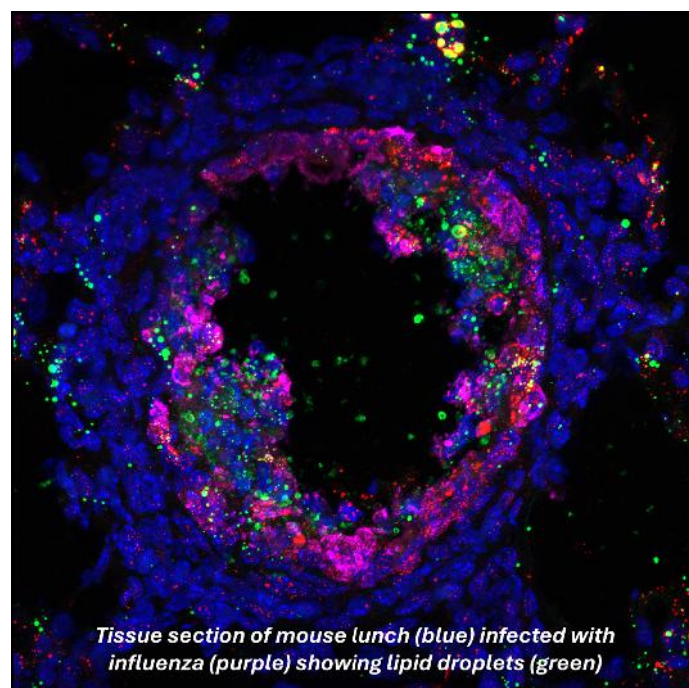
Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

Our research investigates the microscopic battles that happen inside our cells during viral infection. We want to understand how viruses enter cells, how cells detect and fight infection, and how viruses hijack cellular machinery to help themselves survive and reproduce. A major focus of our research is on lipid droplets: tiny fat-filled structures inside cells that are emerging as important players in immunity and viral infection. We are particularly interested in an intriguing possibility: can lipid droplets carry antiviral messages from an infected cell to its neighbours? We are investigating how lipid droplets might leave one cell, enter another, and help neighbouring cells prepare their antiviral defences. But getting into a cell is only half the challenge. Incoming material is often trapped inside membrane-bound compartments called endosomes that act a little like the cell's sorting and recycling system. We want to discover what happens to lipid droplets once they enter a recipient cell and, importantly, whether they can escape from endosomes to deliver their cargo where it is needed. These questions also have exciting industry applications. Endosomal trapping is one of the major challenges facing new medicines based on RNA, proteins and other biological molecules. By learning how cells and viruses naturally move biological material between and within cells, we hope to uncover new strategies for delivering future medicines.

Theme 1. How do cells fight viruses, and how can we use those same pathways to deliver new medicines? A project in this space is flexible- come and chat if you are at all interested in virology, cell biology, immunology and biotechnology and want to learn how to use very high-end microscopes and cutting-edge cell biology tools. Ultimately, we want to understand how cells communicate and defend themselves and how we can harness those processes to fight disease. This project will be completed within the lab of Professor Karla Helbig.



Prof. Steve Petrovski

Bundoora



Microscopy - light & electron (TEM, SEM)



Bacterial overexpression of proteins



Bioinformatics



Genetic sequencing



Gene expression analyses (PCR assays)



Cell transfection



Molecular cloning incl. CRISPR-Cas9 editing



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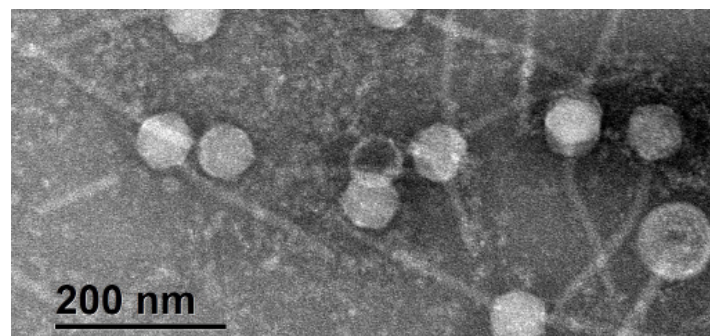
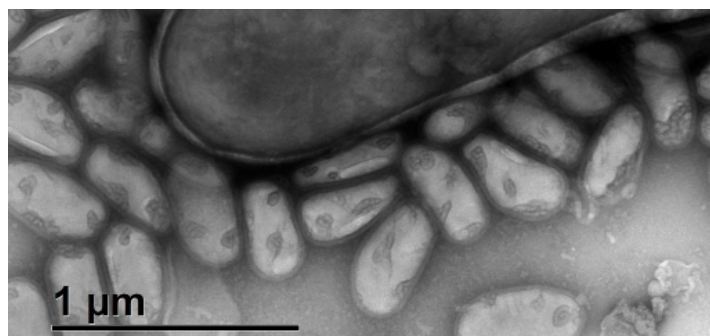
Website: [click here](#)

Number of projects: 1

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

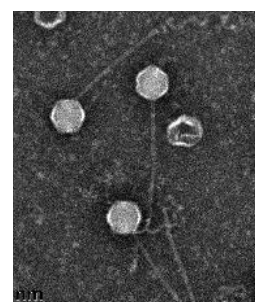
Masters conversion: **Yes**



Horizontal gene transfer (HGT) is the mechanism of gene-swapping and genetic exchange between bacteria. HGT provides opportunities for bacteria to evolve over long and short timespans. The best-known contribution of HGT has been the rapid dissemination of numerous antimicrobial-resistance determinants amongst diverse, clinically significant, bacterial species, a situation that now threatens the usefulness of antimicrobials in the treatment of bacterial infections. Plasmids, transposons and bacteriophages are vital components of HGT and are the subjects of our research.

Our research group uses a range of techniques including molecular genetic techniques, transmission electron microscopy, next generation sequencing, microbiological techniques to understand molecular mechanisms involved in HGT and ways to prevent the dissemination of antimicrobial resistance genes. Biocontrol of recalcitrant bacterial species in both clinical and environmental settings are investigated using phages and parasitic bacteria. We screen and isolate phages that specifically infect bacteria responsible for topical infections and organisms implicated in operational problems in wastewater treatment plants. These phages are used in the development of novel products that can be used to treat clinical infections or environmental problems. We have also started to isolate parasitic bacteria that are able to lyse their host as phages are able to do. We are interested in the bacterial interactions with the parasite and ways we can manipulate their growth to solve environmental problems.

Project 1. Characterisation of bacteriophage and understanding their interactions with host bacteria. Bacteriophages can lyse their host bacteria and this can be a useful tool in controlling the proliferation of its host in different settings. This project area will involve the isolation and characterisation phages and their use in biocontrol of phage therapy.



*Project 2. Fertility inhibition of IncP plasmids using the *fipB* locus.* Plasmids that belong to the IncP family are broad host range and transfer at high frequency to many different bacterial species disseminating antimicrobial resistance genes. The expression of three genes from another plasmid within a cell reduces the transfer of the IncP plasmids. This project will investigate the molecular mechanism involved in the inhibition of plasmid transfer.

*Project 3. Investigation of growth kinetics of *M. amalyticus*.* *M. amalyticus* is a novel parasitic bacterium that has the ability to lyse its host bacterium. *M. amalyticus* has the ability to lyse at least 20 different bacterial strains. This project will investigate the similarities and differences on the diverse host strains.

Other projects are available but you will need to speak with Steve.

Dr. Jennifer Wood

Bundoora



Ecological assays



Field work



Next generation sequencing



Bioinformatics



Gene expression analyses
(PCR, qPCR)



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Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

Our research group advances holistic approaches to restoration, agriculture, and conservation by investigating microbial communities and their functional traits. These traits aid microbial survival and significantly impact ecosystem health. Using cutting-edge Omics technologies and environmental measures, we explore the ecology and function of microbiomes associated with soil, plants, animals, and overall ecosystem health. Our work shapes sustainable practices and develops real-world solutions for pressing environmental challenges.

