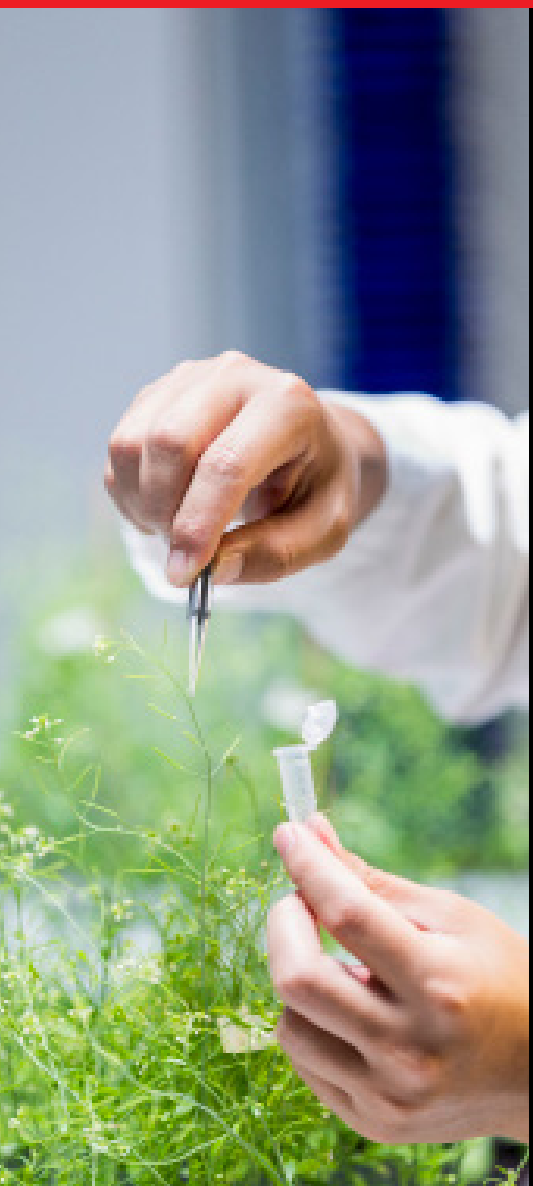
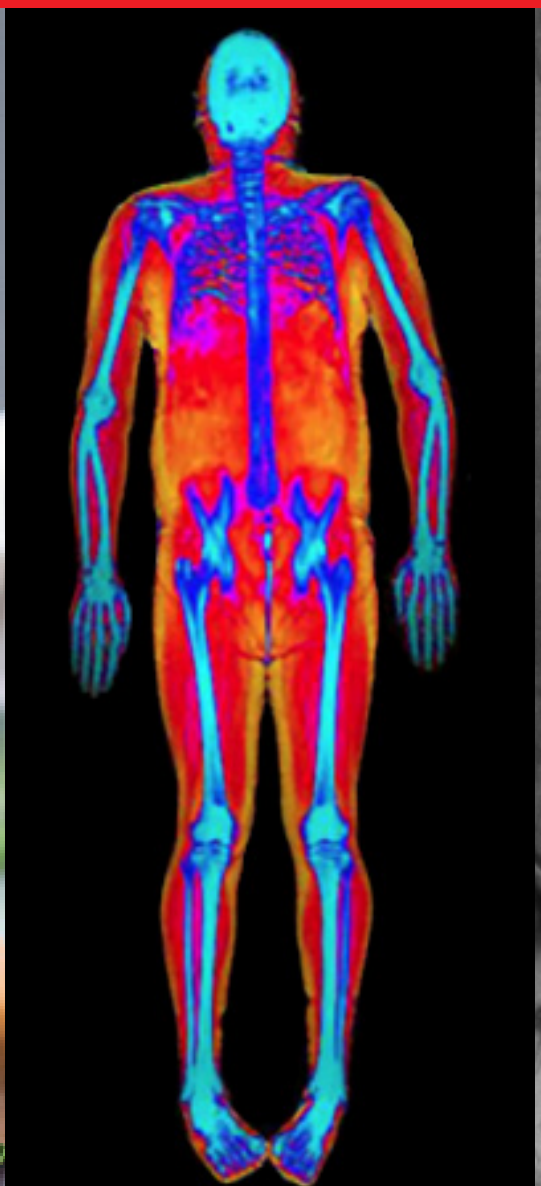
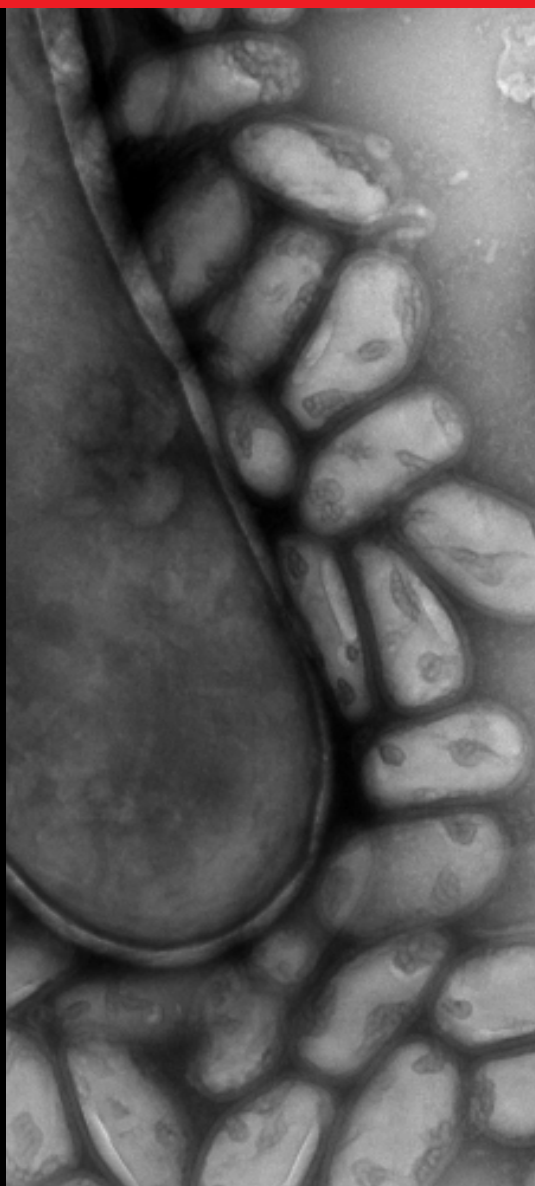
2026 Honours in the School of Agriculture, Biomedicine & Environment







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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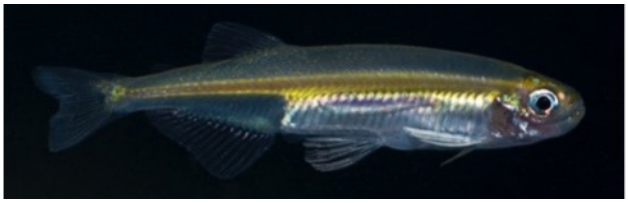

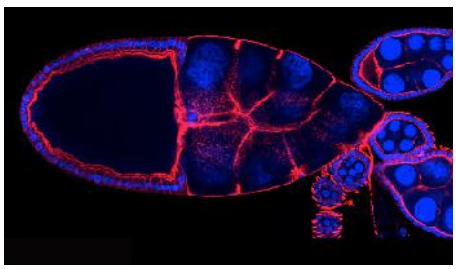

General Information

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 edge of known 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

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. Firstly, 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

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General information

What is Honours?

As an Honours student in our school, you will embark on a new set of adventures, very different to your undergraduate experience. 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 (SABE)?

Students who undertake Honours in SABE 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: learning to read and understand technical and scientific literature, evaluate published data and interpret your own results.
- Communication skills (both written and oral) required to present your research to scientific and generalist audiences.

What are the entry requirements for Honours in SABE?

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).
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

Note: 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 SABE offered?

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

- in February, concluding mid-November
- in 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 SABE 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 SABE 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.

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Scholarships and financial aid

La Trobe Access Scholarships

Honours is a very intense year, and it is often difficult for students to juggle their personal employment(s) and the time required for their research project. Access scholarships and bursaries are intended to support Australia students from all backgrounds to reach their potential at University. These are designed to support students who may have:

- Experienced financial difficulties
- Gone through personal hardship
- Come from a disadvantaged or underrepresented background.

All new and continuing La Trobe students are eligible to apply. Unfortunately, international students are not eligible.

Access scholarships are worth $5000 per year.

Bursaries are usually valued at a $1000 one-off payment.

- Richard Zann Bursary: Bursary of $3000. Available to Animal and Veterinary Biosciences (Honours) students who come from a rural area. Applications for Feb and Jul intakes due 10 October 2025.

Applications for Semester 1, 2026

Applications for Access Scholarships and Bursaries for Semester 1, 2026 are processed through VTAC:

- Applications open at the start of September and close at the start of October.
- Please see https://www.latrobe.edu.au/study/scholarships for dates and how to apply.

Applications for Semester 2, 2026

Applications for Access Scholarships and Bursaries for Semester 2, 2026 are processed by La Trobe scholarshops office:

- Applications open at the start of May and close at the start of July.
- Please see https://www.latrobe.edu.au/study/scholarships for dates and how to apply.

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 Memorial Scholarship: Award of $1000. Available for students with a research topic on the ecology of Australian fauna.

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.

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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 undertake further postdoctoral research, within Australia or overseas. Others, including those listed below, pursue diverse non-academic roles in industry, medicine, biotechnology and others:

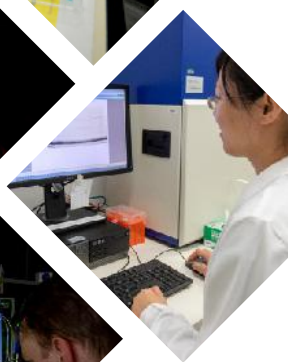
- Dr Nicole van der Weerden (Honours 2003, PhD 2007) is now the Chief Executive Officer of Hexima (a successful biotechnology company).
- David Bloomer (Honours 2012, PhD 2017) is also working in the biotechnology industry, within the recombinant proteins sector at CSL.
- Will Graf (Honours 2018) is now employed at the Police Forensics Laboratory.
- Stephanie Paone (Honours 2013, PhD 2018) works as Clinical Research Coordinator at Nucleus Network.
- Dr Luke Duncon (Honours, PhD 2017) works as a researcher at Bayer Crop Science.
- Dr Ellen Reid (PhD 2012) is a patent scientist at Jones Tulloch.









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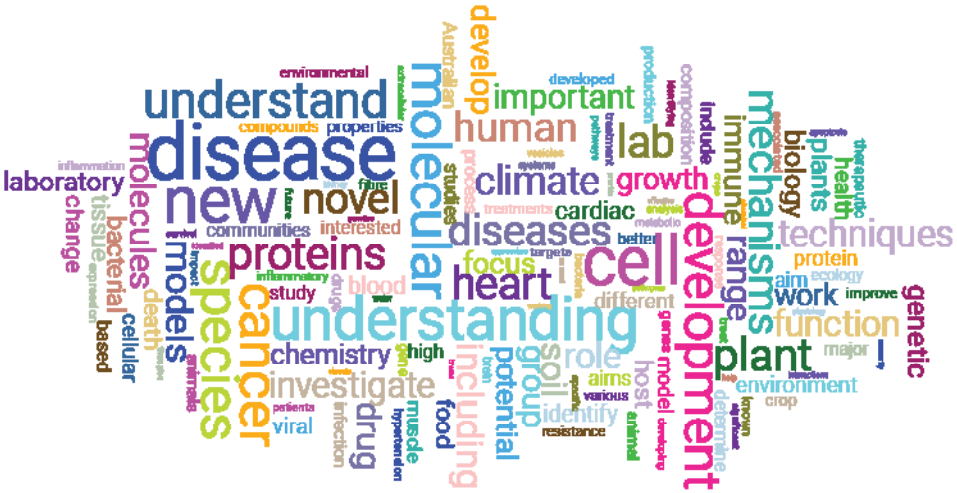
How do you choose a project?

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

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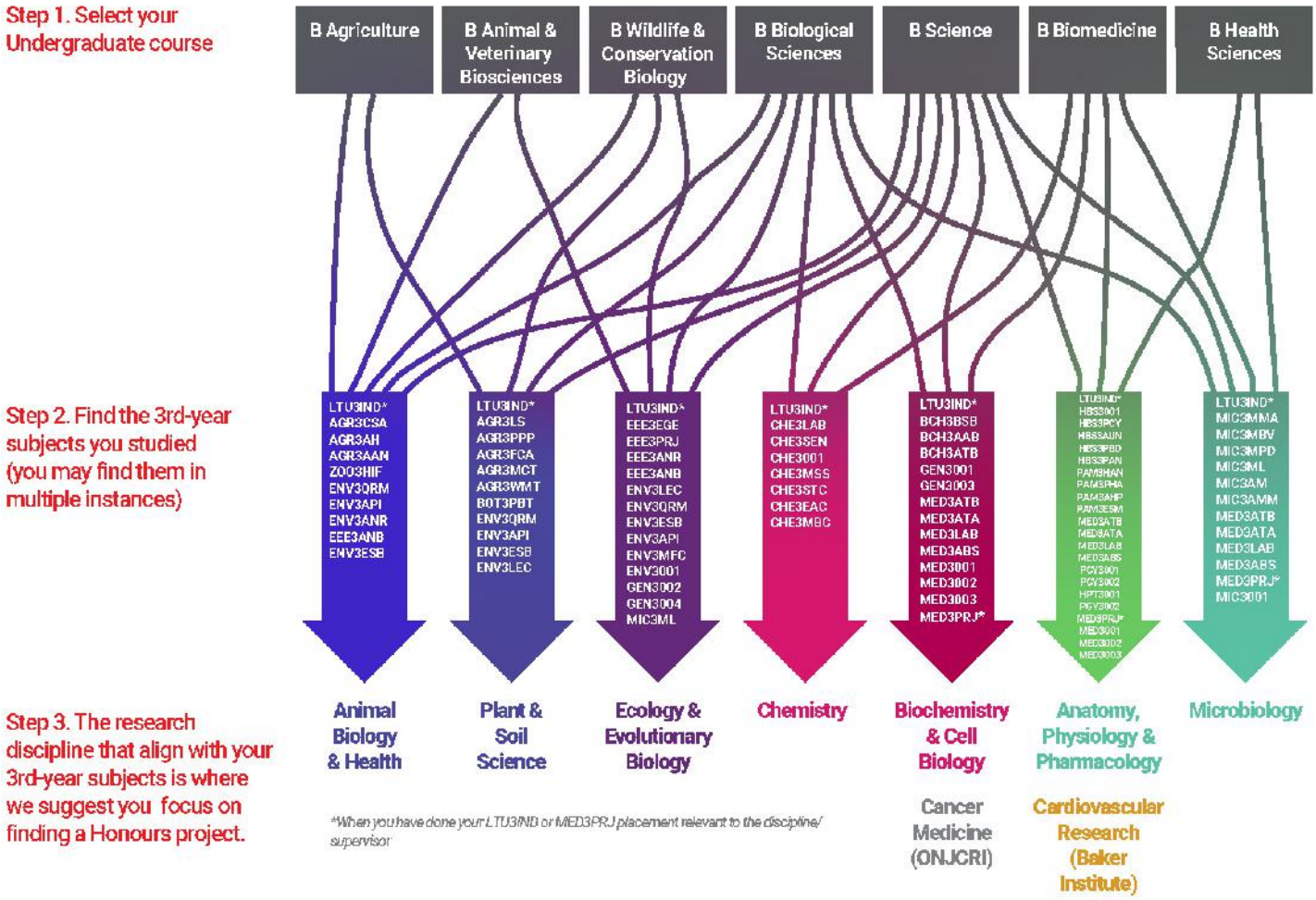
How to use this booklet to find your perfect project

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 expertisie/interest for multiple disciplines.**



Now you have a feel for the research disipline 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.

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Getting help

Need help finding a project?

Finding a research project and supervisor is the most critical part of the application process... but, this can also be an overwhelming experience for students. We have a lot of people ready to help you!

You can contact any of the following people through our SABE Honours email address: sabehonours@latrobe.edu.au

Dr. Keith White

SABE Honours coordinator

General SABE Honours enquiries, course & subject selection.

Dr. Brooke Huuskes

Microbiology, Anatomy, Physiology and Pharmacology Honours coordinator

Advice on Microbiology, Anatomy, Physiology & Pharmacology Honours projects.

Dr. Emma Grant

Biochemistry and Chemistry Honours coordinator

Advice on Biochemistry and Chemistry Honours projects.

Prof. David Wilson

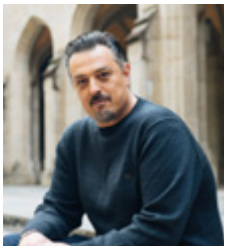
Biochemistry and Chemistry Honours coordinator

Advice on Biochemistry and Chemistry Honours projects.

Dr. Aleicia Holland

Ecology & Evolutionary Biology Honours coordinator

Advice on Ecology & Evolutionary Biology Honours projects.



Dr. Tom Karagiannis

Cardiovascular Research (Baker Institute) Honours advisor

Advice on Honours projects located at the Baker Institute.

Dr. Doug Fairlie

Biochemistry and Chemistry / Olivia Newton-John Cancer Research Institute Honours coordinator

Advice on Honours projects located at the Olivia Newton John Cancer Research Institute (ONJCRI)

Projects Available in 2026

SABE research disciplines

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Animal Biology & Health

Prof. Travis Beddoe
AgriBio

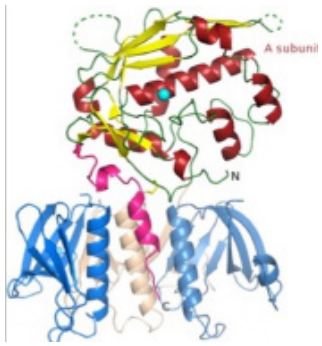
E-mail: t.beddoe@latrobe.edu.au
Website: click here

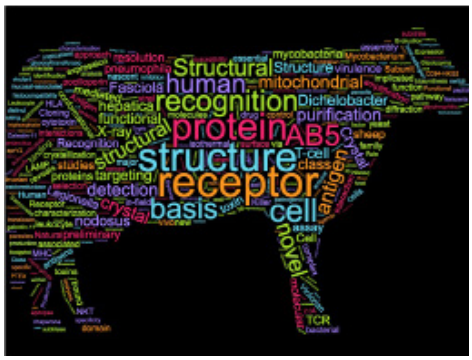
Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

- Bacterial overexpression of proteins
- Animal models of disease
- Protein biochemistry
- Molecular cloning
- PCR assays
- Immunoassays
- Protein purification

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. The Varroa–virus–honey bee disease complex is the most significant biological threat to global apiculture and pollination-dependent agriculture. The focus will be on interrupting virus transmission in honey bee colonies by targeting the Varroa destructor vectoring pathway and enhancing colony resilience through nutritional support. We will explore antiviral interventions, including the use of algae-based compounds or immune-priming additives, to disrupt virus replication and transmission via Varroa. Concurrently, we will evaluate the formulation and performance of artificial diets designed to support brood rearing during pollen scarcity. These diets will be tested under Australian environmental conditions for palatability, nutritional adequacy, and their ability to support colony health and reduce viral susceptibility.