Project 1: Investigating Soil Health in Agriculture and Urban Agriculture. Current land-use practices have reduced soil organic matter by 20-70% in the top 10 cm of Australian soils, impacting water retention, nutrient availability, and productivity. This project examines soil microbial responses to various organic matter (OM) inputs in a restoration context and in traditional and urban agricultural settings, focusing on inputs with differing carbon-to-nitrogen (C:N) ratios and levels of carbon complexity. By examining microbial activity and community structure in response to different OM inputs, we aim to understand their long-term effects on soil function and develop strategies for restoring and maintaining soil health.



Project 2: Discovering Functional Indicators of Soil Health. Current metrics for measuring soil health are inadequate, leaving a critical gap in our ability to accurately assess and manage soil ecosystems. This project explores novel strategies for evaluating soil health, focusing on developing functional indicators that are meaningful and translatable for farmers and land managers. By examining innovative metrics such as DNA and RNA ratios, microbial activity, and alternative methods for measuring soil organic matter, we seek to provide a comprehensive understanding of soil health and support sustainable agricultural practices.

Project 3: Microbial Indicators of Wetland Health and Resilience. Wetlands are essential for agricultural sustainability and biodiversity, providing crucial ecosystem services such as water filtration, detoxification, nutrient cycling, and carbon and methane sequestration. Our research indicates that wetlands exhibit high metabolic diversity, a potential indicator of their health and ability to provide ecosystem services. This project aims to identify microbial indicators of wetland health and resilience by studying microbial communities and their functional traits across a gradient of wetland states, from pristine to degraded. We will investigate how these communities respond to drought conditions, exacerbated by climate change, and their capacity to reestablish critical functions post-drought. By understanding wetland resilience, we aim to develop strategies to maintain their essential ecosystem services amidst environmental changes.





Anatomy, Physiology & Pharmacology

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Dr. James (Jim) Bell Bundoora



Cell culture - eukaryotes
incl. primary & cell lines



Protein biochemistry (SDS-
PAGE, western blotting)



Animal models of disease



Light microscopy



Histology



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Number of projects: **2**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**

The Cardiac Disease Mechanisms lab seeks to understand the cellular and molecular mechanisms driving heart diseases.

We focus on examining the underlying causes and pathological consequences of cardiac rhythm and relaxation irregularities (arrhythmias and diastolic dysfunction respectively) and heart attacks (myocardial infarction), and how these may differ in men and women. The overall goal is to validate novel molecular targets that advance sex-specific preventative therapies for aged and obese populations at risk of developing heart disease.

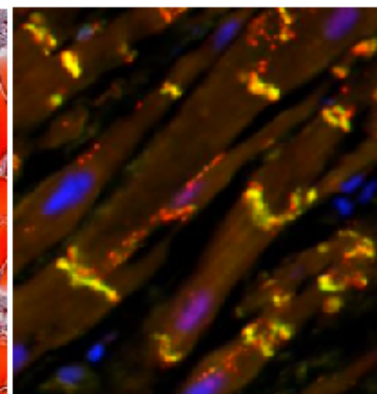
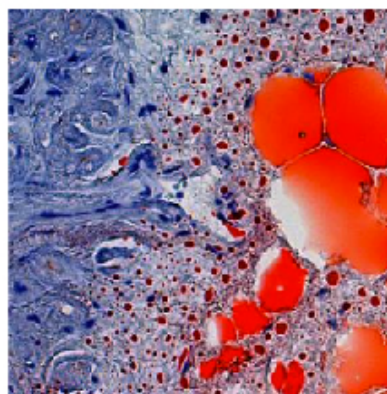
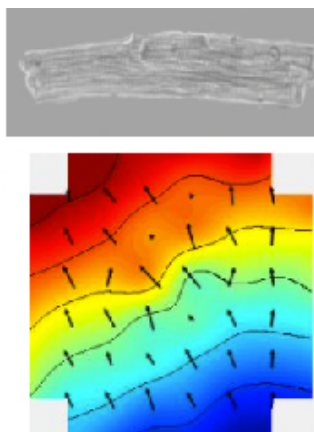
The lab has two primary research themes – specifically, the pathological influence of ‘heart fat’ as an emerging mediator of heart disease and the role of sex and sex steroids in determining heart health. The fat immediately surrounding the heart increases markedly in obesity, with aging, and post-menopause – all important risk factors for heart disease. We are investigating how the fat interacts with heart muscle to cause cardiac dysfunction and identifying the factors released from the fat (including locally synthesised estrogens) that convey communication between these two neighbouring tissues.

Honours projects include:

Project 1. Showing how a fatty heart drives cardiac pathologies

Project 2. Understanding the role of locally synthesised steroids in the heart

Our research scope is facilitated through an extensive expertise in in vivo, ex vivo, in vitro and molecular methodologies, and further supported by ongoing pre-clinical/clinical collaborations developed both nationally (University of Melbourne, Macquarie University) and internationally (University of Birmingham, UK).



Dr. Michael De Silva Bundoora



Animal handling



Genetic sequencing & expression analyses



Animal models of disease



Histology



Animal behaviour studies



Microscopy - light, confocal & super resolution



Flow cytometry



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Number of projects: **1**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

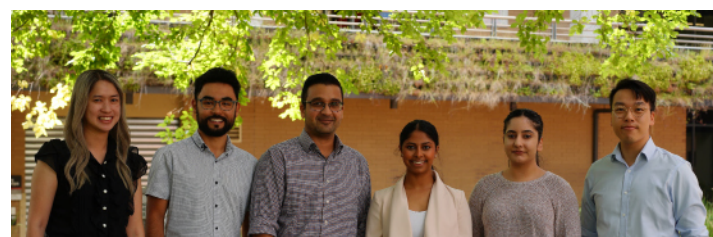
Masters conversion: **Yes**

Cerebrovascular diseases (stroke, dementias) are a major health concern in Australia and throughout the world.

The brain and its circulation are particularly sensitive to disease. Cardiovascular diseases disrupt the function of cerebral arteries which leads to a dysregulation of cerebral blood flow. This may lead to altered blood flow to the brain which may starve neurons of the continuous supply of oxygen and other nutrients essential for their function. Insufficient delivery of oxygen and nutrients to the brain is a major factor in neuronal dysfunction and may contribute to the development of cognitive impairment (e.g. loss of memory).

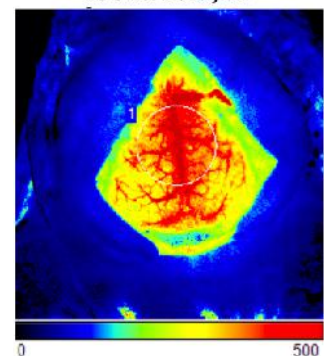
Our research focuses on the effects on cardiovascular diseases (e.g. hypertension, ischaemic stroke, metabolic syndrome) on the brain and its circulation. We utilise animal models of disease as well as state of the art imaging, molecular and behavioural testing techniques to determine the impact of disease on the brain and identify potential targets for therapy.

Project 1. Effect of human amniotic stem cells on brain injury and cognitive function. Cardiovascular diseases (hypertension, metabolic syndrome) are known to promote brain injury and may therefore, result in impairment of cognition. The complex mechanisms that underly these diseases mean that a single therapeutic agent is unlikely to be effective. Human amnion epithelial cells (hAECs) have many properties (eg. anti-inflammatory, antifibrotic, regenerative and immunologically inert) that make them attractive candidates for a cell-based therapy for disease. This project will determine whether hAECs can treat cardiovascular disease-induced brain injury and cognitive impairment.