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Dr. Lucille Chapuis
Bundoora

E-mail: l.chapuis@latrobe.edu.au
Website: click here

Number of projects: **1-2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Whole organism bioimaging
- Machine learning
- Animal behaviour studies
- Field work

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 and to use this knowledge to guide marine conservation.

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.

Project 2. Inner ear diversity in elasmobranch fishes. This project will investigate how sensory systems adapt to different marine lifestyles by focusing on the inner ear morphology of sharks, rays, and their relatives. Using high-resolution microCT scans, students will segment and reconstruct inner ear structures, then compare their shapes across species with contrasting ecologies and behaviours. The work will reveal how balance, hearing, and spatial orientation are shaped by evolution, and contribute to a broader understanding of sensory diversity in elasmobranchs.

Project 3. Nervous system and hearing structures in crustaceans. Although there is growing evidence that many crustaceans can both sense and generate sounds, the mechanisms remain poorly understood. This project will explore how crustaceans detect and produce sound by examining their central nervous systems and sound-producing organs. Using advanced microCT scanning and 3D segmentation, students will reconstruct these structures across several species and compare their anatomy.

Project 4. Machine learning for coral reef soundscapes. This project will apply advanced machine learning to long-term acoustic coral reef recordings to develop new ways of monitoring reef health. Student will design and train a deep learning model that combines convolutional neural networks (CNNs) with a structured sequence state-space model (S4) to extract both spectral and temporal features from reef soundscapes. This project is particularly suited to a student with strong interests in computer science, machine learning, or computational ecology, and could serve as a pathway into a Masters degree.

Supervision team can involve: Lucille Chapuis, Shaun Collin, Caroline Kerr and Travis Dutka.

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Prof. Shaun Collin
Bundoora

Whole organism bioimaging (CT)

Microscopy - electron, light

Field work

Animal handling

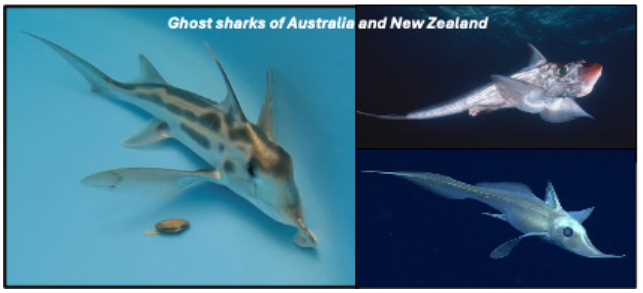
Histology

E-mail: s.collin@latrobe.edu.au
Website: click here

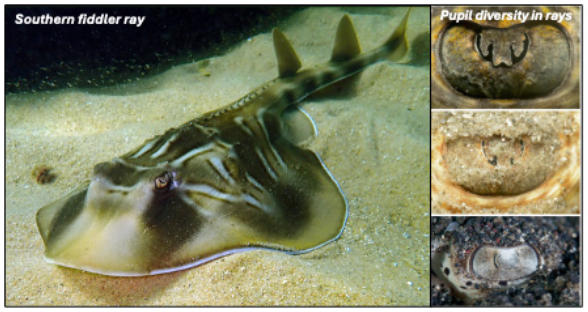
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

The 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 and Caroline Kerr.

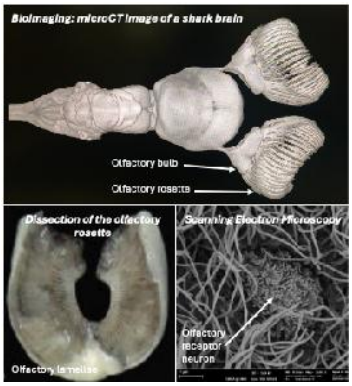
Project 1. Chemoreception in ghost sharks.This project explores how ghost sharks, a little-known group of deep-sea cartilaginous fishes, use smell (olfaction) and taste (gustation) to survive. Occupying different depth ranges, they use chemical cues to find (and digest) food, avoid predation, find reproductive partners and migrate over long distances. Preserved specimens of different species will be studied using microscopy, immunohistochemistry, and bioimaging techniques (microCT) to predict the relative importance of chemoreceptive sensitivity. The results will ultimately assist in assessing the vulnerability of these species to chemical pollutants. This project provides a rare opportunity to study the biology of deep-sea animals and develop practical skills in laboratory imaging and analysis.



Project 2. Visual adaptations in fiddler rays. Fiddler rays are bottom-dwelling cartilaginous fishes that rely on different senses to survive in their sandy habitats. This project investigates how their visual system is adapted for life on the seafloor and how vision compares in importance to other senses. Using microscopy, bioimaging (microCT), and possibly 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 insight into how early marine vertebrates process visual information and how they may cope with future environmental change.



Project 3. Ecotoxicological impacts on sensory systems in fishes Pollutants pose an important environmental risk to fish life, including their ability to feed, avoid predators and reproduce. This project will investigate how different species of fish process olfactory (smell) and gustatory (taste) stimuli and how this may be impacted by ecotoxicants. The sensory organs of preserved specimens will be studied using microscopy, immunohistochemistry and bioimaging techniques. The project provides insights into how human impacts disrupt sensory processing, while offering valuable laboratory experience and conservation relevance.



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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: **1**
Full-time or part-time: **Either**
Feb or July start: **July only**
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.

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A/Prof. Richard Peters
Bundoora

Animal behaviour studies

Robotics

Field work

Animal handling

E-mail: richard.peters@latrobe.edu.au
Website: click here

Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

We are seeking a motivated student to join a unique behavioural ecology project investigating how animals use visual signals to defend key resources. The focus is the Qinghai toad-headed agama (Phrynocephalus vlangalii), a dragon lizard native to China, which uses tail displays to compete for burrows. While these movements likely reflect an individual's quality, little is known about how signal structure influences contest outcomes—either in this species or across dragon lizards more broadly.

Project 1. Robotic Lizards & Signalling in Dragon Lizards. This project will involve designing and building robotic lizards to experimentally test how motion signals relate to signaller quality. The successful applicant will help develop these tools and conduct playback experiments in the field in China, in collaboration with Prof Yin Qi at the Chengdu Institute of Biology. Fieldwork is scheduled for mid-2026 at the Xiaman Conservation Station in the Zoige Wetland Reserve of NW China. This is a great opportunity to develop skills in animal behaviour, bio-robotics, and experimental design in an international research setting.

Left: Xiaman Conservation Station within the Zoige Wetland Nature Reserve. *Middle*: *Phynocephalus vlangalii* lizard at their burrow. *Right*: Tail coiling display by male lizard, which is used to defend resources, including burrows.

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Plant & Soil Science

Dr. Ali Bajwa
AgriBio

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Number of projects: **3**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Light microscopy
- Plant phenotyping
- Glasshouse work
- Bioinformatics
- Gene expression analyses
- Metabolomics
- Analytical skills
- Industry experience

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 form 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.

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A/Prof. Berin Boughton
AgriBio

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Number of projects: **3**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

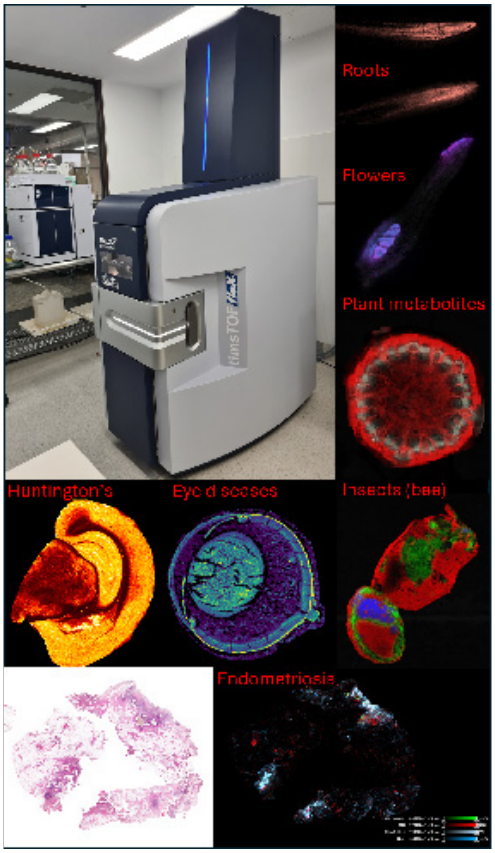
- Mass Spectrometry Imaging
- Animal models of disease
- Bioinformatics
- Chemical synthesis - organic
- Proteomics & Metabolomics

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. 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 localized 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.

Project 2. Synthesis and development of novel bio-orthogonal charge-tag ion mobility probes. This project will develop cutting-edge biorthogonal labelling strategies to spatially measure biomolecules, including turnover in vivo, by synthesizing modular chemical probes. These probes will be validated by mapping the distribution of specific metabolites and newly synthesized proteins using 2022 Nobel Prize winning Click Chemistry techniques in plant and mammalian systems. Ability to identify newly synthesized proteins and specific metabolites spatially will provide new insights into how cells and tissues respond to stress, critical to many pathological conditions.

Project 3. Exploring spatial metabolite fluxes in Huntington's disease mouse model. Spatial and temporal complexity are at the forefront of challenges to our understanding of eukaryotic metabolism under both normal and pathological conditions. Understanding the flux of biomolecules, including lipids, through metabolic pathways in vivo is essential to understand key aspects of biology. This project will map lipid changes in Huntington's disease at high spatial resolution by decoding stable isotope labelling of lipid species within the brain providing new insights into the pathophysiology of neurodegenerative conditions.



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Prof. Phil Brewer
AgriBio

- Molecular cloning
- Bioinformatics
- Genetic sequencing
- Plant molecular biology
- PCR assays
- Gene expression analyses
- Chromosomal and/or nucleotide extraction assays

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Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

When crop plants spend more effort dealing with stress, they put less effort into growing. This can put breeders and growers in a difficult situation to decide between crop varieties that provide high resilience or high yield. But we need both, especially as soil and climate conditions worsen in future. One problem is that the interactions between plant hormones involved in growth and defence are very complex. Genetically altering crops for growth can lead to confounding results in defence, and vice versa. This can be very difficult to untangle in breeding. In addition, breeders may seek to genetically alter hormone pathways to produce a trait, such as shorter crops, but the plant hormones that regulate crop height also influence defence and other traits in complex ways. Understanding the complex relationships between defence and growth hormones may unlock new ways to develop hyper-efficient and resilient crops.

The world's most productive crop just got shorter. Bayer Crop Science USA have released new short corn cultivars developed using gene silencing technology. Short stature crops are easier to manage and are less prone to falling over in wind or drought (lodging). Now, Bayer is partnering with La Trobe University to better understand how plant hormones regulate crop height, which will help refine short corn genetics, which also relates to other crops like sorghum and tomato.

Project 1. Find combinations of plant hormones and inhibitors that provide unique growth and defence benefits using one of our model crop species. Examine the effects on biomass, plant architecture and antioxidants. Research may extend into gene expression responses and disease tolerance.

Project 2. Develop a synthetic gene switch that turns on growth and/or defence at the same time. Building on successful international research, develop similar results in one of our model crop species.

Project 3. Find combinations of plant hormones and inhibitors that provide unique height benefits using one of our model crop species. Examine the effects on height and other traits such as branching. Research may extend into gene expression responses.

Project 4. Develop a synthetic gene switch that represses plant height at a specific time to create a super compact crop. Building on successful research from overseas, develop similar results in one of our model crop species

These projects may involve collaborations with the ARC Centre for Plants4Space, industry partners and other research organisations. he world's most productive crop just got shorter. Bayer Crop Science USA have released new short corn cultivars developed using gene silencing technology. Short stature crops are easier to manage and are less prone to falling over in wind or drought (lodging). Now, Bayer is partnering with La Trobe University to better understand how plant hormones regulate crop height, which will help refine short corn genetics, which also relates to other crops like sorghum and tomato.

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A/Prof. Marisa Collins
AgriBio

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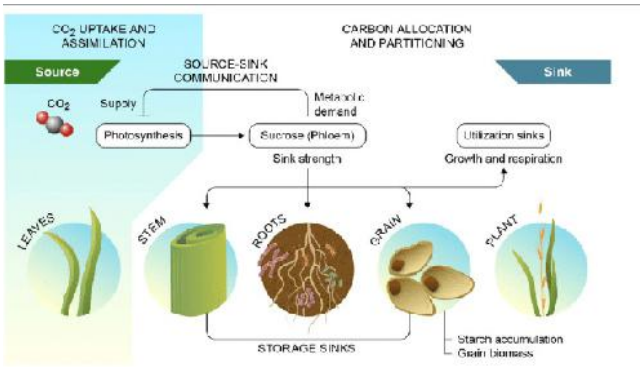
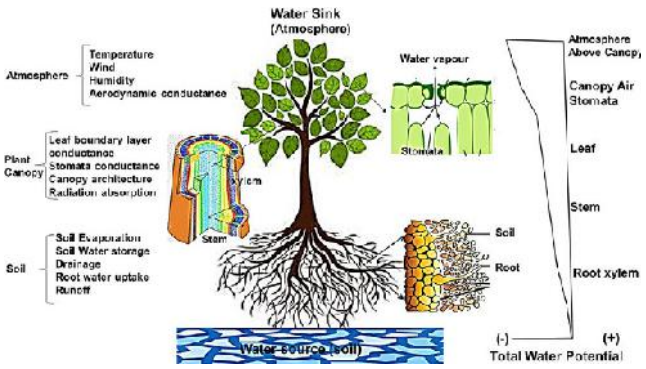
Number of projects: **3**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

Field work

Crop physiology

Glasshouse work





Our research aims to improve crop productivity under challenging conditions by examining drivers of yield and sensitivity of crop species to abiotic stressors such as high temperatures and drought.

Research theme 1. Climate change. In legume crops (also known as pulses such as chickpea, lentils, mungbean and fababean) we investigate and develop understanding of the tolerance sensitivity to high temperatures, drought and interactions between heat/and drought that are likely to impact production under future climate conditions. This research allows identification of useful traits for increasing stress tolerance and yield stability in new varieties and particularly legume crops which generally perform poorly under stress. Understanding crop physiology, or the way crops interact with environment also enables us to build crop models that can directly examine the predicted impacts and risks associated with climate change on future crop production in Australia.

Project title 1. Does foliar potassium (K) improve yield and drought tolerance of major legume crops in Australia?

Project title 2. Can we improve yield in legume crops through better understanding of factors affecting flowering and pod-set?

Research theme 2. Improving global food systems. Global food systems will need to almost double their yield to feed the projected global population in 2050. To meet this challenge, we need to substantially increase production and consumption of healthy and sustainable alternative proteins, such as those from legume crops. Legumes have the potential to deliver food ingredients which support a healthy balanced diet and contribute to a reduced demand on foods from animal origins. In Australia, legume seed yield improvement has traditionally focussed on disease resistance and herbicide tolerance rather than nutritional traits such as protein content. Protein abundance and composition is known to differ between species and is variably impacted by stress conditions. What determines the flux of metabolism between protein, carbohydrates (starch and dietary fibre) and other nutrients in legume grains and how this is influenced by growing environments is mostly uncharacterised. The project will select germplasm to begin preliminary assessment of these traits in legume crops as a pathway towards attempting to address some of these knowledge gaps

Project 1. To assess the suitability of existing legume germplasm for development of plant-based protein production in Australia. This will focus on preliminary investigation into the impact of environmental conditions on protein and carbohydrate dynamics in legume seed.

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A/Prof. Monika Doblin
AgriBio

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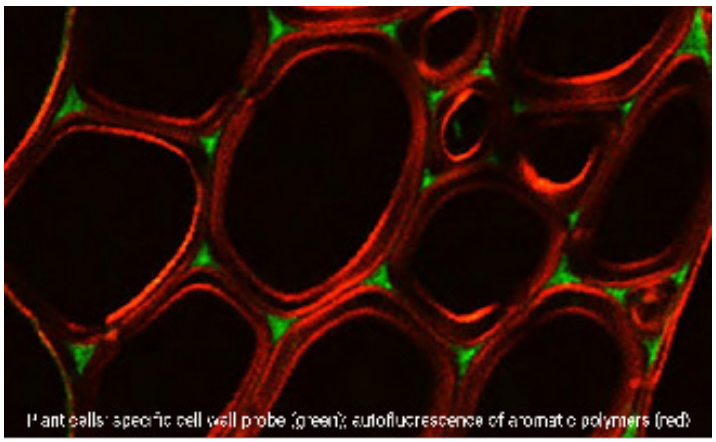
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Microscopy - light, confocal and super resolution fluorescence
- PCR assays
- Gene expression analyses (incl. PCR, qPCR)
- Molecular modelling
- Protein biochemistry (SDS-PAGE, western blotting)
- Molecular cloning and CRISPR-Cas9 gene editing

The Plant Cell Walls and Bioactive Secondary Metabolite Group investigates how biopolymers and specialised metabolites are produced and regulated. These carbon-rich molecules—key to biomaterials, food, and medicine—are among the most abundant and renewable resources on Earth. By understanding how bioactive levels are controlled, we aim to breed plants with tailored traits for specific uses. Our group is part of the ARC Protected Cropping Hub, which aims to enhance the production and quality of horticultural and medicinal crops in an indoor setting.