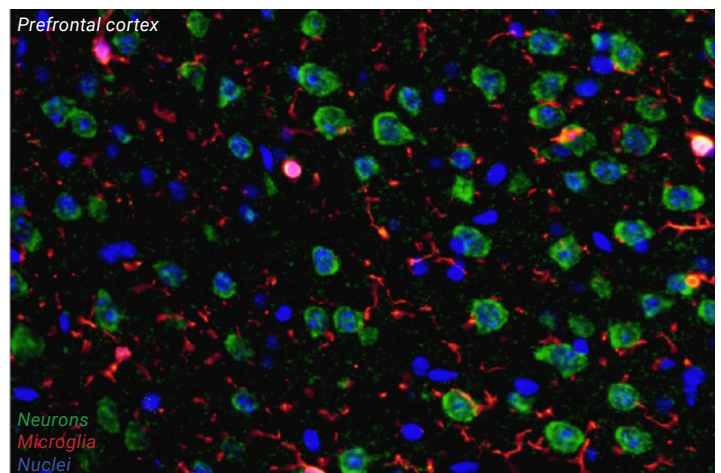


Project 2. Targeting estrogen signalling to reduce dementia risk. We have found postmenopausal women with hypertension to have the greatest reduction in brain health between ages 60-80. This decline is greater than in groups regarded as "unhealthier" (e.g. males with multiple cardiovascular diseases). Loss of protection by estrogen after menopause is a likely contributor. We have shown that activation of the G protein-coupled estrogen receptor (GPER) is protective in cardiovascular disease models, including hypertension and stroke. Importantly, selective activation of GPER avoids unwanted effects that result from activation of classical estrogen receptors. In this project we will study menopause-accelerated brain atrophy and cognitive decline in female mice with hypertension and if these changes to brain health can be prevented by pharmacological targeting of GPER.

Cerebral blood flow



Prefrontal cortex



A/Prof. Seb Dworkin Bundoora



Animal handling



CRISPR-Cas9 gene editing



Animal models of disease



Genetic sequencing & expression analyses



Zebrafish microinjection



Microscopy - light, confocal & super resolution



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Number of projects: **2**

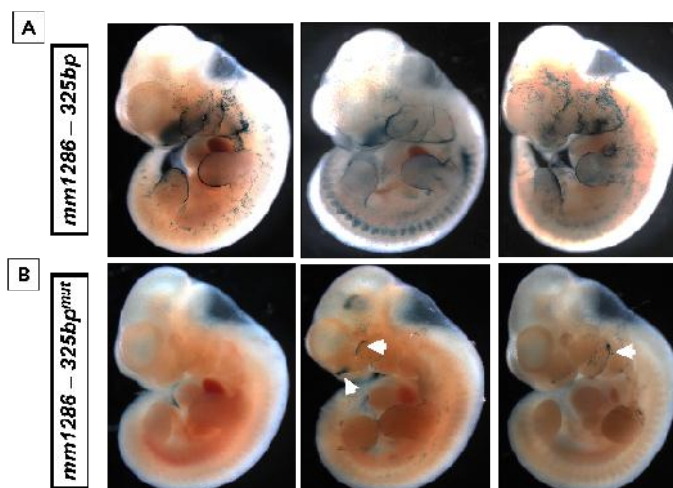
Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**

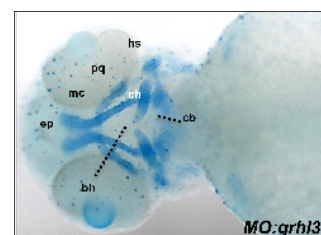
Understanding how a single, fertilised cell develops into an entire, fully functioning baby, is one of the most incredible fundamentals of life. It is also a process across the entire animal kingdom. Amazingly, this process usually works perfectly well - that is, the baby develops without any problems. However, in ~4-5% of cases, things do go wrong, resulting in problems with structure or function in the baby that we term "birth defects".

Understanding the genetic and non-genetic causes of these birth defects is the major focus of my groups' work. In particular, we aim to understand what are the factors that allow for correct formation of the brain, head, face, jaws and skin. In my group we use animal models - zebrafish and mouse - that harbor defined genetic mutations in order to understand how these genes function in regulating development.



Moreover, we are now also using our models to better understand how we can "rescue" birth defects of genetic origin through supplementing the fish water (or mouse diet) with safe bioactive natural product compounds (such as vitamins and plant extracts). Ideally, we hope to discover novel molecules that may be safely given in pregnancy to reduce the incidence or severity of potential birth defects.

The various Honours projects in the lab will involve analysis of zebrafish models to identify the functions of new genes in development, particularly craniofacial development, and will identify novel bioactive compounds to prevent, or reduce, defect severity. Each project will be tailored to individual student backgrounds and interests; a working (minimum 2nd year undergraduate level) knowledge of genetics is essential, and an interest in embryology and developmental biology would be advantageous.



Dr. Brooke Huuskes Bundoora



Cell culture - eukaryotes
incl. primary & cell lines



Gene expression analyses



Animal models of disease



Histology



Animal handling



Light microscopy



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Number of projects: **2**

Full-time or part-time: **Either**

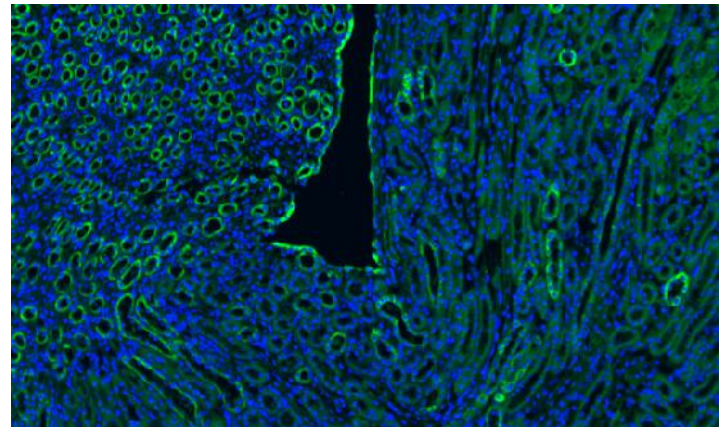
Feb or July start: **Both**

Masters conversion: **Yes**

The mission of the Cardiorenal Division is to lessen the burden of those living with chronic kidney disease (CKD). There is no cure for CKD, which affects more than 10% of the world's population. Current therapies for CKD only slow the progression of disease and a significant number of people progress to end-stage kidney disease requiring either dialysis or kidney transplantation. People on dialysis are more likely to die of a cardiovascular event before getting a transplant, and there is a significant shortage of available organs to be transplanted.

To do this we aim to understand the cellular and molecular mechanisms that cause kidney inflammation and fibrosis in a range of kidney diseases, including in the pathology of hypertension and genetic kidney conditions. By understanding these pathways, new therapeutic strategies can be identified and targeted for patients suffering kidney disease.

We additionally use applied qualitative research methods to perform research priority setting activities and to understand the perspectives of those living with chronic kidney disease. This research helps inform practice and policy for improved patient-centered outcomes.

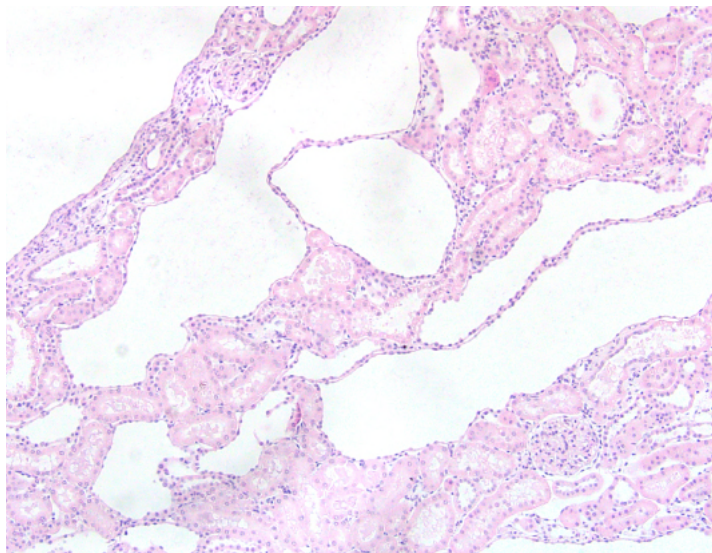


Project 1. Understanding the role of the immune system in polycystic kidney disease

Project 2. Unravel the role of cell death in kidney disease

Project 3. Modeling polycystic kidney disease using zebrafish

Project 4. Research priority setting in xenotransplantation



Dr. Maria Jelinic Bundoora



Cell culture - eukaryotes
incl. primary & cell lines



Immunoassays



Bioinformatics



PCR assays



Flow cytometry



Microscopy - Light,
confocal



Histology

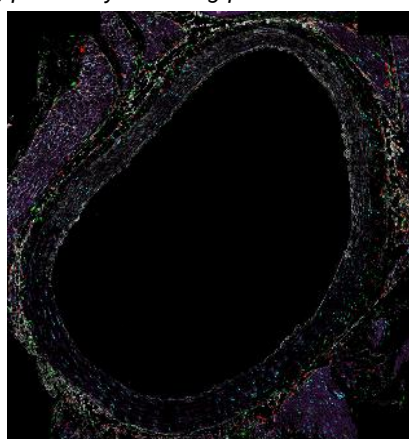


Proteomics

Imagine a future where heart attacks and strokes are no longer leading causes of death. The AtheroImmunology Research

Division is working towards this goal by uncovering new ways to prevent coronary artery disease, the underlying cause of most heart attacks. This disease develops gradually as fatty deposits and chronic inflammation accumulate within the artery wall, often without symptoms until a sudden and life-threatening event occurs. While many current approaches aim to suppress the immune system to reduce inflammation, these strategies can compromise the body's natural defences. Our research takes a different approach by investigating how damaged and stressed cells within atherosclerotic plaques trigger harmful immune responses. By understanding how stressed vascular cells communicate with immune cells, we aim to identify new therapeutic targets that prevent plaque destabilisation and rupture without impairing normal immune function. Using human tissue samples, advanced molecular and imaging technologies, and computational analysis, we are uncovering the cellular interactions that drive cardiovascular disease and informing the development of safer, more targeted therapies.

Project 1. Characterise immune synapse formation between stressed vascular smooth muscle cells and cytotoxic T cells. Vascular smooth muscle cells (VSMCs) are critical for maintaining plaque stability, yet their loss is a hallmark of vulnerable atherosclerotic plaques. Using our established human VSMC models of cellular stress and senescence, this project will characterise the immune synapses formed between VSMCs and cytotoxic T cells using proximity-labelling proteomics. The project aims to identify the ligand-receptor interactions that drive immune-mediated VSMC killing and contribute to plaque instability.



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Number of projects: **2**

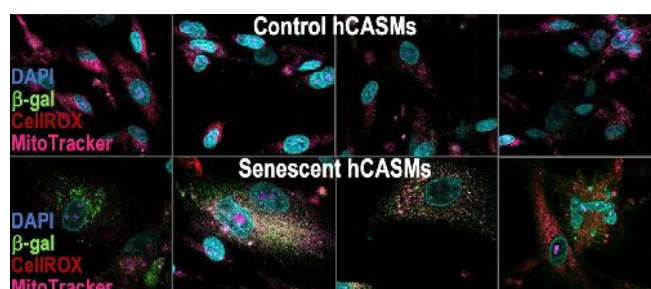
Full-time or part-time: **Either**

Feb or July start: **Both**

Masters conversion: **Yes**



Project 2. Map stress signalling pathways across human atherosclerosis progression. Using imaging mass cytometry in human coronary artery specimens, this project will investigate how stress-induced signalling pathways are expressed and spatially organised throughout atherosclerosis progression. Focusing on stress ligands such as MICA and BTN3A1 and associated cytotoxic immune populations, including $\gamma\delta$ T cells, the project will define how these pathways change across distinct stages of disease and determine their association with plaque vulnerability, fibrous cap integrity, and plaque rupture. The findings will provide new insights into the cellular mechanisms that drive progression to heart attack and stroke.



Dr. Helena Kim Bundoora



Animal behaviour studies



Gene expression analyses



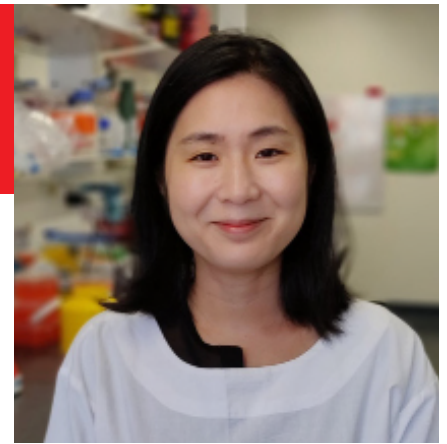
Data analysis



Genetic sequencing



Histology



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Number of projects: **1**

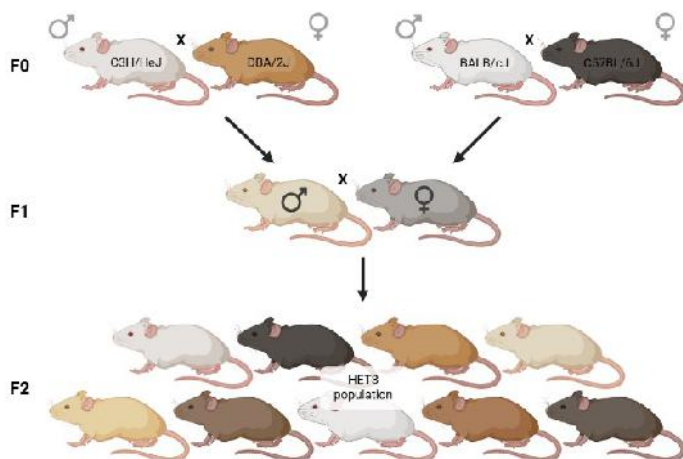
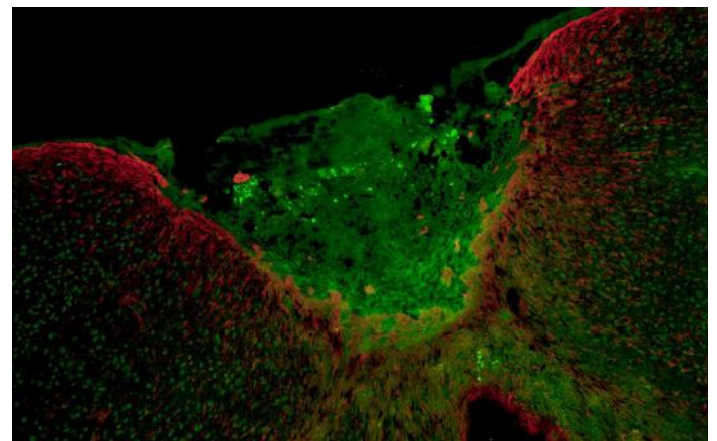
Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

The stroke and Brain Inflammation Division aims to understand how inflammation contributes to brain injury and recovery following ischemic stroke. Stroke remains one of the leading causes of death and long-term disability worldwide. Although clot-removing therapies such as tissue plasminogen activator (tPA) can be highly effective, only a small proportion of patients are eligible for treatment because of the narrow therapeutic window. As a result, there is an urgent need to identify new therapeutic targets that can protect the brain and improve recovery after stroke.

Our research focuses on uncovering the molecular and cellular mechanisms that drive post-stroke inflammation and brain damage. A major challenge in stroke research is that many preclinical studies are conducted in young, genetically identical animals, which poorly represent the clinical population most affected by stroke. Older adults are at the highest risk of stroke, and human populations are genetically diverse. To address this gap, our Centre for Cardiovascular Biology and Disease Research has established Australia's first colony of HET3 mice, a genetically heterogeneous mouse model designed to improve the clinical translatability of experimental findings.



This Honours project will contribute to our efforts to develop more clinically relevant models of stroke by investigating age-related changes in the brain and circulation of aged mice (20 months and older) from both C57BL/6 and HET3 strains. The project will examine genomic and proteomic profiles associated with ageing, generating foundational data that will support future studies of stroke and brain inflammation in more representative preclinical models. Primary supervisor: Dr Helena Kim, Dr Richard Zhang.

Students will become part of a multidisciplinary and supportive research team and gain hands-on experience in a wide range of laboratory techniques, including animal behavioural assessment, tissue processing, PCR-based analyses, proteomics, histology, fluorescence microscopy, and data analysis. This project provides an excellent opportunity for students interested in neuroscience, ageing, immunology, and translational biomedical research to contribute to a research program aimed at improving outcomes for stroke patients.