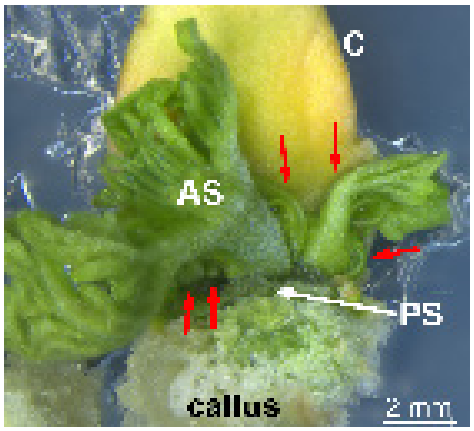
Most plant biomass is made up of carbohydrate-rich cell walls, a major carbon sink and renewable resource that influences the quality and quantity of plant-based products (food, fibre, fuel). Primary cell walls provide soluble dietary fibre, vital for human health. Secondary cell walls form insoluble fibre used in textiles, paper, timber, and increasingly in biofuels and biocomposites. Understanding their composition and mechanics enables us to engineer 'designer walls' using biotechnology tools such as genetic transformation and gene editing.

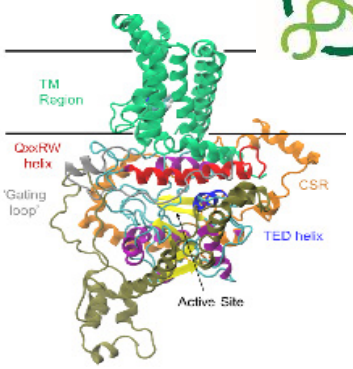
Project 1. Dietary Fibre for Human Health. Mixed linkage glucan (MLG), a key soluble fibre in cereals, varies in solubility—higher in oats and barley than wheat. This project explores how MLG production and solubility is regulated, aiming to boost its levels and solubility in wheat via biotechnology approaches.



Project 2. Plant Synthetic Biology (in partnership with the PSBA Victoria node). Transient gene expression using Agrobacterium is a fast, cost-effective method for gene function analysis. This project will develop and optimise transient expression systems for monocots and/or medicinal plants, enabling rapid gene screening and synthetic biology applications. Additional projects may involve designing new plant gene circuits. These projects integrate biotechnology (plant transformation including CRISPR), genetics, molecular biology (cloning, PCR), biochemistry (assays), and cell biology (microscopy).

PLANT SYNBIO AUSTRALIA





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Dr. Peter Dracatos
AgriBio

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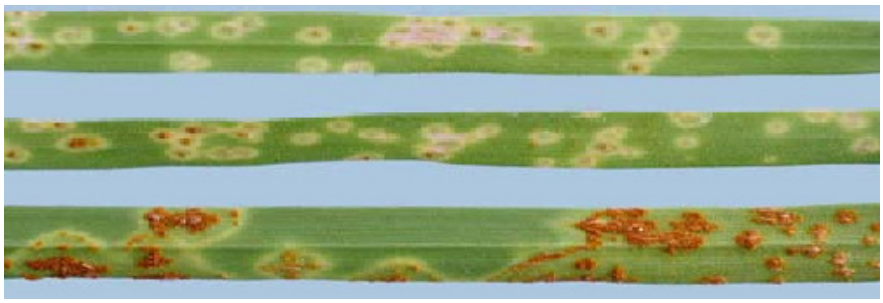
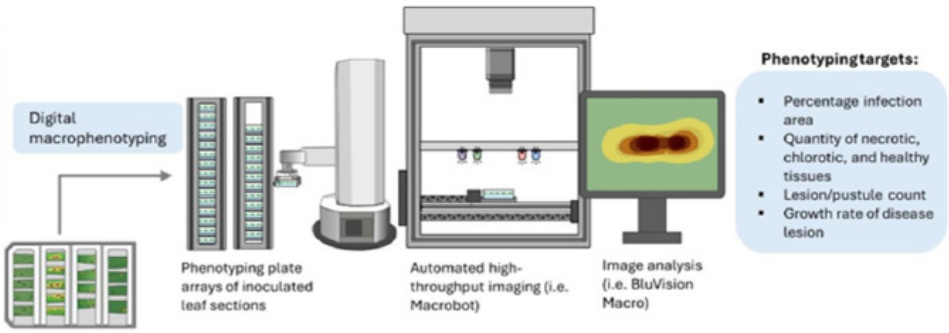
- Plant genetics
- AI-based image analysis
- Genetic sequencing
- Plant pathology
- Bioinformatics
- Digital agriculture

Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

The cereal disease lab at La Trobe University focusses on the identification and genetic characterisation of fungal disease resistance in economically significant grain crops to Australia. The research we do uses an intregrated approach utilising digital agriculture/AI, plant genetics and the latest genomic technologies to unravel the molecular basis of genetic resistance to foliar fungal diseases. More recently the Dracatos lab has implemented and optimised a digital phenotyping method to accurately measure and quantify disease response at different time-points after the pathogen has colonised the host plant. This has also involved the development of image analysis modules based on using AI and machine learning in collaboration with colleagues from computer sciences that are specific to different types of fungal diseases.

The honours project being offered is to identify the genetic basis of rust resistance in four different durum wheat (the wheat species used to make pasta) biparental (resistant x susceptible) populations. By identifying the chromosomal location of the respective resistance genes we can determine if they are known or represent new widely effective resistance genes. The project will benefit from the availability of the robotic phenotyping platform mentioned above and the recent release of a chromosome-scale reference genome for durum pasta wheat.





The skills acquired during the project include but are not limited to:

1. Plant pathology
2. Molecular and quantitative genetics
3. Digital agriculture and image analysis/AI
4. Fluorescence microscopy
5. Gene Expression/bioinformatics

Major outcomes for the project are to develop closely linked diagnostic markers that can be used by Australian breeding companies to track the resistance in breeding programs that will ultimately enhance food security.

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A/Prof. Kim Johnson
AgriBio

Plant physiology

Light microscopy

Gene expression analyses

Metabolomics

PCR assays

Molecular cloning

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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 bio-resource 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 soil compaction tolerance mechanisms of native grasses. 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:shoot biomass and nutrient allocation in response to different soil types and compaction levels to attempt to uncover the mechanisms by which kangaroo grass tolerates challenging environments.

Project 2. Optimizing food quality traits in protected cropping environments. With increasing environmental challenges from climate uncertainty, farmers are moving towards Protected Cropping systems for food production. Protected Cropping has potential to produce quality foods and higher yields more reliably with fewer inputs (e.g., water, fertilizer) in shorter time frames. PC systems currently use simple light and temperatures regimes and the potential for varying to improve growth remains largely unexplored. Fine-tuning environmental inputs throughout development can reduce production (energy and resource) costs and enhance traits that increase market value. This project aims to modify environmental conditions, such as temperature, light and nutrient supply, to induce mild stress pre-harvest and determine the influence on fruit quality in tomato, strawberry or lettuce. The impact on biomass, metabolite production (such as antioxidants and phenolics) and nutrient levels will be investigated.

Project 3. Developing an engaging educational STEM experience for secondary and undergraduate students Plants for Space is a national research program that includes an education and engagement initiative to engage K-12 teachers and students, tertiary students and the public and showcase the opportunities and career paths in Agriculture, Food and Space. Education initiatives include hands on, authentic experiences aligned to curriculum and P4S research. This project will design, test and assess a hands-on experiment for a secondary school student in/excursion that can also be adapted as a practical for a third year plant science subject. This project will explore how students felt about the activity and try to understand the influence on attitudes towards STEM, learning and understanding of the P4S topic, career aspirations, language and identity.

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Prof. Mathew Lewsey
AgriBio

Gene expression analyses

PCR assays

Plant development analysis

Light microscopy

Bioinformatics

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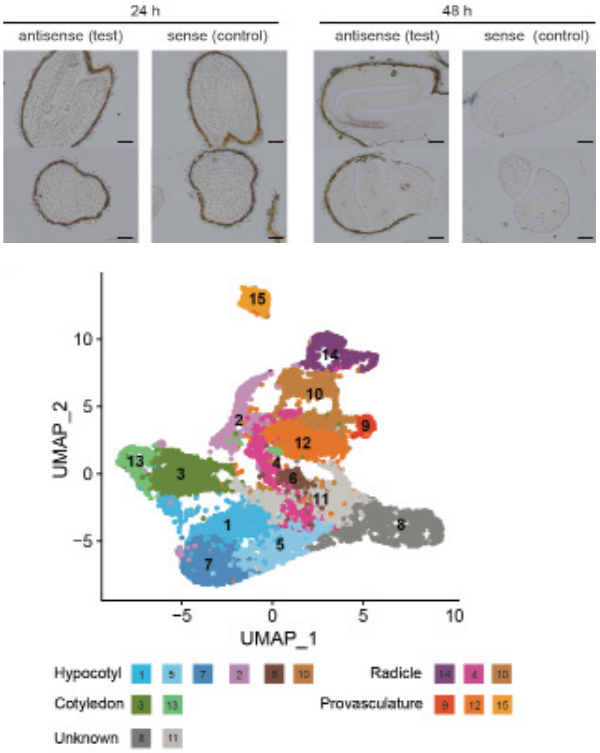
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

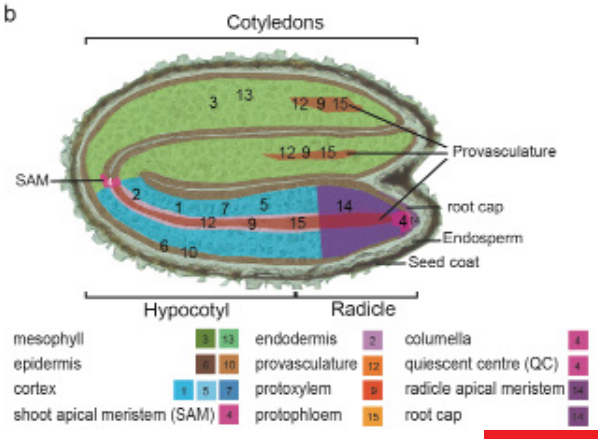
My lab studies how plants perceive the world around them and interact with their environments by regulation of their genomes. We apply this work with commercial partners who grow a range of agricultural crops including cannabis, opium poppies, barley, oats and peas. In a project co-supervised with senior 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 comfirm 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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Dr. Dugald Reid
AgriBio

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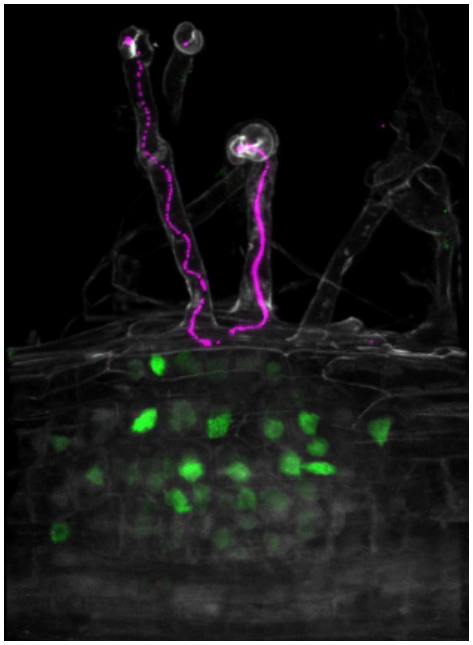
Number of projects: **1 Feb, 1 Jul**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Bioinformatics
- Plant phenotyping
- CRISPR-Cas9 gene editing of cells
- Gene expression analyses
- Molecular cloning



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.

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A/Prof. Penelope Smith
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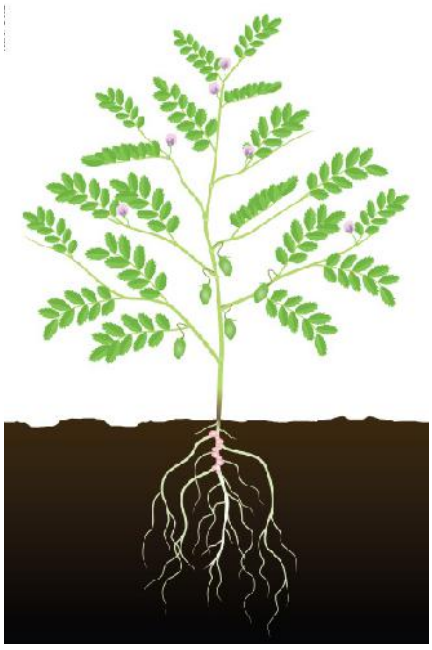
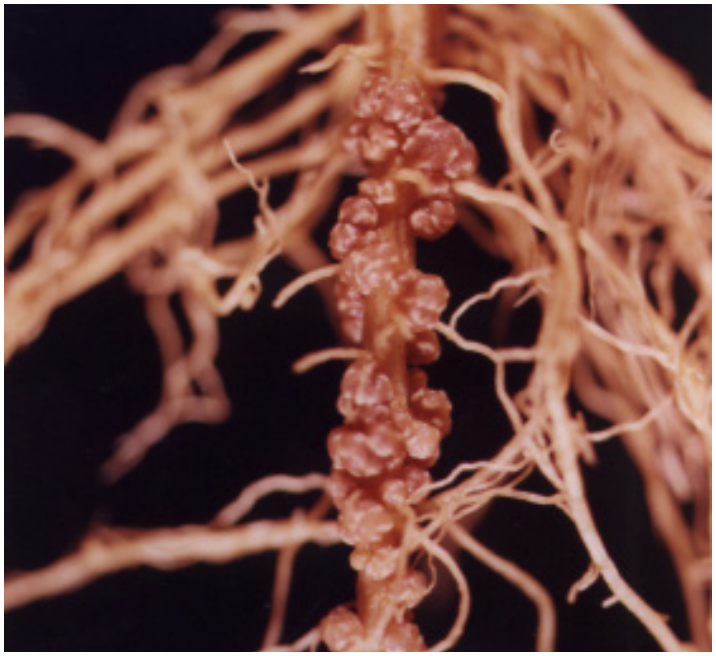
Number of projects: **1**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Plant transformation
- Molecular cloning (e.g. expression vectors)
- Gene expression analyses
- Bioinformatics
- Cell culture - eukaryotes, incl. primary and cell lines

With the world's population increasing we need to produce more food sustainably, without contributing to global warming and other environmental problems. Agriculture relies on nitrogen fertilizers that are chemically synthesized and production requires lots of energy which is expensive and contributes to carbon emissions and global warming. When applied in excess these fertilizers can also pollute waterways. An alternative to use of N fertilizers is to harness biological nitrogen fixation (BNF) involving microbes that can fix nitrogen from the atmosphere. Legume crops can form a symbiosis with rhizobia bacteria which fix N and provide it to the plant reducing its requirement for N fertilizer. Some of the fixed N is also left in the soil reducing the need for fertilizers in subsequent non-legume crops. As part of the symbiosis a new organ called a nodule develops on roots to house the rhizobia and the rhizobia are enclosed in a membrane in infected cells in these nodule.





Project 1. Characterizing transporters and regulatory proteins essential for N fixation. In exchange for fixed N the plant provides a range of nutrients to the rhizobia. My group is investigating the transport of nutrients to rhizobia and its regulation. This project will use new single cell transcriptomic data to identify transporters or regulatory proteins in infected nodule cells. They will then be characterised using knockouts in transgenic root systems, real-time PCR and expression in yeast.

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Prof. Caixian Tang
AgriBio

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Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

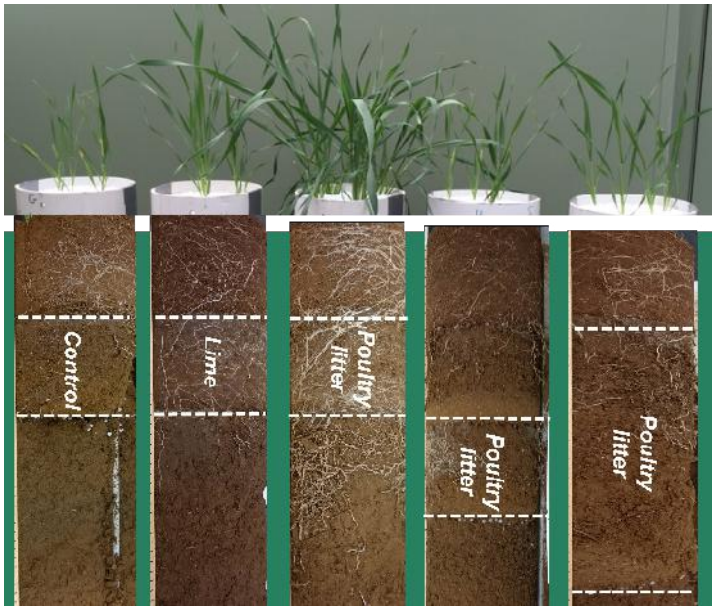
- Soil management
- Analytical skills
- Industry experience
- Glasshouse trials

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. 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.

Projects 2. Comparing the effectiveness of new fertilizer types: associated with industry Incitec Pivot Fertilizers. The project compares the performance and efficiency of fertiliser products (slow released, controlled released coated fertilisers), examines the effects of microbiological stimulants on their effectiveness, and understand how the fertiliser products affect soil properties and crop nutrient uptake. Controlled-environment studies will be conducted. Plant growth, physiological responses, plant nutrient concentration, soil properties, and fertilizer-use efficiency will be determined.

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.



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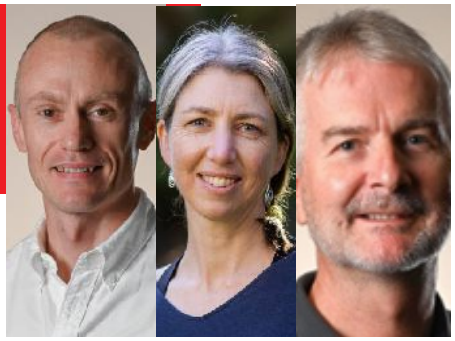
ARC Center of Excellence - Plants for Space (AgriBio)



- 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

PLANTS FOR SPACE
ARC CENTRE OF EXCELLENCE

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Number of projects: **2**
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. Current crop varieties that are ultra compact and short often exhibit defects in cell wall structure and vascular development, leading to warped leaves and impaired water use. The impact of these traits on overall productivity remains unclear. This project will investigate how cell walls and vascular tissues are essential for optimal plant function. Insights gained will support alternative strategies to reduce plant height by modifying cell wall architecture, while maintaining or enhancing nutrient and water transport, stress resilience, growth, and yield.

Project 2. The balance of hormones plays a critical role in regulating plant height. While our understanding of individual hormone signalling pathways has advanced significantly in recent years, a major unresolved question is how these pathways interact. Alterations in hormone levels that reduce plant height often lead to side effects—some beneficial, others detrimental. This project aims to deepen our understanding of the hormonal regulation of plant height with the goal of designing more compact crop varieties that maintain optimal performance.