Dr. Chris van der Poel Bundoora



Animal handling



Animal behaviour studies



Histology



Data analysis



Immunoassays



Protein biochemistry



Live-cell metabolism assays



Protease activity assays



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Number of projects: 2

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

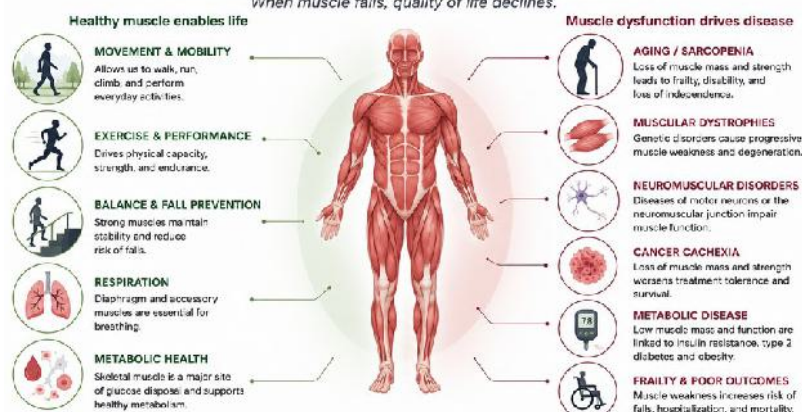
The Integrated Muscle Biology Laboratory, co-led by Professor Robyn Murphy, studies how nutrition, exercise, ageing, and disease influence biochemical regulation, and physical function of skeletal muscle. Our research spans from whole-body physiology to detailed studies of individual muscle fibres, helping us understand how muscle works, how its biochemistry changes across life, and how we might protect it. We are particularly interested in diet-based strategies, supplements, and food-derived compounds that may support muscle, metabolic, and healthy ageing outcomes. Our projects combine physiology, muscle function, nutrition, and biochemistry, with a focus on research that can ultimately inform real-world health strategies.

Project 1. Creatine and menopause: can nutrition protect muscle and metabolic health? Co-supervised with Dr Michael de Silva (MAPP). Menopause is associated with changes in muscle, metabolism, body composition, and physical function. Creatine is a widely used nutritional supplement, best known for its role in muscle energy, but its potential benefits during and after menopause are still being explored. This project will use a mouse model of menopause to investigate whether creatine can help protect muscle and metabolic health. Students may examine outcomes such as muscle function, tissue health, metabolic markers and cognition. This project would suit students interested in women's health, ageing, nutrition, physiology, and translational biomedical research.

Project 2. Digestion-Derived Food Bioactives and Their Effects on Skeletal Muscle Contractile Function. Co-supervised with Dr Deepa Agarwal (Centre for Food Science). Many foods contain compounds that may only become biologically active after they are digested. This means that testing whole food extracts alone may miss important effects that occur once food is broken down in the gut. This project will investigate whether digestion-derived compounds from selected foods, such as legumes, seaweed or pine bark, can directly influence skeletal muscle function. Students will help generate digested food samples using a laboratory digestion model, then test whether these samples alter muscle fibre performance, including force production and calcium-related processes that control contraction. This project would suit students interested in nutrition, functional foods, muscle physiology, food bioactives, and hands-on laboratory techniques.

Why Skeletal Muscle Matters

Skeletal muscle is essential for movement, metabolism, and health.
When muscle fails, quality of life declines.



Understanding skeletal muscle function is essential for developing therapies that preserve mobility, independence, and quality of life.

A/Prof. Antony (Bill) Vinh Bundoora



Animal handling



Animal models of disease



Flow cytometry



Bioinformatics



Histology



Genetic expression analyses



Immunoassays



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Number of projects: **1**

Full-time or part-time: **Full-time**

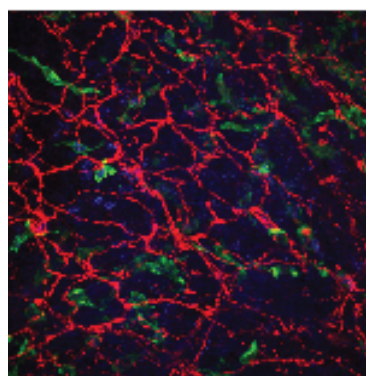
Feb or July start: **Feb only**

Masters conversion: **Yes**

The Hypertension and Immunobiology Research Division aims to discover and validate novel cellular and molecular mechanisms and targets to treat hypertension and related end-organ damage.

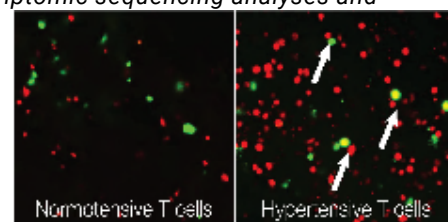
High blood pressure (BP) remains the leading cause of death worldwide. Despite the availability of several drugs to treat hypertension, 50% of patients still have uncontrolled high BP. Furthermore, in 90% of cases of hypertension, the cause remains unknown, which clearly indicates a lack of understanding of the mechanisms that drive sustained elevations in BP.

At the Hypertension and Immunobiology Research Division at the Centre for Cardiovascular Biology and Disease Research, we study novel mechanisms that drive hypertension and related end-organ damage. We have identified that non-classical physiological pathways of BP control such as inflammation, the immune system, fibrosis and the gut microbiome are major influencers of hypertension. Our team specialises in using a multidisciplinary approach to study hypertension, which includes expertise in pharmacology, physiology, immunology, molecular and cellular biology. Our world-leading capabilities in several pre-clinical models of hypertension (e.g., angiotensin II, DOCA-salt, metabolic syndrome), with gold-standard in vivo tools (radiotelemetry, ultrasound imaging, transdermal GFR) has allowed for the discovery and validation of novel targets and drug therapies to treat hypertension and related pathologies such as heart disease, chronic kidney disease, aortic stiffening and fibrosis.



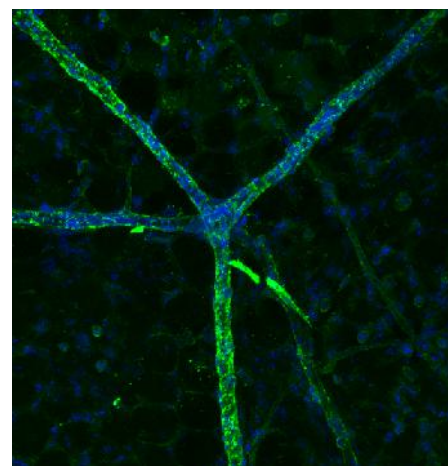
Sympathetic nerves (red) and macrophages (green) infiltrate the perivascular fat of hypertensive mice.

Project 1. B and T lymphocytes/cells in hypertension. Primary supervisor: Dr Hericka Figueiredo Galvao, A/Prof Bill Vinh. B and T cells have been shown to be required for the full development of hypertension. However, the precise mechanisms remain understudied. This project will combine pre-clinical models of hypertension, next-generation single-cell transcriptomic sequencing analyses and machine learning to interrogate the contribution of the adaptive immune system to hypertension. Techniques and skills that will be learnt include animal handling and BP detection, flow cytometry and complex bioinformatic analysis.



Visualising dynamic T cell-APC interactions in the perivascular fat of hypertensive mice (Hox: T cells; Green: APCs)

Project 2. Bacteriophages and Hypertension. Primary supervisor: A/Prof Bill Vinh, Prof Grant Drummond, A/Prof Steve Petrovski. Loss of "healthy promoting" gut bacteria - or microbiome - is recognised as an important driver of cardiovascular disease such as high blood pressure (also known as hypertension). Much of the focus in this area of research has been associated with bacteria, while much less attention on the virome and more specifically, bacteriophages - virus that kill bacteria - which outnumber bacteria almost 10-fold. We have isolated a world-first lytic bacteriophage that targets one of the most abundant gut commensal bacteria. This project aims to test the impact of administering this lytic phage on the gut microenvironment, and determine whether these changes impact the development of hypertension. Techniques and skills that will be learnt include animal handling and surgery, blood pressure detection, flow cytometry and histology.