Project 3. Plant hormone balance coordinates stress and growth responses, yet the interplay between hormonal pathways - particularly the antagonism between defence and growth - is still poorly understood. A central biological question is whether these pathways can be uncoupled to sustain robust stress responses without compromising growth and yield. This project seeks to unravel the mechanisms underlying hormone crosstalk to inform strategies for optimising plant productivity.

Project 4. Metabolic responses to stress in plant cells share notable similarities with those in animal cells, particularly under extreme conditions such as space environments, where both plants and astronauts face elevated stress and radiation exposure. In these contexts, enhanced antioxidant production may be vital for the health and resilience of both crop plants and humans. This project will investigate key aspects of oxidative stress and antioxidant biosynthesis in plants, with the aim of identifying mechanisms that support crop performance and contribute to broader applications in human health.

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Ecology & Evolutionary Biology

Dr. Charles Feigin
Bundoora

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Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

- Genetic sequencing
- Light microscopy
- Animal handling
- Bioinformatics
- Histology
- Chromosomal and/or nucleotide extraction assays

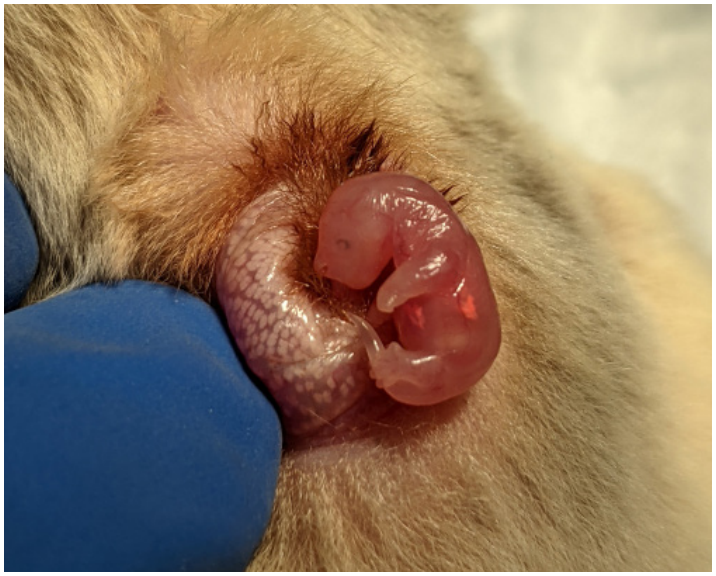
My lab aims to clarify the role of molecular and developmental mechanisms in shaping trait diversity. DNA encodes the information that underpins the 'endless forms' of biodiversity on our planet. In animals, the critical stages of embryonic and juvenile development are where much of these genetic instructions are realized, leading to the formation of adaptive traits. However, genes do not function in isolation. The effects of genetic variation are heavily influenced by the dynamic molecular interactions in which they are involved. To fully explain animal diversity, modern evolutionary theory must incorporate the mechanisms that link genotypic changes to their phenotypic outcomes during development.

In the Developmental Evolution Group, we harness the remarkable diversity of non-traditional model species to explore how the structure of developmental programs shapes patterns and biases in trait variation across the tree of life. Our research delves into the formation of adaptive traits using a variety of techniques, including functional genomics, imaging, and in vitro and in vivo manipulations. We place our findings within an evolutionary context through comparative studies at the genomic, developmental and phenotypic levels. To support this work, we train new lab members to be proficient in both wet lab techniques and basic computational skills.

Current research in our lab includes:

- The genomic and developmental basis of skin traits
- Evolutionary drivers of morphological stasis in 'living fossils'
- Control of diapause, DNA repair, and embryonic survival

Students have the opportunity to work on projects involving marsupial or arthropod models, with options for both wet lab and/or computational approaches. In 2026 we are especially keen to attract students interested in comparative development and genomics. Our lab also collaborates with the Melbourne-based Thylacine Integrated Genetic Restoration Research (TIGRR) Lab, with co-supervision opportunities available for projects related to conservation genetics and biotechnology in marsupials.



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Dr. Shannon Hedtke
Bundoora

E-mail: s.hedtke@latrobe.edu.au
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Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

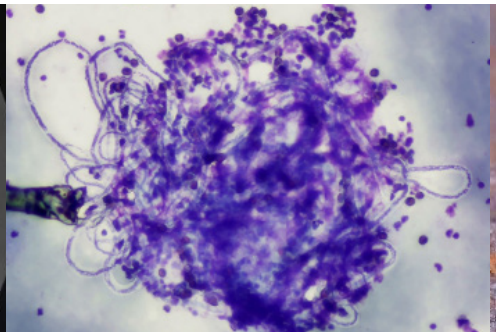
Genetic sequencing

Molecular modelling

Bioinformatics

PCR assays

Light microscopy



The vision of our group is to develop molecular, genomic, and modelling tools to aid in the elimination of parasitic diseases worldwide. In communities affected by parasites, drugs are distributed to all people to disrupt parasite transmission and thus stop people from being infected. However, persistent parasite infection continues in many areas despite the use of multiple drugs. Elimination of these diseases is possible only if the reasons for continuing infection are identified; whether it's because of evolution of drug resistance, re-introduction of new infection, or inadequate monitoring protocols. 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: The mosquito-borne disease 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 (Wuchereria bancrofti) 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 sequencing the microscopic larvae to determine whether there is evolution of multidrug resistance, whether people from the same household are more likely to be infected (local transmission), or whether people spread the parasite when they travel (long-distance transmission). We are also developing approaches for detecting multiple pathogens in the mosquitoes, including parasites and viruses such as dengue.

Project 2: The parasite that causes river blindness in Africa. This parasite (Onchocerca volvulus) is transmitted by the bites of blackflies. Disease symptoms are caused by the microscopic larvae, which move through the skin and can cause irreversible eye damage. Adult females are ~80cm long and are found coiled up in skin nodules. This project involves sequencing the parasite across life stages, and sequencing the genomes of blackflies, to determine whether there is evolution of drug resistance and whether blackfly migration between different areas is spreading the disease. We are also examining the microbiomes of these blackflies to determine whether they might be transmitting other diseases.

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Dr. Susan Hoebee
Bundoora

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Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Either**
Masters conversion: **Yes**

- Field work
- Population genomics; plant reproductive assessments
- Bioinformatics
- Microscopy - Light, electron

The research in my group combines studies of plant reproduction, together with genetic/ genomic studies. Our focus is typically related to issues of native species conservation. We work in the field and the lab to explore issues including pollen viability, floral visitors and their effectiveness for seed set, as well as population connectivity and species delineation using sequencing and bioinformatics. I welcome enquiries from students with interests in these areas and encourage them to meet and speak with current students in my lab. For 2026, I have two honours projects on offer and others available where I would be a co-supervisor:

Project 1: Population genomics of the critically endangered Mt Cole Grevillea. This species contains two subspecies found on adjacent mountain tops in central Victoria but there are knowledge gaps relating to connectivity via gene flow (recent vs. historic).

Project 2: Pollination studies and genomics of a recently discovered gentian at Wilsons Promontory. This genus is threatened by changing hydrological conditions and is somewhat of an Australian enigma - understanding its biology has been a challenge because the species are cryptic and typically very small. The population at Wilsons Prom was found in 2023, is the largest of all known Australian populations and offers us a rare chance to begin to better understand the biology of the genus.

Additionally, I am looking to co-supervise a study on brushtailed possums with Kylie Robert (supported by Nangak Tamborree) and am open to shared projects with other colleagues within EPAS. Feel free to come and have a chat!

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Dr. Aleicia Holland
Albury-Wodonga

Field work

Ecotoxicology

Animal handling

Ecological assays

Animal or plant identification

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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**

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.

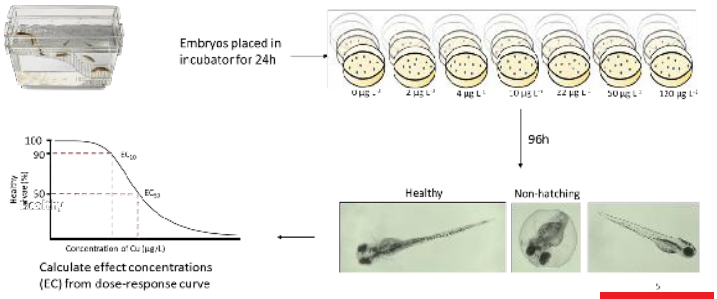
I currently have interest in recruiting students for the following topics:

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



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Dr. Vanessa Kellermann
Bundoora

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Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Field work
- Ecological assays
- Animal handling
- Drosophila melongaster models
- PCR assays

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.

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A/Prof. John Morgan
Bundoora

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Number of projects: **1-2**
Full-time or part-time: **Either**
Feb or July start: **July**
Masters conversion: **Yes**

Field work

Plant identification

Ecological assays

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 2026:

Project 1: What holds up climate-change plant migration? Determining the germination microsite requirement of herbaceous high mountain species may help better understand their capacity to establish into new habitats as a result of climate change. Seed dispersal will be crucial if plants are to migrate to new places to keep pace with climate change. But what happens when those seeds arrive at new places? What is the likelihood that seedling establishment can occur, particularly where habitats are already occupied by other plants? We have quantified alpine plant species dispersal, but wish to now ask – what conditions are necessary for those seeds to be successful? What are hostile vs favourable microsites for establishment?

Project 2: Seed dormancy – can we generalize about patterns? Tropical savannas and temperate grasslands have very different environmental settings in Australia, but we still don't have a very good understanding of the importance of seed dormancy in these contrasting settings, despite the plants being similar (i.e. herbaceous). There is much experimental evidence that fire-type temperatures (greatly exceeding summer temperatures) increase germination of many species that have physical dormancy, whereas hot summers do not have the same impact. It would be expected that fires in tropical savannas are so frequent that fire-released seed dormancy is almost redundant for species there, whereas it might be more common in Mediterreanean-climate grasslands where fire is highly stochastic but guaranteed within the lifespan of the seeds. In this project, we can choose selected species (of grasses and herbs) and expose them to fire and summer-type heat treatments. What sort of patterns might we see, and might we be able to predict these outcomes? This will enhance our understanding of regeneration in grassy ecosystems, and potentially feed into restoration strategies.

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A/Prof. Nick Murphy
Bundoora

Phylogenetics

Ecological assays

Population genetics

Genetic sequencing

Field work

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Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Either**
Masters conversion: **Yes**

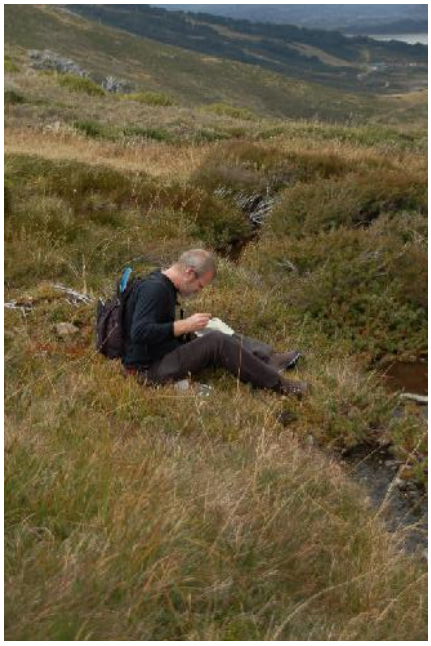
My lab uses genetic tools to better understand biodiversity. Techniques such as DNA sequencing, phylogenetic reconstruction, and population genetic analyses are used to understand why species are found where they are and how changes in environmental impact distributions occur. We also utilise state-of-the-art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

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, with many undescribed species of terrestrial isopods, millipedes, pseudoscorpions, and velvet worms. This project will choose one of these groups and undertake DNA sequencing studies, phylogenetics, population genomics, and morphological analyses to understand the drivers of short-range endemism. You are guaranteed to find a new species!

Project 2. Yellow crazy ants on Christmas Island. Yellow crazy ants (YCA) are among the world's most invasive species. This is particularly the case on Christmas Island, where YCA are killing iconic red crabs. Utilising the insatiable appetite of yellow crazy ants for sugar and protein, this project will undertake genetic analysis of YCA diets. You will examine the interaction between ants and honeydew producing scale insects in raging YCA supercolonies to highlight potential avenues for YCA control and determine protein and sugar sources in apparently "friendly" ant colonies, where ants and crabs appear to co-exist.

Project 3. Identifying optimal source populations for Growling Grass Frog introductions. The La Trobe Wildlife Sanctuary is investigating the establishment of a growling grass frogs (GGF) population. This project will use physical surveys and population genomics and analyses such as habitat suitability and population viability modelling, to identify source populations to create a genetically diverse and locally representative GGF population with the best chance for survival within the wildlife sanctuary.

Project 4. Deer dynamics on the urban fringe. Deer have established populations along the Yarra River billabongs into urban Melbourne. Deer leave genetic signatures in faecal pellets and analysis of these samples show that male deer move among billabong sites, but it is still unknown how these sites are connected to the urban fringes such as Warrandyte. This project will undertake surveys of faecal pellets and genetic analysis to examine urban deer population dynamics and help understand the likelihood of urban deer repopulation after control efforts.



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Dr. Ryan Phillips
Bundoora

Ecological assays

Animal or plant identification

Field work

Experimental design

Plant reintroduction

Animal behaviour studies

E-mail: R.Phillips@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 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 identify the ecological interactions needed to support rare 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.

Project 2: Floral adaptations to specialised pollination strategies. Although having a range of 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 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 the threatened Brisbane Ranges Grevillea (co-supervised with Susan Hoebee).

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A/Prof. Jim Radford
Bundoora

Fauna surveys

Habitat assessment

Field work

Remote sensing

Animal or plant identification

Data analysis

Geographic information systems (GIS)

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Website: click here

Number of projects: **3**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

Our lab undertakes research that is focused on how to conserve species, ecological communities and ecosystems in human-modified landscapes. We often adopt a landscape perspective that looks at the influence of factors like the extent, configuration and composition of landscape elements on the distribution of species, and the diversity and composition of communities. Our aim is to identify strategies and management responses that are most likely to sustain wildlife in regions experiencing change associated with agriculture, fire, and urban development. Our research uses field surveys and experimental manipulations, statistical modelling and analysis of spatial data using GIS.

Major research topic areas include:

- Landscape change and nature conservation (especially birds) in agricultural environments
- Fire ecology and the relationship between fire regimes and conservation of species and communities
- Conservation biology of wildlife (especially birds)
- Provision of ecosystem services by wildlife in agricultural landscapes
- Innovative ways to detect, monitor and manage wildlife species

Project 1. Farmland conservation: transitioning to higher biodiversity farmland futures (co-supervisor, Dr. Alex Maisey). This project will test the outcomes of selected management actions (e.g., fertiliser use, grazing management) on farms for one of the following groups: birds, invertebrates or plants (depending on the student's interest and skills). You will undertake field surveys on farms in western Victoria and south-east South Australia to examine the influence of sustainable agricultural management approaches on biodiversity.

Project 2. Field Validation of a Grazing Pressure Index for Mallee Conservation Reserves (co-supervisor, Dr. Alex Maisey). This project will ground-truth and refine a new Grazing Pressure Index, developed from satellite data in the South Australian mallee region. You will conduct field surveys in conservation reserves such as Calperum and Gluepot Stations, collecting data on vegetation composition, grazing impacts, and, if of interest, bird communities. The project will suit a student with an interest in botany, ecology, or remote sensing, and offers training in field survey methods, GIS, and ecological data analysis. This project provides valuable opportunities to connect with Australian Landscape Trust, BirdLife Australia, and the Murraylands and Riverland Landscape Board.

Project 3. Response of plants and birds to fire in heathland communities. This project will examine the response of (either) plant or bird communities to time since fire, fire severity and fire frequency in heathland communities of western Victoria. You will conduct field surveys in areas that have experienced different fire history, collecting data on vegetation or bird communities. The project will suit a part-time student but could also be completed full-time.

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A/Prof. Kylie Robert
Bundoora

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Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

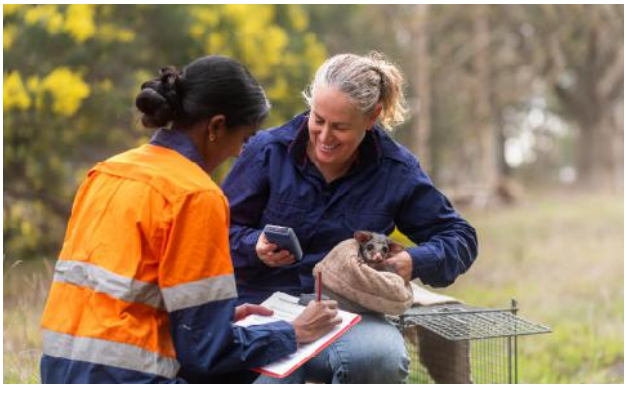
- Animal handling
- Animal behaviour studies
- Field work
- Animal or plant identification
- Ecological assays

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.

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.



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Dr. Michael Shackleton
Albury-Wodonga

Field work

PCR assays & genetic sequencing

Ecological assays

Light microscopy

Animal behaviour studies

Metabolomics

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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**

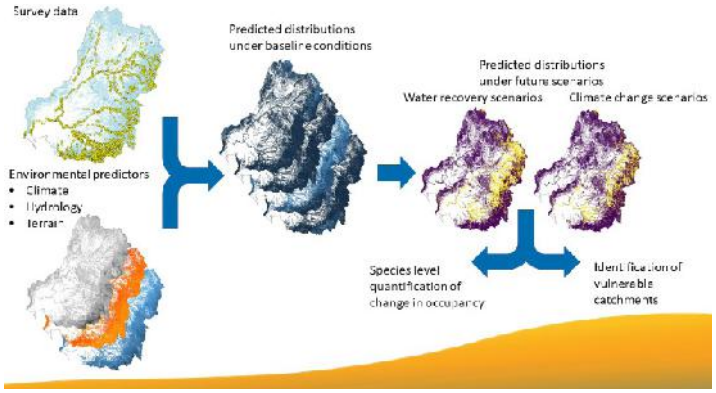
My lab is primarily interested in aquatic ecology, specifically around understanding species distributions and responses to environmental parameters - especially those impacted by climate change. I use traditional and molecular (i.e. metabarcoding) survey techniques to characterise communities and model 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.



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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**
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.

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Biochemistry & Cell Biology

Dr. Lesley Cheng
LIMS

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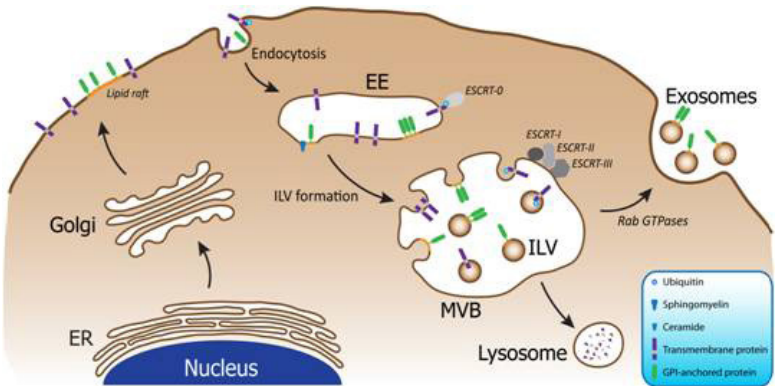
Website: click here

Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

- Cell culture - eukaryotes incl. primary & cell lines
- Protein biochemistry (SDS-PAGE & western blotting)
- Genetic sequencing
- Gene expression analyses (PCR, qPCR)
- Proteomics
- Immunoassays (ELISAs, I-P)
- Molecular cloning
- Bioinformatics

Neurodegenerative diseases, such as Alzheimer's disease (AD) is one of the leading causes of death world-wide. At the early stages of AD, neurons that control memory and thinking are attacked by toxic proteins that causes pre-mature neuronal death. Brain tissue becomes damaged, and patients begin to experience symptoms such as dementia related memory and cognitive impairment – a stage of disease when it is difficult to repair with disease-modifying drugs. Currently, the diagnosis process involves invasive procedures such as brain imaging and cerebrospinal fluid testing but is often performed at the symptomatic stage when damage to the brain has begun. Hence, there is currently an unmet need for an early, convenient, low-invasive blood-based test to diagnose AD. Our group focuses on developing diagnostic tests for neurodegenerative diseases such as Alzheimer's and Parkinson's disease but, also other similar dementia disorders to allow for differential diagnosis.



Project 1. It's in the blood – Extracellular Vesicles. Exosomes are extracellular vesicles (EVs) that are secreted from cells and tissues where they can then be found circulating throughout the body. They can carry protein and genetic material which have been shown to reflect the host cell. EVs can be isolated from blood making them a potential source of disease biomarkers. Our hypothesis is that EVs secreted from neurons within brain tissue can migrate through the blood brain barrier (BBB) into the blood whereby brain biomarkers are readily detected and reflective of disease occurring the brain, equivalent to a 'liquid biopsy' of the brain. We utilise 'Next-Generation' deep sequencing to identify all the RNA species, in particular microRNA, in EVs isolated from human post-mortem brain tissue and blood of patients with neurodegenerative diseases.

Project 2. Brain-derived EVs. Historically, it has been challenging to develop biomarkers for brain diseases as neurological biomarkers do not cross the BBB so sampling peripheral whole blood is not reflective of the brain. However, brain-derived EVs (BDEVs) can cross the BBB through specialised transport channels that allow BDEVs to pass the BBB. Our research group has the capability to isolate BDEVs from human brain tissues, a complete game-changer from using cell culture models. We can now investigate the contents and role of EVs isolated from the brain of patients diagnosed with a neurodegenerative disease from an entirely new perspective.

Projects will be developed around investigating the biology of EVs at the interface of the brain and blood to identify specific biomarkers for neurodegenerative diseases and further our knowledge about EVs.

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Dr. Pamali Fonseka
LIMS

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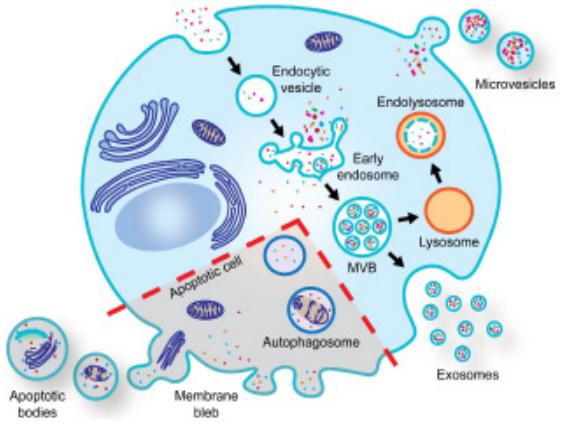
Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

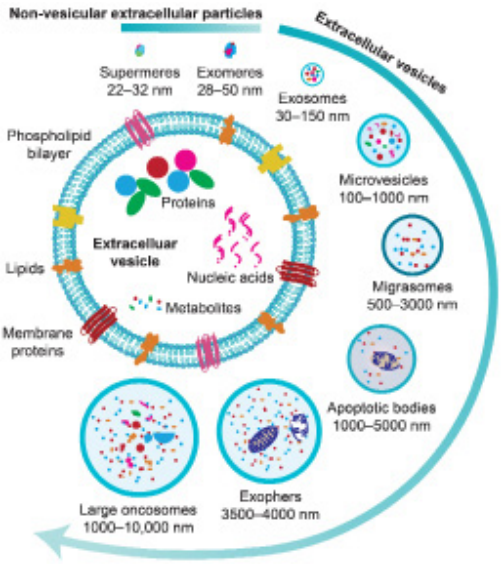
- Cell culture - eukaryotes incl. primary & cell lines
- Proteomics
- Bioinformatics
- Animal models of disease
- Cell transfection
- CRISR-Cas9 gene editing of cells

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.



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Prof. Stephanie Gras
LIMS

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Number of projects: **4**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **No**

- 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

Viruses and pathogens are part of day-to-day encounters that the immune system needs to deal with. How the immune system "sees", recognises and eliminates viral infection is not fully understood. Indeed, viruses can mutate and as a result escape the immune system surveillance. If we were to develop better vaccine and drugs, or even vaccine against viruses like HIV, it is essential to understand the mechanism of viral recognition and viral escape prior to this. Our lab use multiple techniques in biochemistry, structural biology, and cellular immunology that students can choose to study.

Examples of projects in our lab:
Influenza virus continue to be a health burden in human, with ½ million death per year globally. We used immunological assays and flow cytometry to assess the response of human immune cells towards influenza virus derived peptides, determining which induce an immune response (immunogenic) and which do not. We also use Xray crystallography to make 3D structures of viral peptides bound to immune system proteins (HLA molecule) in complex with T cell receptor (TCR) at the Australian Synchrotron. We discover new Influenza epitopes as potential target for therapeutics/ vaccine development.

FIG 1. First TCR-HIV-MHC-II complex. Galperin, *Science Immunology*, 2018

FIG 2. T cells recognition of SARS-CoV-2 and other seasonal coronaviruses. Lineburg et al, *Immunity*, 2021.

HIV virus has of very high mutation rates and despite the dramatic life improvement provided by current antiretroviral therapy, HIV and AIDS are still health burdens. To tackle these issues, our work focus on a subset of individuals– named controllers – known to control HIV infection and/or delay AIDS disease progression. We will employ flow cytometry to assess T cell functionality and X-ray crystallography to create 3D structures of HIV epitopes and better understand the interaction between the peptide and the TCR, and link those observations with the function of the T cell (FIG 1).

SARS-CoV-2 virus is responsible for COVID and we have join the fight against SARS-CoV-2 infection, and our previous work on viral immunology places us naturally to provide and understanding of the T cell immune response to this new virus. We use protein chemistry, crystallography, as well as cellular immunity to provide a basis and better understanding of the impact of the SARS-CoV-2 infection. We have published the first structures of SARS-CoV-2 epitopes presented by Human Leukocyte Antigens (HLA) molecules that are the target of killer T cells. We are studying the immune response to SARS-CoV-2 and to COVID vaccines (FIG 2).

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Prof. Stephanie Gras & Dr. Anurag Adhikari
LIMS

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- 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

Number of projects: **1**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **No**

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.

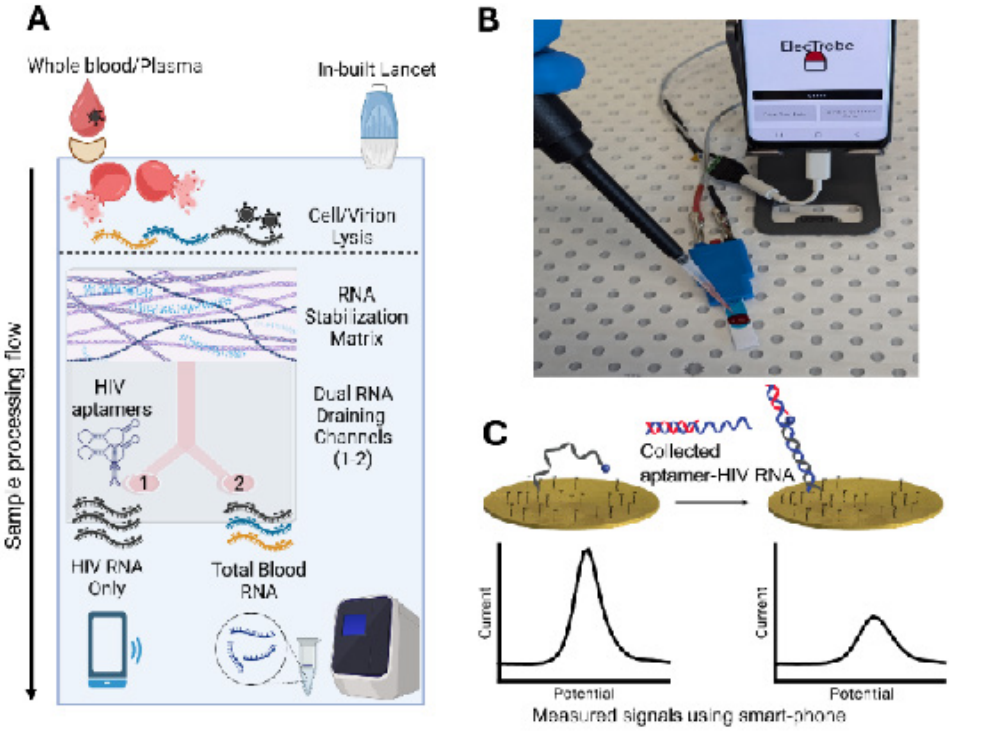

Figure 1: A) Prototype microfluidic device for RNA extraction/stabilization, detection, and storage. **B)** Image of patented, instrument-free, smartphone-based electrochemical detection using disposable test strips in fluids. **C)** Surface chemistry on test strip for detecting HIV RNA-aptamer material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

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Prof. Begona Heras
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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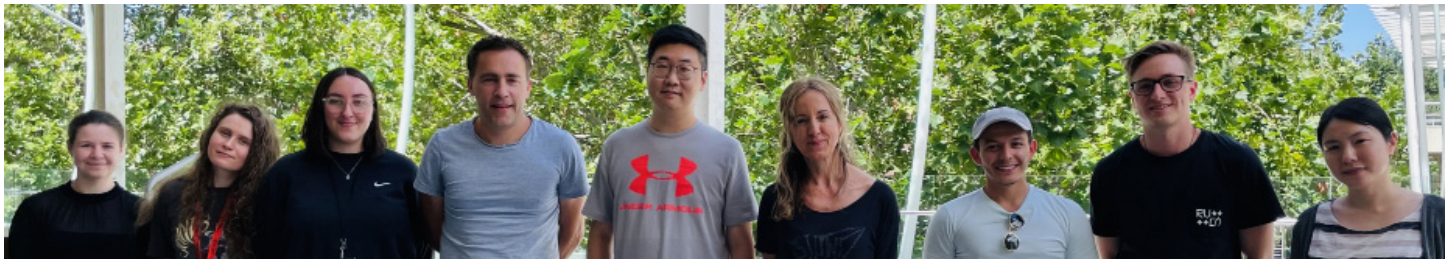
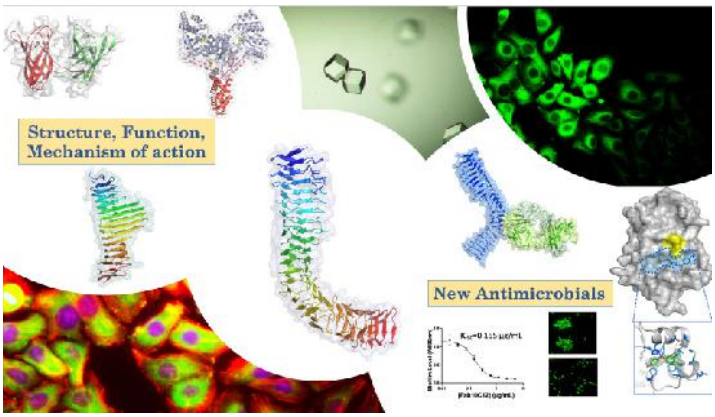
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**



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 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 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.

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Prof. Mark Hulett
LIMS

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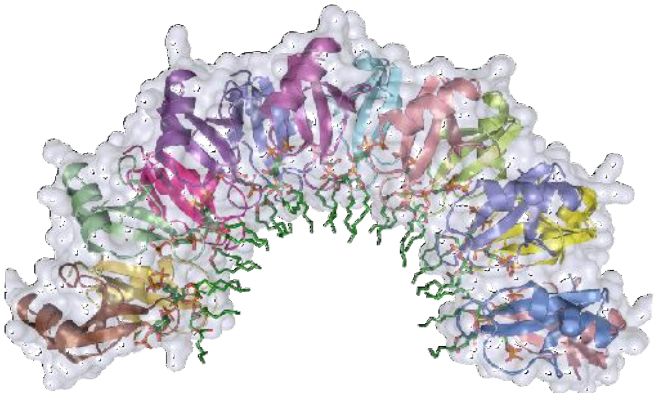
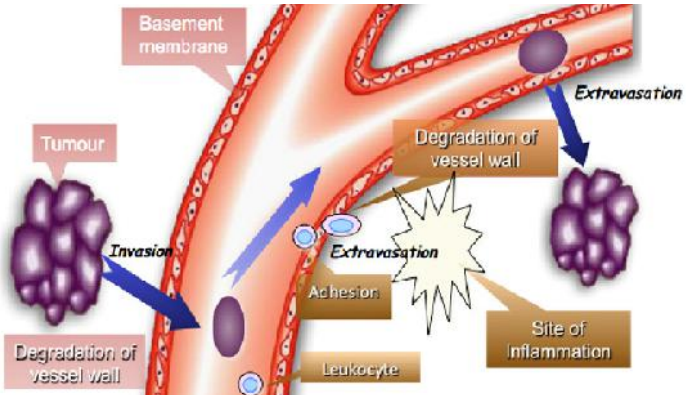
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **February**
Masters conversion: **Yes**

- Infection & Immunity
- Cancer
- Mammalian cell culture
- Flow cytometry
- Animal models of disease
- Microscopy - electron, confocal, light
- CRISPR-Cas9 gene editing
- Protein biochemistry





Cancer and infectious diseases are major global health problems. There is an urgent need for more effective anti-cancer therapies and new antibiotics to address the rise of antimicrobial resistance. Our research focuses on two key areas (i) defining the molecular basis of the enzyme heparanase in tumour progression to develop inhibitors as anti-cancer drugs, and (ii) understanding the mechanism of action of innate defense peptides against target cells for development as anticancer and antimicrobial therapeutics. In consultation with prospective honours students we will design projects that are appropriate to your interests under the following themes.

Project 1. Heparanase function in tumour progression. The ability of malignant tumour cells to escape from primary tumour sites and spread through the circulation to other sites in the body (metastasis) is what makes cancer such a deadly disease. An essential process in metastasis is cell invasion - where tumour cells move into and out of the vasculature. The activity of heparan-sulphate (HS)-degrading enzymes has been shown to play a key role in cell invasion by degrading extracellular matrices. We have shown that heparanase is the dominant HS-degrading enzyme in mammalian tissues, making it an attractive drug target. We are trying to (i) understand the molecular basis of heparanase function, (ii) defining heparanase expression in cancer, and (iii) using heparanase knockout mice in disease models to define the precise role and contribution of heparanase in tumour progression.

Project 2. Innate defense molecules as novel antimicrobial and anti-cancer agents. Defensins are innate immune molecules found ubiquitously in the animal and plant kingdoms that often exhibit broad activity against microbial pathogens and mammalian cancer cells. We have described a conserved mechanism of action by defensins against pathogenic bacteria, fungi and enveloped viruses, as well as cancer cells. The defensins target and kill such pathogens and cancer cells using a novel cell lysis mechanism via direct binding to specific plasma membrane phospholipids. Our aim is to define the defensin mechanism of action to engineer improved forms for development as novel antimicrobial and anticancer therapeutics. We have extensive research programs dedicated to (i) investigating the molecular basis of the antimicrobial and anti-cancer activity of defensins using a range of biochemical and biophysical methods including in vitro pathogen and cell viability assays, live cell imaging, electron microscopy and X-ray crystallography (in collaboration with the Kvansakul lab); and (ii) in vivo testing and pharmacokinetic properties of defensins in models of infection and tumour progression.

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Prof. Patrick Humbert
LIMS

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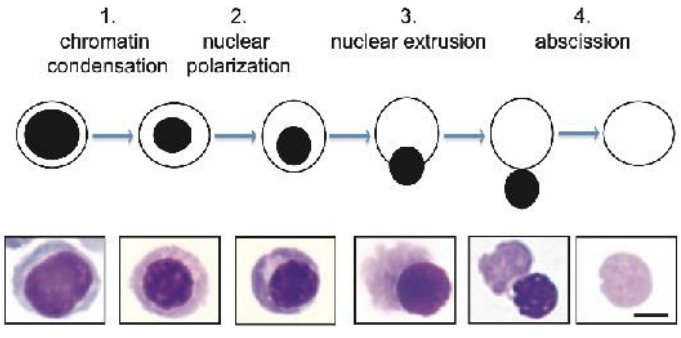
Number of projects: **1**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

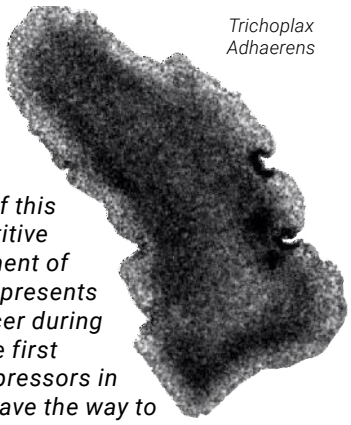
- Cancer
- Animal models of disease
- Mammalian cell culture
- Microscopy - electron, confocal, light
- CRISPR-Cas9 gene editing
- Flow cytometry
- 3D cell culture
- Protein biochemistry

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



Trichoplax Adhaerens

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.

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.