Dr. Richard Zhang Bundoora



Animal behaviour studies



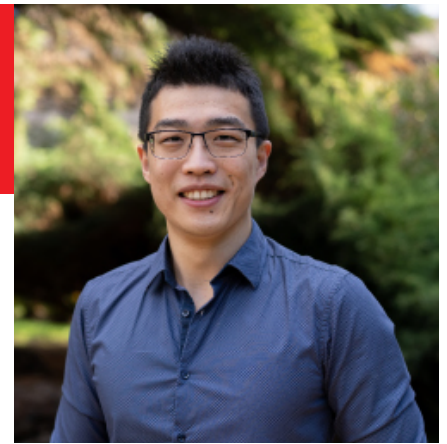
Animal handling



Animal models of disease



Artificial Intelligence



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Number of projects: 1

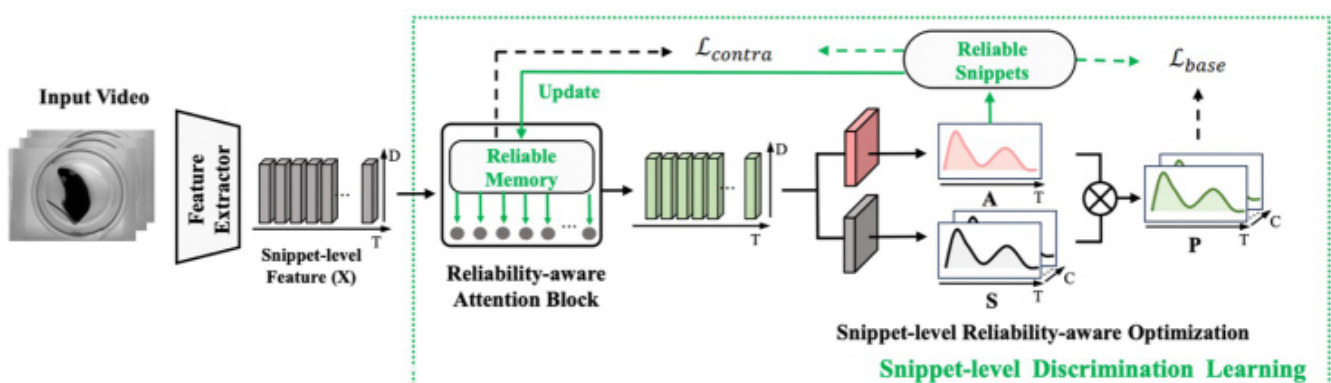
Full-time or part-time: **Full-time**

Feb or July start: **July only**

Masters conversion: **Yes**

Our stroke division at the Centre for Cardiovascular Biology and Disease Research focuses on the mechanisms behind ischemic strokes, with the goal of discovering new therapies to prevent or mitigate their detrimental effects. Stroke occurs when brain tissue is deprived of blood due to the blockage of a cerebral artery. Our lab has been using animal models of stroke to mimic human stroke conditions. This allows us to investigate disease pathways that contribute to arterial blockages, as well as the inflammatory responses in various organs post stroke.

We utilise grid walking video analysis in mice to assess their coordination as a measure of stroke injury and the effectiveness of potential treatment. Traditionally, mouse behavioural videos are analysed manually, which is not only time consuming, but also prone to human error and subjective bias. Artificial intelligence carries the potential to perform these analyses within seconds, whilst offering faster, objective results with frame-by-frame accuracy. This Honours project will form a collaboration between Australia Centre for AI in Medical Innovation (ACAMI) (Dr Lu Yu) and the Stroke Division of our Centre. We aim to create the ground truth data using our existing mouse grid walking videos and then develop a reliable machine learning model to automate the process with high accuracy.





BAKER

HEART & DIABETES INSTITUTE

A member of
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Res
+ All

Cardiovascular Research (Baker Heart and Diabetes Institute)

Prof. David Greening 98

Prof. Peter Meikle 99

A/Prof. Tom Karagiannis, Dr Julia
Liang & Eleni Pitsillou 100

A/Prof. David Greening

Baker Heart and Diabetes Institute



3D cell culture



Cell culture - eukaryotes
incl. primary & cell lines



Bioinformatics



Light microscopy



Proteomics



Multi-omics



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Number of projects: 1

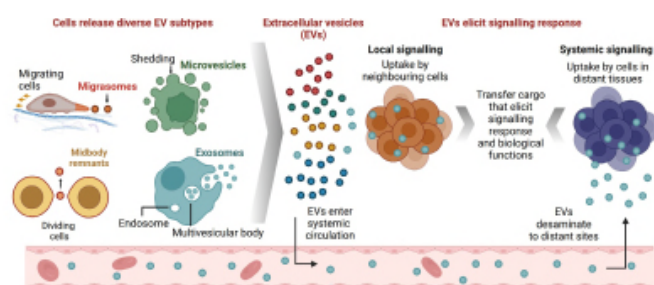
Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

Masters conversion: **Yes**

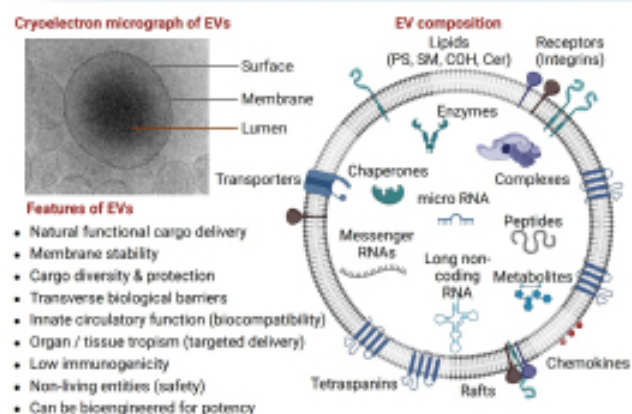
The Molecular Proteomics laboratory explores intercellular signalling and apply advanced omics in the context of the heart and circulation. Our research program seeks to understand cell signalling through nanovesicles as a therapeutic strategy and integrate multi-disciplinary technologies to understand cardiac remodelling and its repair. We develop advanced approaches to understand cell signaling through quantitative mass spectrometry and multi-omic technologies. Our research program has led to significant new knowledge in the molecular form and function of EVs, how they shape biology, and impact in therapeutic & clinical utility.

Our programs continue to shape how mass spectrometry is applied to understand complex biological systems, including human health and biology, spatial biology, and precision therapeutics. These studies have led to understanding the molecular landscape of the heart and circulation networks, phosphorylation signalling and spatial proteomics of the heart, and the focus on how signaling and targeting specific regulatory networks in complex conditions such as heart disease.



Key areas of ongoing research (projects will be tailored based on experience, interest, and scope):

- Leveraging multi-omics and machine learning strategies to decipher subcellular proteome of the heart
- Integrate multi-omics to define mechanisms of extracellular vesicle function in heart
- Sequential multi-omics to capture the molecular form of extracellular vesicles
- Building an omic atlas of the heart
- Understand circulating EV surfaceome as interactive, tissue-specific vascular platform
- Bioengineer extracellular vesicles for cardiovascular therapeutics
- Advances in transcription factor delivery for cardiac therapeutics
- Vascular function of human circulating extracellular vesicle subtypes



Prof. Peter Meikle

Baker Heart and Diabetes Institute



Animal handling



Data analysis



Cell culture - eukaryotes,
incl. primary & cell lines



Metabolomics (incl.
lipidomics)



Bioinformatics



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Number of projects: **4**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**

Dysregulation of lipid metabolism is a key contributor to numerous chronic diseases, including obesity, type 2 diabetes, cardiovascular disease, and age-related dementia.

Although lipid metabolic pathways are well characterised, the mechanisms by which environmental and genetic factors disrupt these pathways—particularly in the context of chronic disease—remain incompletely understood. The Metabolomics Laboratory using advanced tandem mass spectrometry has developed Australia's only high-throughput lipidomics platform and has conducted some of the largest clinical and population-based lipidomics studies to date. These studies have enhanced our understanding of lipid metabolic pathways and identified lipidomic biomarker profiles that improve the prediction of disease risk and therapeutic response. Importantly, these same metabolic pathways represent promising targets for interventions aimed at preventing, slowing, or treating major chronic diseases. Leveraging our state-of-the-art lipidomics capabilities, we are investigating the relationship between lipid metabolism and cardiometabolic disease. The translation of these findings into clinical practice has the potential to deliver novel diagnostic, risk assessment, and disease-monitoring tools, as well as innovative therapeutic strategies for the management of chronic disease.