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Dr. Travis Johnson
LIMS

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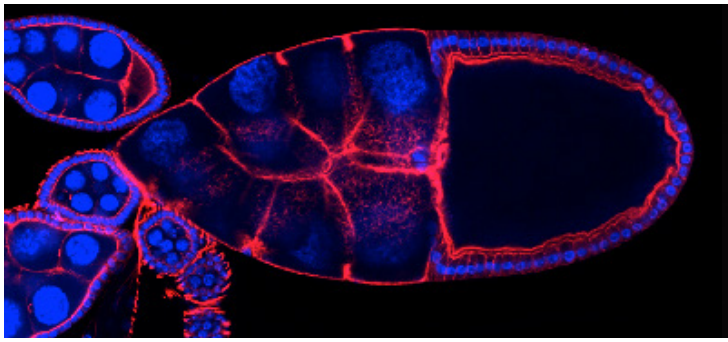
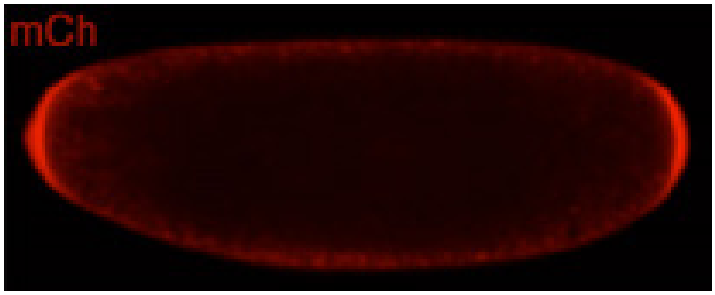
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Drosophila melongaster models
- Bioinformatics & molecular modelling
- Confocal & super resolution fluorescence microscopy
- Protein biochemistry (SDS-PAGE, western blotting)
- Animal behaviour & models of disease studies
- Histology (incl. immunohistochemistry)
- Metabolomics
- Molecular cloning & PCR assays



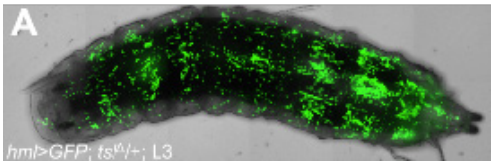
The Johnson Lab uses the powerful genetic model organism, the fruit fly (Drosophila melanogaster), to understand the actions of critical developmental and environmental factors that are involved in cellular decision making processes (growth, proliferation and differentiation). His lab uses sophisticated genetic experiments, including genome-wide screens, and the generation of transgenic strains to discover new genes and novel mechanisms of cell communication. The Johnson Lab further extends to using flies to study human disease via the discovery of the genetic and molecular bases of human diseases, as well as developing novel treatments. We use advanced imaging (e.g. confocal microscopy), genetic technologies (e.g. CRISPR/Cas9 mutagenesis), biochemistry (protein purification and analysis), cell biology, and molecular and 'omics approaches.



Project 1. Growth factor trafficking and secretion in early embryo patterning. This project aims to use fixed and live cell imaging, as well as molecular genetics to investigate the secretory pathway taken by a unique growth factor involved in a critical developmental event in the very early Drosophila embryo. It will reveal new information about specialised secretory pathways and how patterning is achieved.

Project 2. Novel mechanisms that control blood cell numbers. This project will use genetic tools to disrupt gene function specifically in fluorescently-labelled blood cells and advanced imaging techniques to learn how blood cells talk to other blood cells and tissues and decide whether or not to proliferate. It will reveal new insights into the mechanisms used to control blood cell numbers for homeostasis and during disease.

Project 3. Using diet to treat a model of metabolic disease. This project will characterise a genetic model of a human inherited metabolic disease and test a variety of potential dietary interventions. This will require Drosophila genetics, tissue analysis and imaging and the quantification of traits such as survival, developmental timing, behaviour and the generation of synthetic diets.



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Prof. Robyn Murphy
LIMS

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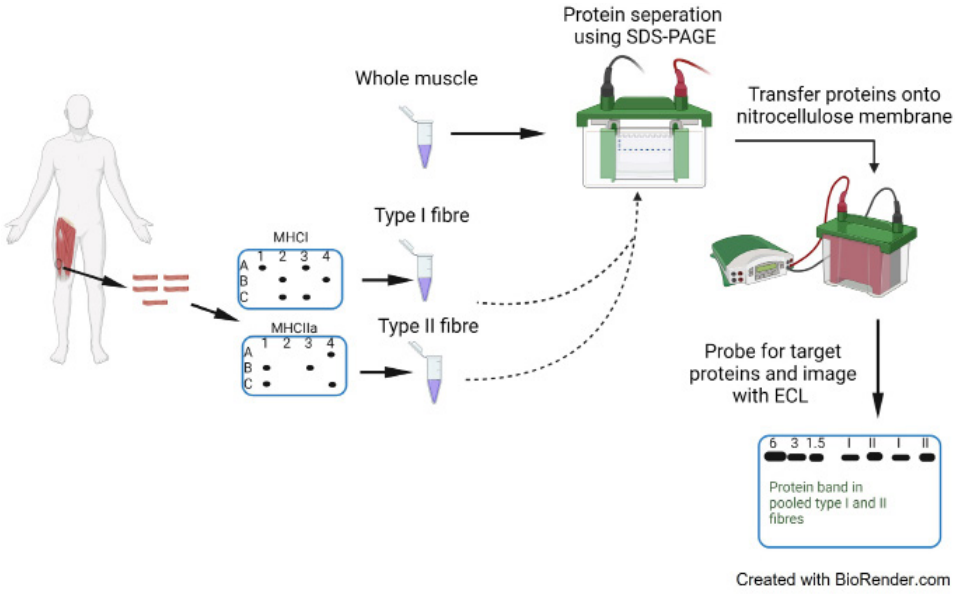
Website: click here

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

- Infection & Immunity
- Protein biochemistry
- Animal models of disease
- Proteomics
- Histology (incl. immunohistochemistry)
- Microscopy - electron, confocal, light

Our group studies the various aspects of skeletal muscle function in health and disease, using exercise and disease models in humans, as well as animal models. We address many problems at a cellular level, allowing the differences that exist between cells (muscle fibres) that sit side by side in a whole muscle. We have discovered that a protein, metallomatrix protein 9 (MMP9) that has known functions outside muscle, is present inside the muscle cells as well. This project will work towards understanding the function of intracellular MMP9. The study will use tissue from rodents and likely also humans.
Given the role of mitochondria in muscle and during exercise, as well as the fibre specific responses to exercise and in mitochondrial abundance and likely function, we explore mitochondrial content, function and/or dynamics in skeletal muscle. Of particular interest are diseases such as Type 2 diabetes and the exploration of any impairments in mitochondrial function in skeletal muscle obtained from old compared with young individuals. This project will work towards understanding the function of Calcium handling in the mitochondria.

Other projects are possible by discussion with Robyn. There are many possibilities that fall under the overall research objectives of the group. These could include animal or human studies.



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Dr. Kha Phan
LIMS

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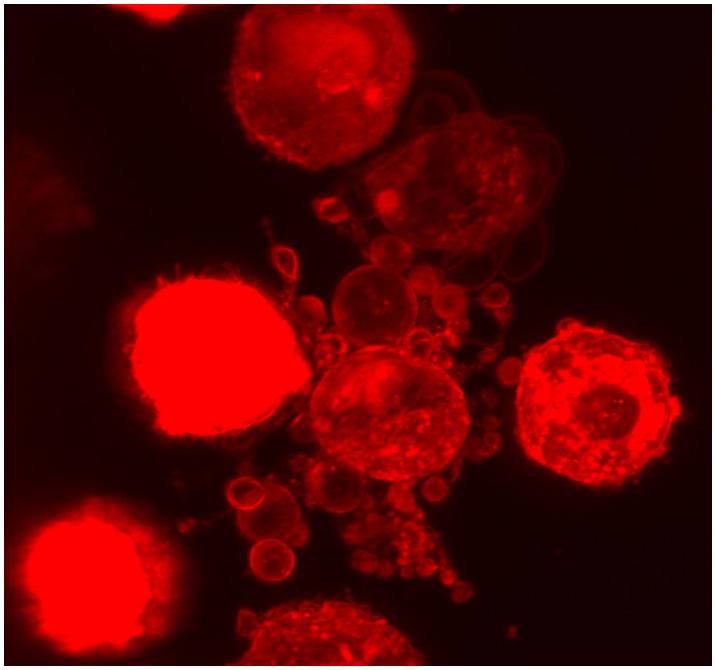
Number of projects: **1 Feb, 1 Jul**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Cell culture - eukaryotes & prokaryotes
- CRISPR-Cas9 gene editing of cells
- Protein biochemistry (SDS-PAGE, western blotting)
- PCR assays
- Flow cytometry & immunoassays
- Animal models of disease
- Light microscopy
- Histology (incl. immunohistochemistry)

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, 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 collaboration with Prof. Ivan Poon (La Trobe) and Prof. Jun Suzuki (Kyoto University), you will identify novel regulators for this processes using a new genome-wide CRISPR/Cas9 screening techniques. You will also functionally characterise the identified positive hits 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.



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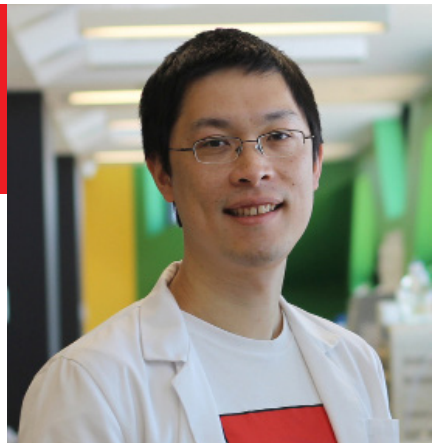
Prof. Ivan Poon
LIMS



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Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Infection & immunity
- Microscopy - electron, confocal, light
- Cell culture - eukaryotes, incl. primary & cell lines
- CRISR-Cas9 gene editing of cells
- Flow cytometry
- Cell transfection
- Animal handling

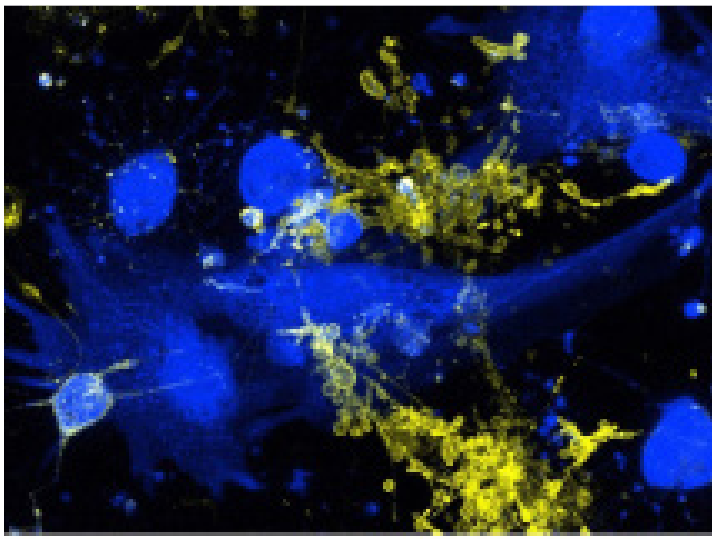
Billions of cells die daily as part of normal turnover in various organs. It is vital that dying cells are rapidly removed as their accumulation has been linked to inflammation, autoimmunity, cancer and infection. To aid efficient removal of dead cells, dying cells often disassemble into smaller fragments 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



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Dr. Stefan Wette
LIMS

- Animal models of disease
- Microscopy - confocal, super resolution fluorescence
- Histology
- Animal handling
- Protein biochemistry
- Proteomics
- Small-angle X-ray scattering

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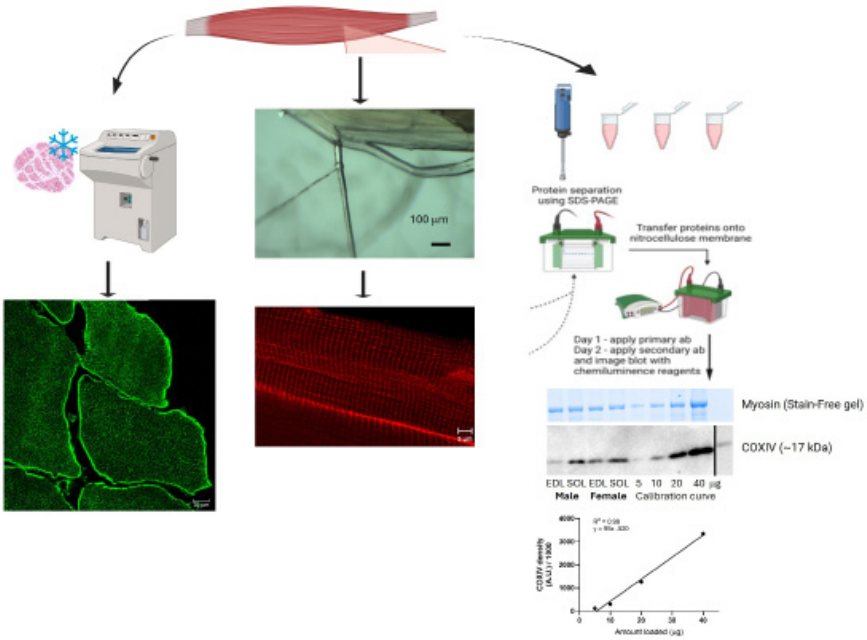
Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

My research interests focus on physiology and biochemistry of skeletal muscle. I am part of the Murphy Lab research group (Prof Robyn Murphy lab head) that examines various aspects of skeletal muscle biochemistry in health and disease, using exercise and disease in humans, as well as animal models of rare muscle diseases known as Limb Girdle Muscular Dystrophies (including Dysferlinopathy and Calpainopathy). We also conduct biochemical analysis and confocal imaging of single fiber segments to measure proteins abundance and localisation (or protein movement), respectively, allowing us to determine the abundance and redistribution of proteins following an intervention or treatment (e.g. Calcium-treatment).

I am also interested in muscle function analysis and small-angle X-ray fiber diffraction, which is used to examine the structure of muscle under physiological conditions in living tissue. This advanced technique is particularly useful for studying the molecular structural changes in various muscle diseases using transgenic animal models, human skeletal and cardiac muscle.



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Dr. Lakshmi Wijeyewickrema
LIMS

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Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Infection & Immunity
- Molecular cloning
- Protease activity assays
- Bacterial over-expression of protein
- Protein biochemistry

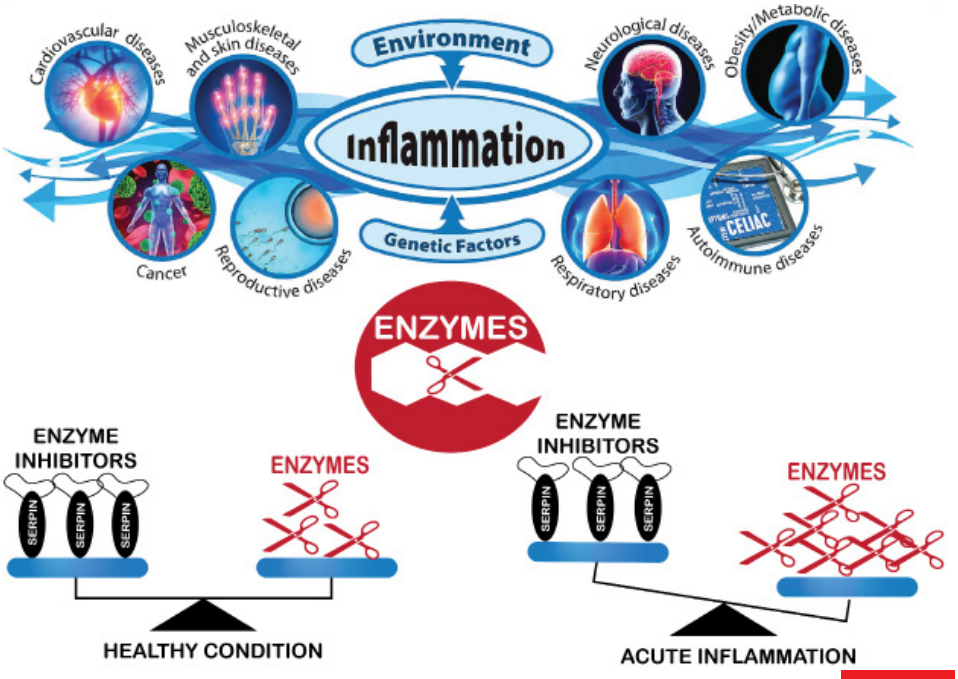
Enzymes are truly remarkable molecular machines that operate tirelessly within our bodies, allowing us to carry out even the most basic biological functions. These unsung heroes keep us healthy and functioning by catalysing essential chemical reactions. But enzymes are not just vital for basic survival – they also play a critical role in regulating inflammation and other immune system functions. Inflammation is one of the body's most important defence mechanisms, protecting us against harm and aiding in the healing process.

By delving into the intricacies of enzyme function, we can unlock the secrets of disease prevention and treatment. Targeting specific enzymes offers a promising approach to developing new therapies for combating inflammation, infection, and a host of other health issues. However, we must also consider the delicate balance between enzymes and their inhibitors. An imbalance of enzymes and their inhibitors can lead to the overproduction of inflammatory molecules, which can contribute to the development of chronic inflammation and various diseases.

By gaining a deeper understanding of the delicate balance between enzymes and their inhibitors, we can develop new strategies to prevent and treat inflammation, leading to better health outcomes for all.

Project 1. The enemy within: targeting the viral entry facilitator of SARS-CoV-2 as a therapeutic strategy.

Project 2. Designing specific enzyme inhibitors: the good, the bad, and the impossible.



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Chemistry

A/Prof. Peter Barnard
LIMS

Chemical synthesis - organic & inorganic

Nuclear magnetic resonance

Light microscopy

Mass spectrometry

X-ray crystallography

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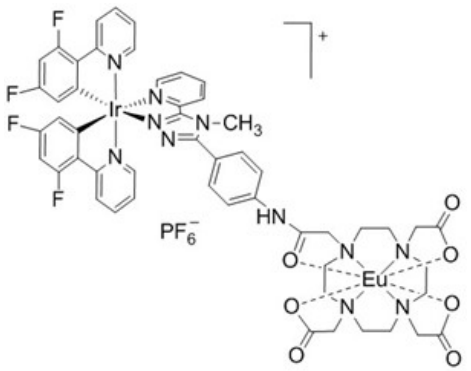
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

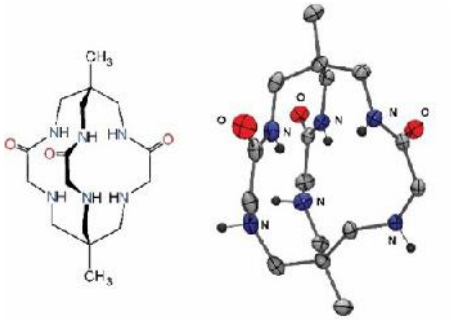
The main focus of the Barnard research lab is the synthesis and development of organic ligands and coordination complexes for medicinal and biological imaging applications. Organic and inorganic synthetic chemistry in combination with a wide range of analytical techniques are used for the generation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

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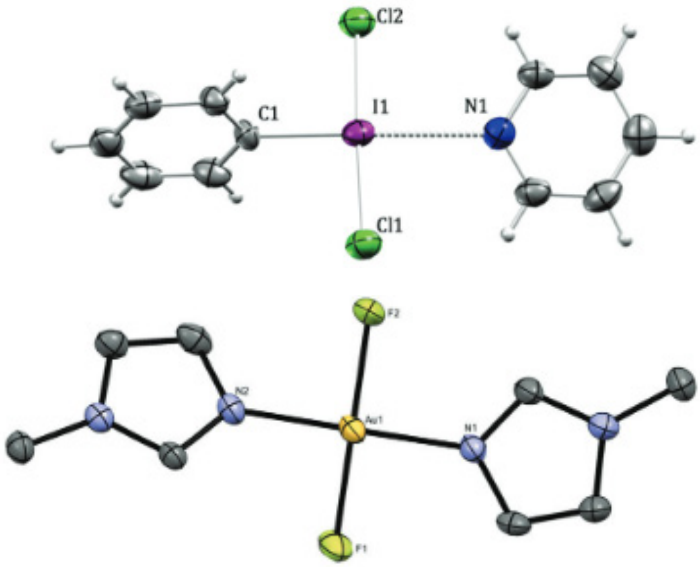
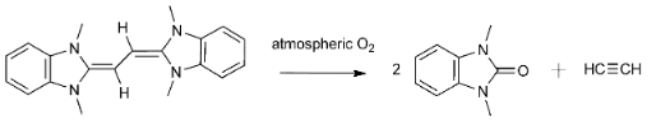
Number of projects: **1 Feb, 1 Jul**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Chemical synthesis - organic & inorganic
- Mass spectrometry
- Nuclear magnetic resonance
- X-ray crystallography

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!

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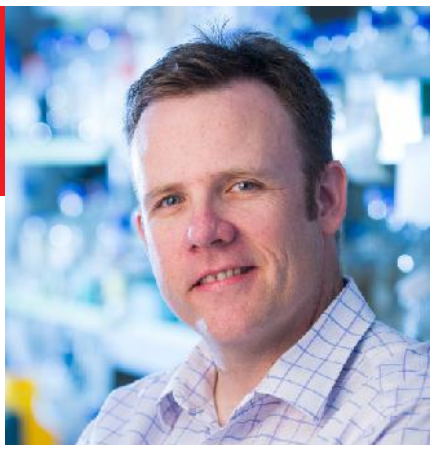
Prof. Conor Hogan
LIMS



- Cyclic voltammetry
- Electrochemiluminescence
- Spectroelectrochemistry
- Electrochemical impedance spectroscopy
- Materials inket printing
- Time-correlated single photon counting
- Photoluminescence spectroscopy

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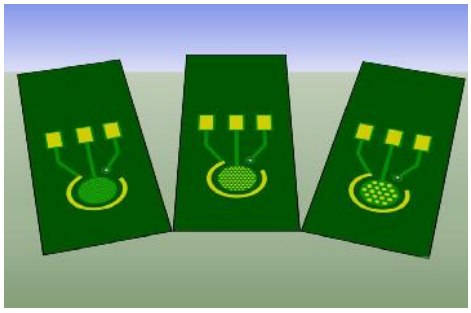
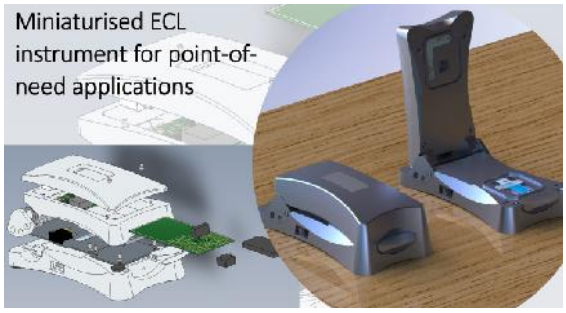
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**





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.

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Prof. Yuning Hong
LIMS

Available for Industry placement

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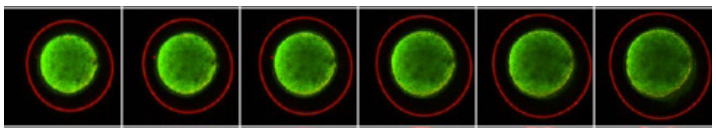
Number of projects: **1 Feb, 1 Jul**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

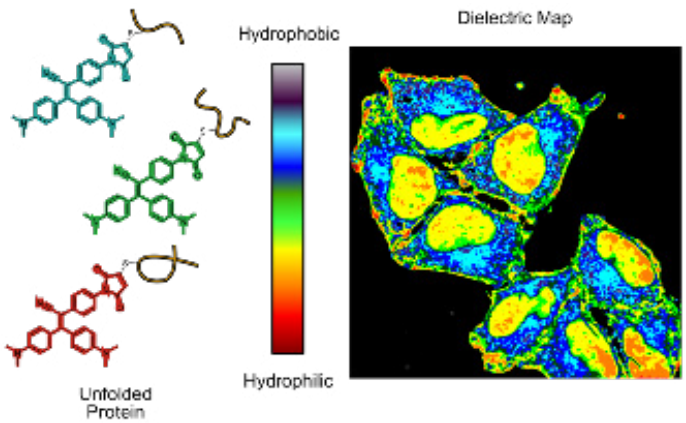
Our Group develops novel chemical compounds, usually with interesting fluorescent behaviors, to study how proteins changes in live cells under drug treatment and in cell models of Parkinson's, Huntington's and Motor Neuron Diseases. The molecules we create can selectively turn on their fluorescence or 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.





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Dr. Wenyi Li
LIMS

- Chemical synthesis - organic
- Biophysical characterisation of materials
- Cell culture - eukaryotes
- Bioinformatics
- Cell culture - prokaryotes
- Protein biochemistry
- Mass spectrometry
- Protein purification

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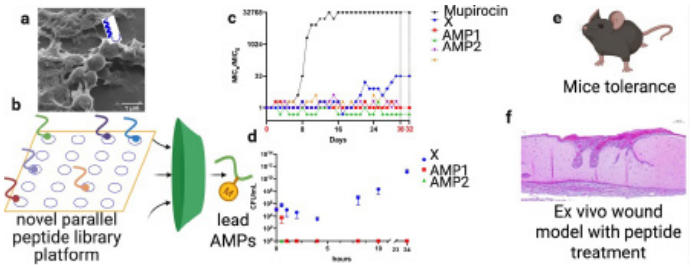
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

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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Prof. Adam Mechler
LIMS

- Atomic force microscopy
- Biophysical characterisation of materials
- Mass spectrometry

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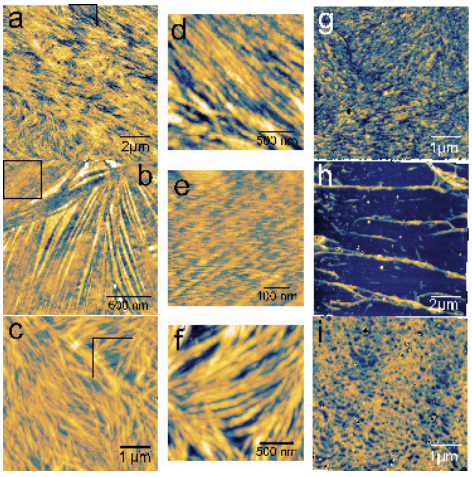
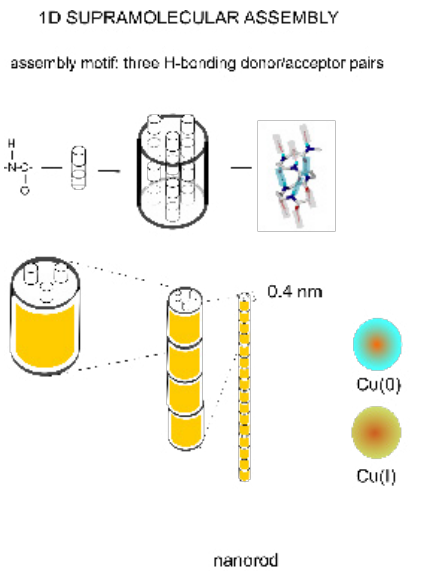
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

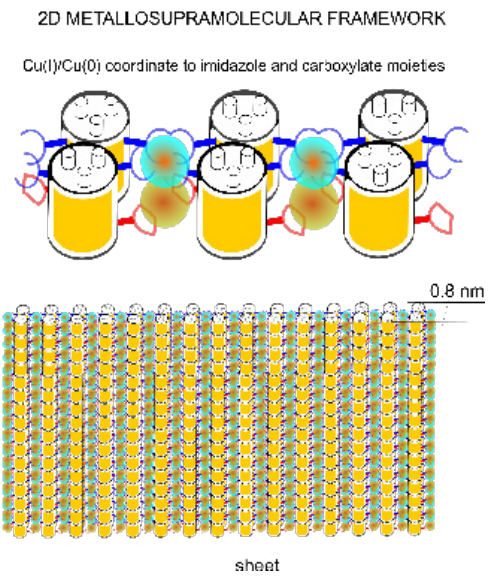
We study the interactions between molecules that lead to a range of phenomena from the simple, such as aggregation of small particles in a solvent, to the highly complex, such as the formation of cell membranes, protein folding and the self-assembly of biomolecular machines. The spontaneous assembly of complex nano-to-microstructures from small molecule precursors opens up new horizons in designing 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.

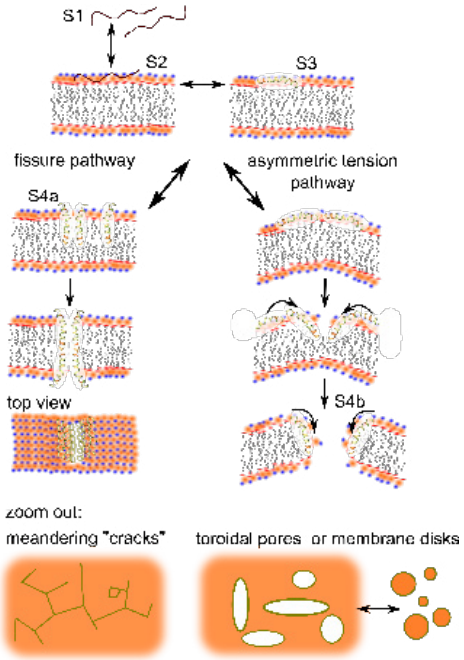
Projects include:

- Physical chemistry of biomolecule interactions, such as structure of cell membranes,
- Membrane disrupting antibiotic/ antiviral/antifungal peptides,
- Design of bioinspired molecular LEGO systems to create functional nanomaterials or devices.









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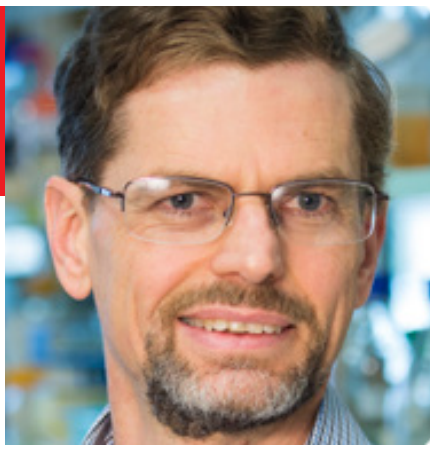
A/Prof. Evan Robertson
LIMS



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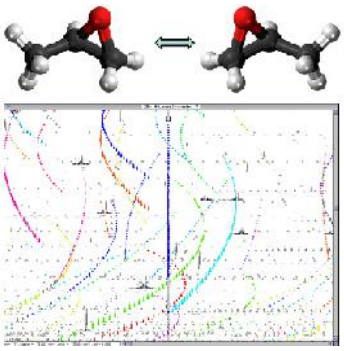
Website: click here

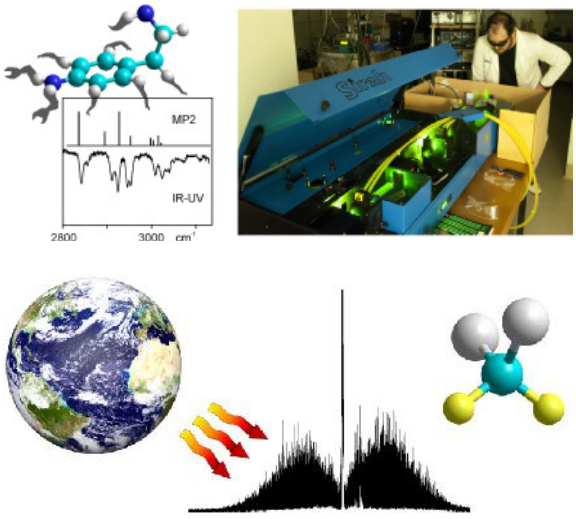
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- IR spectroscopy
- Molecular modelling
- Raman spectroscopy
- Pulsed ns lasers
- Electronics

We exploit powerful light sources such as infrared, visible and ultraviolet lasers, or the Australian Synchrotron's infrared beamline to study molecules relevant to pharmaceutics, 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 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.

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Dr. Saimon M. Silva
LIMS

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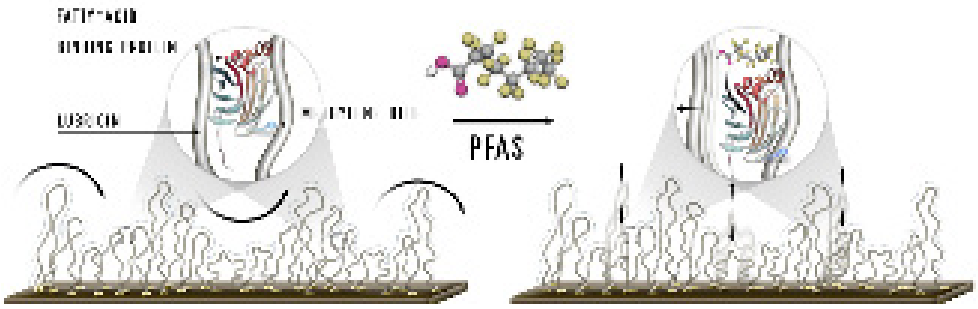
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Analytical chemistry
- Electrochemical sensing
- Sensors & Biosensors
- Point-of-care diagnostics



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.

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Dr. Keith White
LIMS

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Website: click here

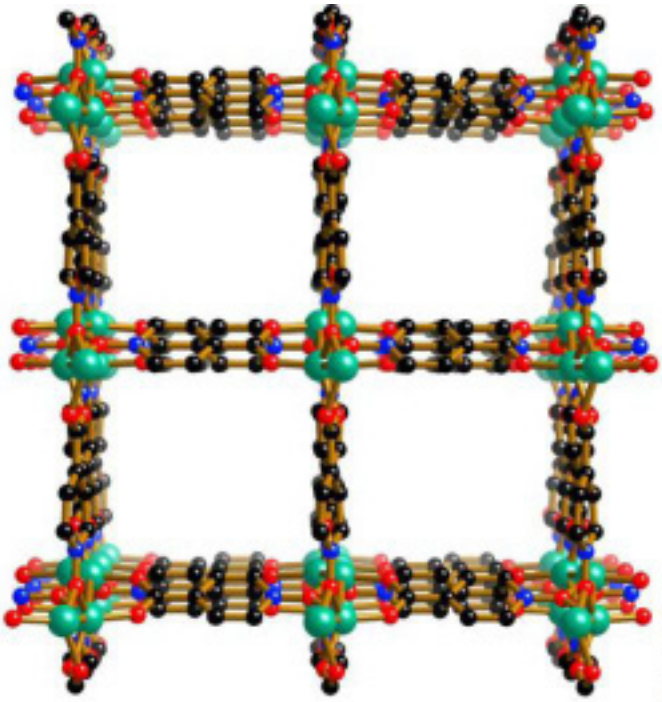
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Feb only**
Masters conversion: **Yes**

- 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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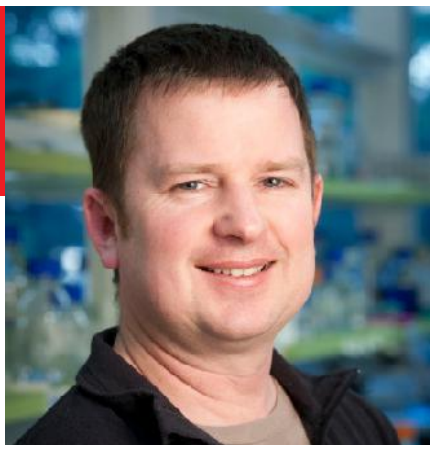
Prof. David Wilson
LIMS



Computational chemistry

Molecular modelling (computational incl. AI)

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Website: click here

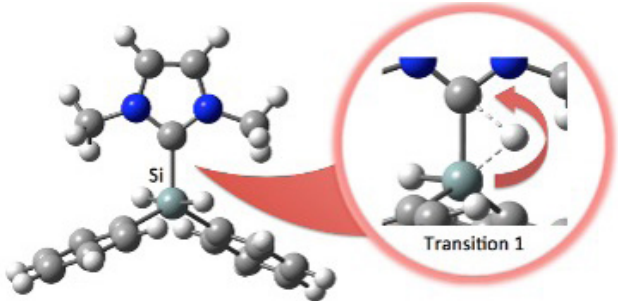
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

Our group "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.

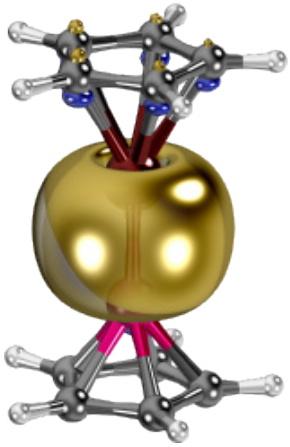
Project 2. Modelling reaction mechanisms to understand critical reactivity. There are several projects, such as the involvement of PhICl2 in catalysing organic reactions or reactions of borole rings with unsaturated molecules.