We have a number of Honours/Masters/PhD projects available for 2027 in areas of lipid metabolism, mass spectrometry and bioinformatics. These include:

1. Characterising myeloperoxidase oxidation on lipids and lipoproteins. *Co-supervisor Dr Kevin Huynh*
2. Development and validation of a high throughput clinical lipidomics platform for Cardiovascular Risk Assessment. *Co-supervisor Dr Thomas Meikle*
3. Impact of milk bank processing on the donor milk lipidome. *Primary Supervisor Alexandra George*
4. Modulating Plasmalogens Lipids to protect the heart. *Primary Supervisor Yow Keat Tham*
5. Role of ether lipids in lymphocyte biology and function. *Primary Supervisor Sudip Paul*
6. Defining the lipidomic landscape across postnatal development and ageing. *Primary Supervisor Sudip Paul*

A/Prof. Tom Karagiannis, Dr. Julia Liang & Eleni Pitsillou Baker Heart and Diabetes Institute



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Number of projects: **3**

Full-time or part-time: **Full-time**

Feb or July start: **Feb only**

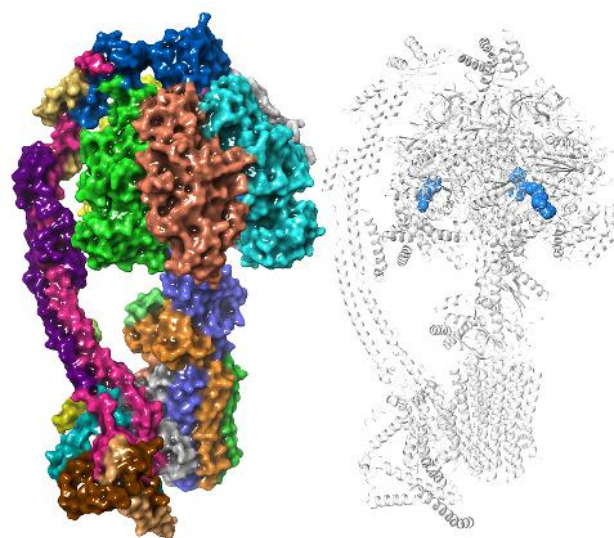
Masters conversion: **Yes**

Our lab investigates how dietary compounds may influence the molecular processes underlying lifestyle-related diseases. Using molecular modelling and other in silico techniques, we study the interactions between bioactive compounds, often derived from food or plants, and proteins involved in various physiological pathways. Students do not require coding experience for successful completion of these projects, and all work will be carried out using freely available software.

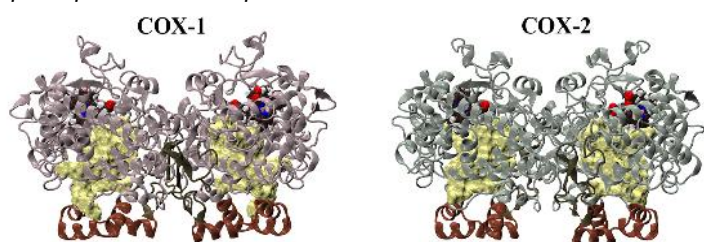
Project 1. Investigation of anti-inflammatory effects of dietary fatty acids using molecular modelling. Chronic inflammation plays a key role in the development and progression of cardiovascular disease. While omega-3 fatty acids are well-known for their anti-inflammatory effects, other dietary fatty acids may also play important roles. This project investigates how dietary fatty acids interact with cyclooxygenase (COX) and lipoxygenase (LOX), two enzymes involved in the synthesis of pro-inflammatory mediators such as prostaglandins and leukotrienes. Students will use molecular modelling and perform molecular docking to predict binding affinities and interactions.

*Project 2. In silico investigation of modulation of circadian rhythm proteins by passionflower compounds. Sleep and circadian rhythms are tightly regulated by core proteins such as CLOCK, BMAL1, PER, and CRY. Disruptions in these pathways are linked to mood disorders, metabolic issues, and cognitive decline. Passionflower (*Passiflora incarnata*), a traditional herbal remedy, has been associated with improved sleep and relaxation, possibly through modulation of circadian proteins. This project uses molecular modelling to explore interactions between passionflower-derived compounds and circadian rhythm-related proteins. Students will identify active compounds, build protein-ligand models, and evaluate binding using molecular docking.*

*Project 3. Computational investigation of saffron-derived compounds and their interaction with neurotransmitter proteins in brain health. Neurotransmitter proteins, such as GABA receptors and dopamine receptors are central to brain function and mental health. Saffron (*Crocus sativus*) has been used traditionally to support mood and cognition, with its therapeutic potential attributed to bioactive compounds. This project investigates how saffron-derived molecules interact with key neurotransmitter-related proteins using molecular docking techniques. Students will model 3D structures of both ligands and target proteins to explore potential neuroprotective mechanisms.*



Human ATP synthase (PDB ID: 8H9V)





**Cancer Medicine
(Olivia Newton-John
Cancer Research Institute)**

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Dr. Quentin Gouil

ONJCRI



Bioinformatics



**Chromosomal and/or
nucleotide extraction
assays**



**Cell culture - eukaryotes
incl. primary & cell lines**



Genetic sequencing



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Website: [click here](#)

Number of projects: **2**

Full-time or part-time: **Either**

Feb or July start: **Both**

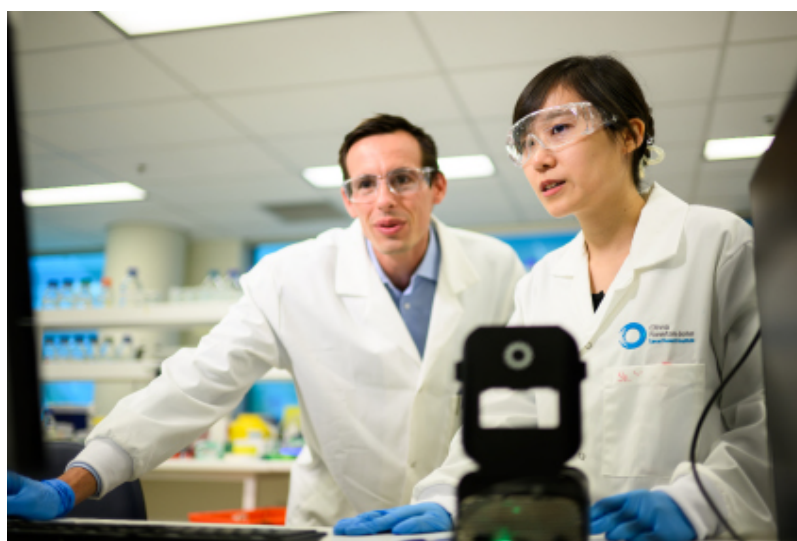
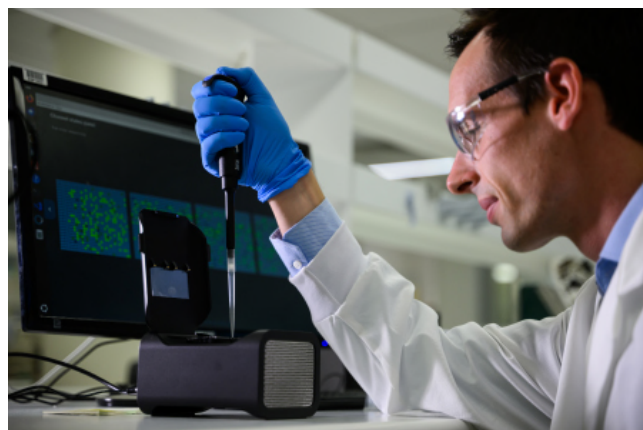
Masters conversion: **Yes**

The Health and Epigenomics Across Life (HEAL) lab is offering multiple placement opportunities in clinical genomics and bioinformatics.

We leverage the latest advances in genomic technologies, in particular long-read sequencing of DNA and RNA, to better understand gene regulation in health and disease. Some of our current interests are:

- Determining the genetic and epigenetic adaptations of cancer during metastasis
- Using epigenetic information to improve the accuracy of genetic diagnosis and risk prediction
- Using nanopore long-read sequencing to improve diagnosis of retinal disorders and brain tumours
- Developing bioinformatic tools to obtain a comprehensive description of the nucleic acids in our cells
- Using AI (genome language models) to model and understand genetic reprogramming in disease

The specific internship project will be adapted to the skills and motivation of the candidate.



Dr. Yi (David) Ju

ONJCRI



Animal handling



Cell culture - eukaryotes
incl. primary & cell lines



Cell transfection



Flow cytometry



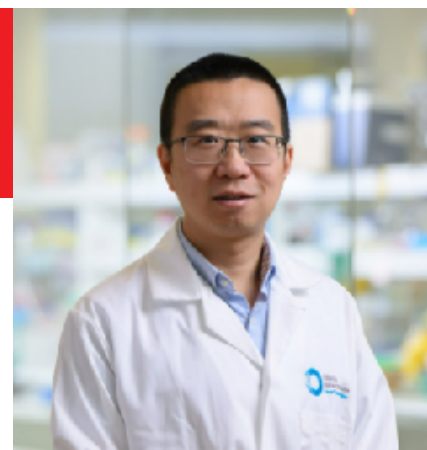
Gene expression analysis



Immunoassays



mRNA-lipid Nanoparticle
formulation



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Number of projects: **1 Feb, 1 Jul**

Full-time or part-time: **Full-time**

Feb or July start: **Both**

Masters conversion: **Yes**

Our lab focuses on designing cutting-edge nanoparticles—especially lipid nanoparticles (LNPs)—to safely and precisely deliver genetic medicines such as mRNA and siRNA into the body. We aim to solve key challenges in drug delivery by targeting specific immune cells while minimising off-target effects. We are also pioneering human blood-based models to better understand how these nanoparticles behave in realistic biological environments. Our work sits at the intersection of nanotechnology, immunology, and gene therapy, with a strong emphasis on translation to clinical applications in cancer and immune-related diseases.

Project 1. Targeting Nanoparticles to Specific Immune Cells. This project aims to design and test lipid nanoparticles that can home in on particular immune cell types, such as T cells, B cells, or monocytes. Students will use chemical conjugation strategies to attach targeting molecules to the nanoparticle surface and evaluate delivery efficiency using cell-based assays and flow cytometry. Co-supervisors: Dr Zhaoran Wang.

Project 2. Understanding Nanoparticle Behaviour in Human Blood. This project investigates how lipid nanoparticles interact with components of human blood, including plasma proteins and immune cells. Students will use fresh blood samples to study nanoparticle stability, immune recognition, and uptake, helping to uncover delivery barriers and safety issues. Co-supervisors: Dr Shiyao Li.

Both projects are based at the Olivia Newton-John Cancer Research Institute (ONJCRI) in Heidelberg and are available for a February or July 2026 start (full-time). Students will gain hands-on experience in nanoparticle formulation, mRNA delivery, flow cytometry, and working with human biospecimens—ideal preparation for future research or biotech careers.

Dr. Teresa Sadras ONJCRI



Cancer



Cell culture - eukaryotes
incl. primary & cell lines



Cell transfection



Flow cytometry



Gene expression analysis



Molecular cloning



Protein biochemistry



Genetic sequencing



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Number of projects: **1-2**

Full-time or part-time: **Full-time**

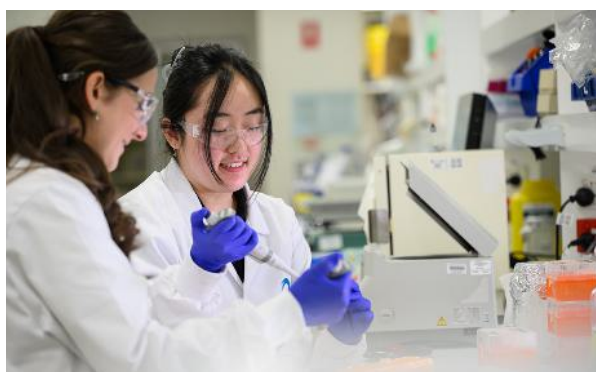
Feb or July start: **Both**

Masters conversion: **Yes**

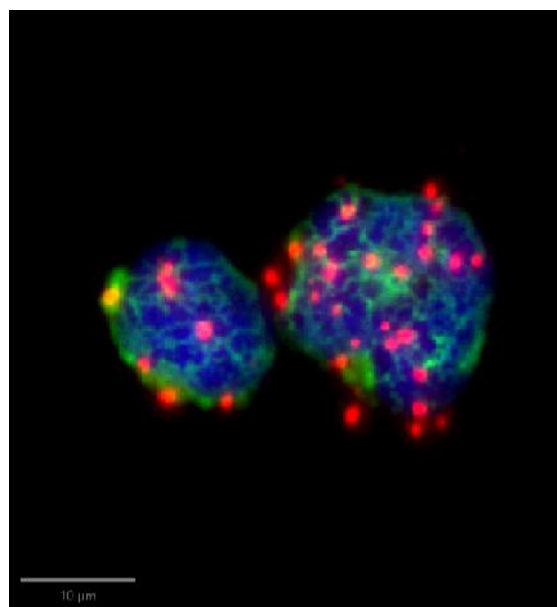
The Leukaemia Biology and Functional Genomics Laboratory investigates how genetic alterations transform normal blood cells into leukaemia and how leukaemia cells adapt to survive treatment. Acute lymphoblastic leukaemia (ALL) is the most common cancer diagnosed in children. Although treatment is successful for many patients, relapse remains difficult to treat and is a leading cause of cancer-related death in children and young adults. Our laboratory combines CRISPR genome engineering, functional genomic screening, molecular and cellular biology, proteomics and advanced sequencing to develop clinically relevant models of leukaemia and identify vulnerabilities that can be therapeutically targeted. We are particularly interested in understanding why some leukaemias resist immunotherapies such as CAR T-cell therapy, and how abnormal signalling proteins and oncogenic gene fusions drive leukaemia development. Students will join a collaborative and translational research environment and gain experience in mammalian cell culture, flow cytometry, CRISPR-Cas9 genome editing, molecular cloning, protein analysis and drug-response assays.

selected candidates promote resistance to CAR T-cell killing. The student will use CRISPR genome engineering to alter candidate genes in B-ALL cells and assess their effects on antigen expression, cell survival and response to CAR T cells.

Project 2. Mapping the protein interactions of an abnormal leukaemia receptor. The cytokine receptor CRLF2 normally has tightly restricted expression during blood-cell development but is abnormally activated or overexpressed in a high-risk subgroup of B-ALL, driving signalling that promotes leukaemia-cell growth and survival. However, the proteins that interact with CRLF2 in leukaemia remain poorly understood. This project will use proximity-labelling proteomics to define the CRLF2 protein interactome in B-ALL cells. The student will generate and validate CRLF2 constructs fused to a BioID proximity-labelling enzyme and use CRISPR-Cas9 genome editing to introduce the tag at the endogenous CRLF2 locus. Candidate interacting proteins identified by mass spectrometry will be validated and investigated for their roles in oncogenic signalling and leukaemia-cell survival.



Project 1. How do leukaemia cells escape CAR T-cell therapy? CD19-directed CAR T-cell therapy has transformed treatment for relapsed B-cell ALL. However, many patients eventually relapse. Some leukaemia cells lose or reduce CD19, becoming invisible to CAR T cells, while others retain CD19 but acquire alternative mechanisms that protect them from immune-mediated killing. Our laboratory has identified candidate genes and pathways altered in leukaemia cells following CD19-directed immunotherapy. This project will investigate how



**If you have any further questions please don't hesitate to email us
at sabehonours@latrobe.edu.au.
We look forward to seeing you in SABE!**