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 H2 to within 0.001 ppm of experiment, and extended the 19F scale by 800 ppm! Projects include (i) NMR shielding including 19F, 9Be, and 15N, (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.

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Microbiology

Dr. Sarah Annesley
Bundoora

- Live cell metabolism assays (Seahorse)
- 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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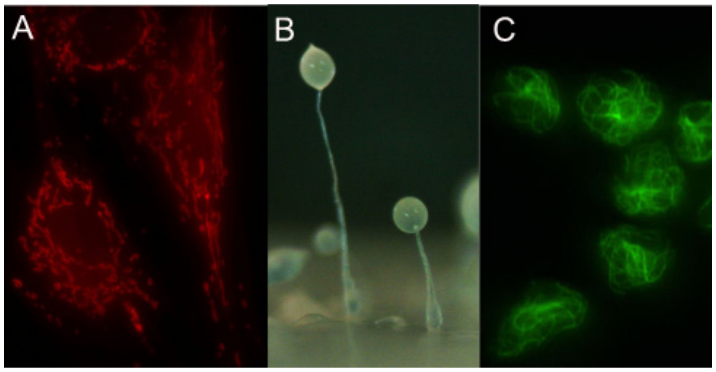
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Feb only**
Masters conversion: **Yes**

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 cells called lymphoblasts) 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 and identify patients early in the disease process prior to clinical diagnosis. We do this via analysing mitochondrial and lysosomal function, activity levels of proteins, measurement of calcium responses and analysis of gene expression changes.



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 has begun to investigate the similarities and differences between the two disease cohorts, identify biomarkers of Long COVID and use these to identify which post-COVID patients are likely to go on and develop Long COVID.

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Prof. Karla Helbig
Bundoora

- Cell culture - eukaryotes incl. primary & cell lines
- Cell culture - prokaryotes
- Animal handling
- Animal models of disease
- Gene expression analyses
- Cell transfection
- Microscopy - confocal & super resolution
- Molecular cloning

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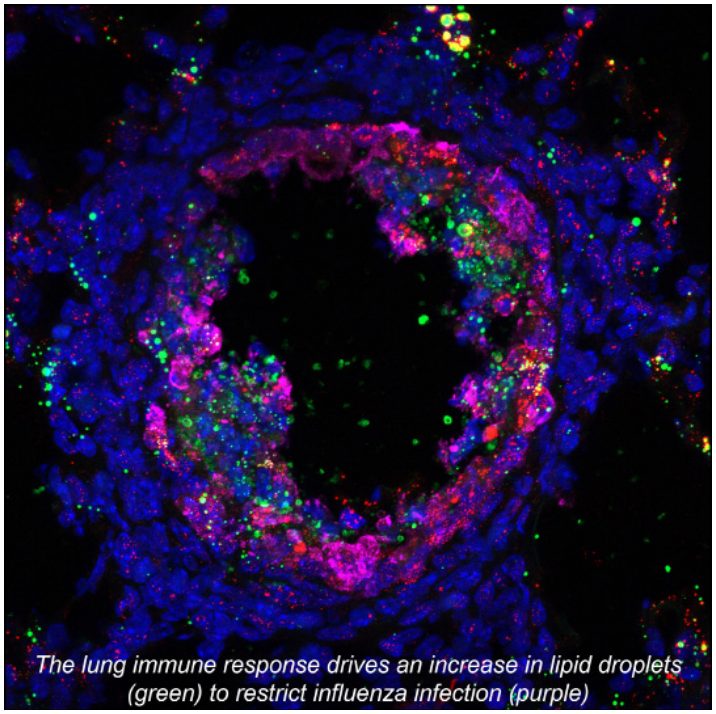
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

Viruses infect all living organisms, and our laboratory studies the early host response to viral infections in humans, and other mammalian and non-mammalian animal hosts, such as abalone. Specifically, we are interested in the role of antiviral cytokines called interferons, and how they orchestrate and control the host anti-viral response.

Our team uses advanced imaging, molecular, and genomic techniques to examine the cellular and molecular mechanisms of the host response to viral infection. Our research aims to better understand how host cells control viral infection, and use this information to development novel strategies to combat viral infection in both humans and animals. Currently our projects centre around two main themes:

Theme 1: Understanding the role of lipid droplets in driving viral clearance from host cells. Our group has recently shown that lipid droplets are upregulated very rapidly following viral infection of a cell, and that these lipid droplets drive heightened expression of antiviral cytokines. Projects in this theme use viruses such as Zika virus, influenza and dengue virus to understand the role of lipid droplets in both infections of the lung and the brain.

Theme 2: Can we protect abalone against lethal Herpesvirus infection? Australian abalone are very susceptible to abalone herpesvirus and our group work together with abalone farmers in Victoria to develop novel solutions to protect these animals against viral infection. We work both with abalone housed in our laboratory as well as farmed abalone. Projects in this theme will investigate basic mechanisms that underpin abalone resistance and susceptibility to viruses, using live animal models of viral infection.



The lung immune response drives an increase in lipid droplets (green) to restrict influenza infection (purple)

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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 (Seahorse)
- Microscopy - electron, confocal & super resolution
- Protein biochemistry (SDS-PAGE, western blotting)

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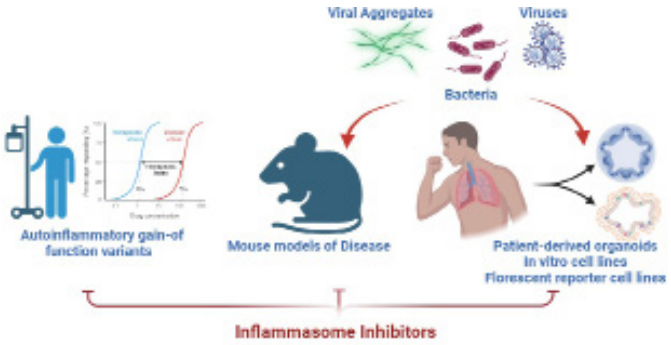
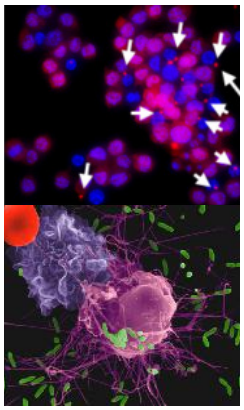
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Either**
Masters conversion: **Yes**

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.

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Dr. Katelyn Mroczek
Bundoora

Pedagogy

Qualitative analysis

Animation

Scientific Illustration

Interviewing

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Website: click here

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

I'm passionate about developing innovative educational resources that help students grasp core microbiological concepts through diverse representations. By understanding how students learn, we can design content that actively supports their success. My focus is on integrating technology—such as animations, scientific illustrations, and educational software—to complement content and reinforce conceptual understanding in practical classes.

Project 1: Co-Designing Technology-Enhanced Resources for Microbiology Education. This project aims to design and evaluate the use of digital tools—including scientific illustrations, animations, and interactive software—to enhance student learning of essential microbiological concepts. By partnering with students in the development process, we will create educational resources that are both pedagogically sound and responsive to learner feedback. The goal is to foster deeper understanding and retention of foundational knowledge in microbiology.

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A/Prof. Steve Petrovski
Bundoora

- Microscopy - light & electron (TEM, SEM)
- Gene expression analyses (PCR assays)
- Bacterial overexpression of proteins
- Cell transfection
- Bioinformatics
- Molecular cloning incl. CRISPR-Cas9 editing
- Genetic sequencing

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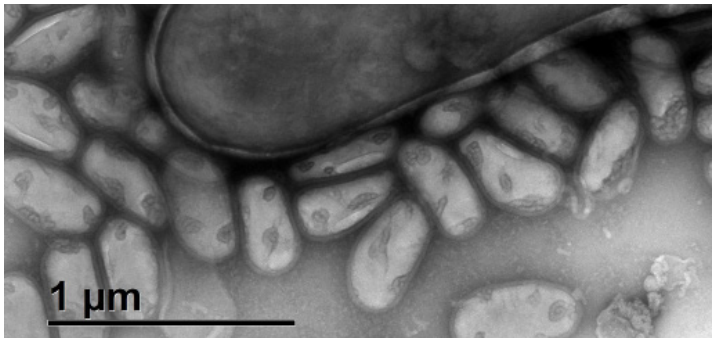
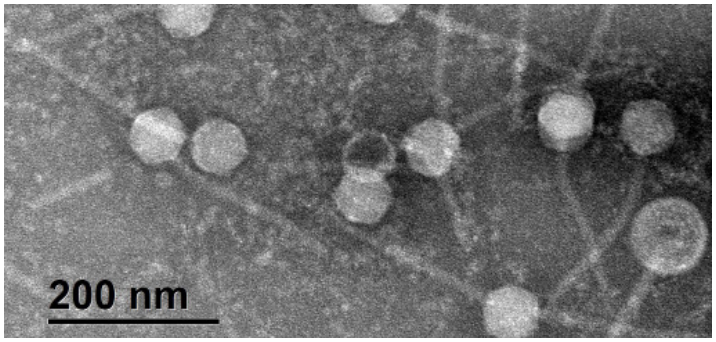
Website: click here

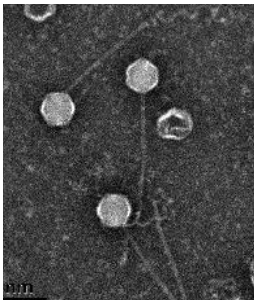
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**





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. amayticus 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.

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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.

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Anatomy, Physiology & Pharmacology

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: **1**
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.

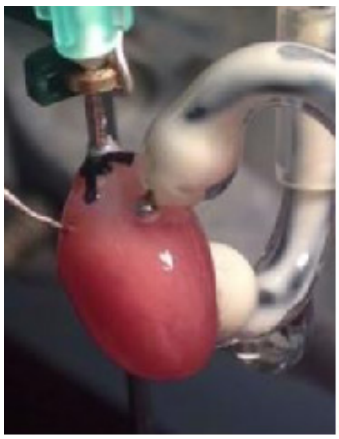
The lab has two primary research themes – specifically, the pathological influence of 'heart fat' as an emerging mediator of heart disease and the role of sex and sex steroids in determining heart health. The fat immediately surrounding the heart increases markedly in obesity, with aging, and post-menopause – 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.

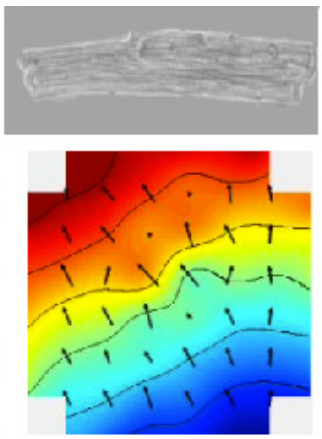
Honours projects include:

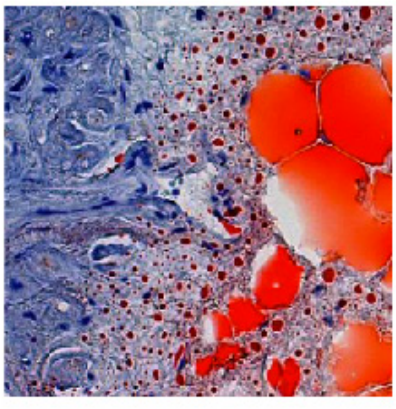
Project 1: Showing how a fatty heart drives cardiac pathologies

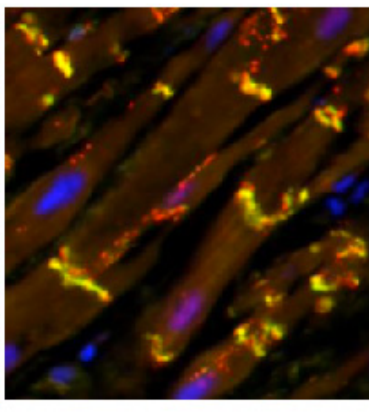
Project 2: Understanding the role of locally synthesised steroids in the heart

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).









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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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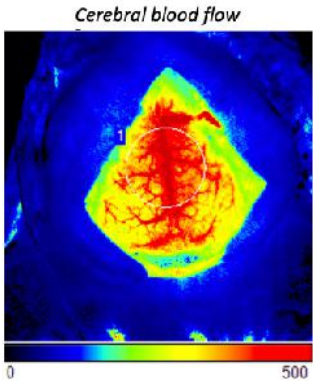
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

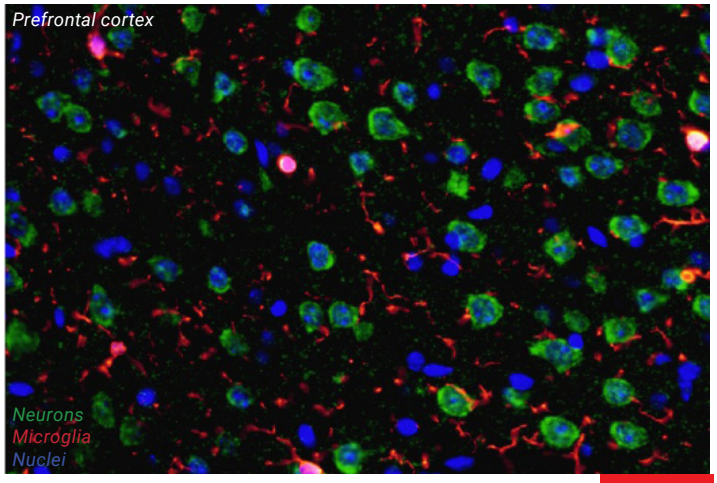
Cerebrovascular diseases (stroke, dementias) are a major health concern in Australia and throughout the world. The brain is and its circulation are particularly sensitive to disease. Cardiovascular diseases disrupt the function of cerebral arteries which leads to a dysregulation of cerebral blood flow. 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.





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A/Prof. Seb Dworkin
Bundoora

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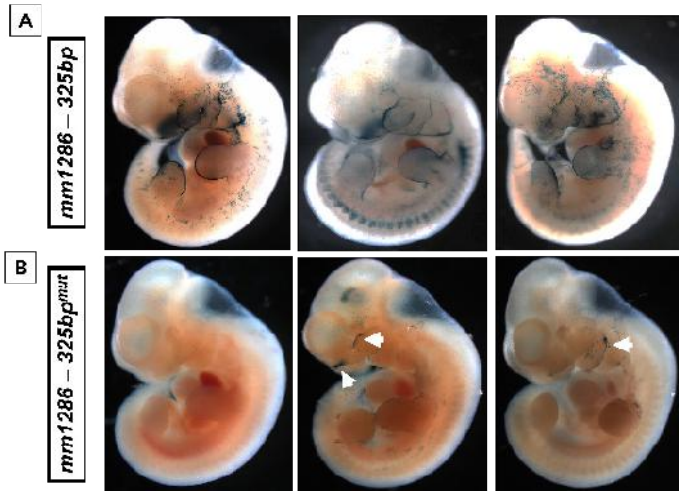
Website: click here

Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Animal handling
- Animal models of disease
- Zebrafish microinjection
- Microscopy - light, confocal & super resolution
- CRISPR-Cas9 gene editing
- Genetic sequencing & expression analyses

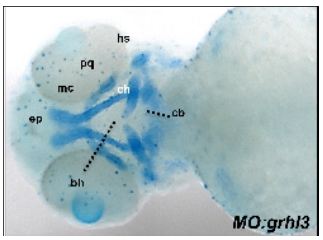
Understanding how a single, fertilised cell develops into an entire, fully functioning baby, is one of the most incredible fundamentals of life. It is also a process across the entire animal kingdom. Amazingly, this process usually works perfectly well - that is, the baby develops without any problems. 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.



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Dr. Brooke Huuskes
Bundoora

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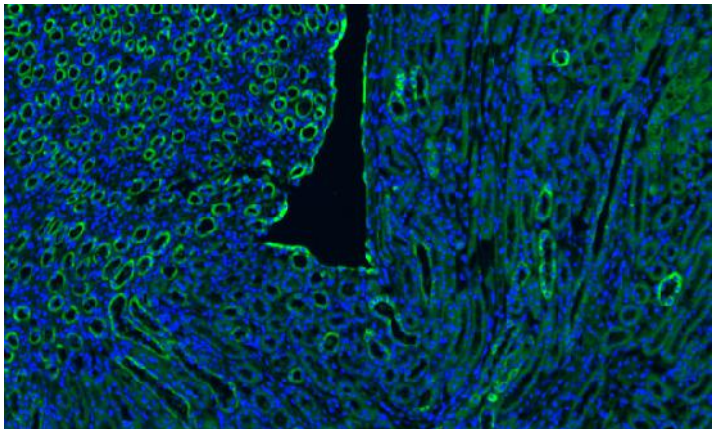
Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Cell culture - eukaryotes incl. primary & cell lines
- Gene expression analyses
- Animal models of disease
- Histology
- Animal handling
- Light microscopy

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 that 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.

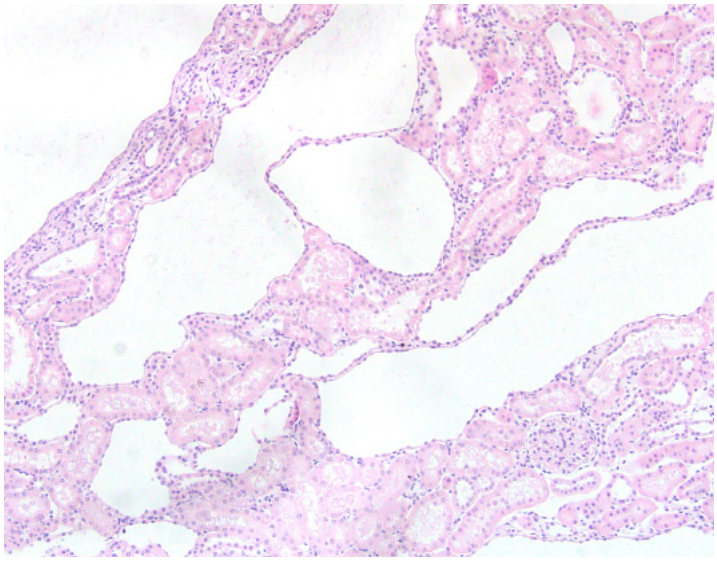


Project 1: Understanding the role of the immune system in polycystic kidney disease

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



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Dr. Chris van der Poel
Bundoora

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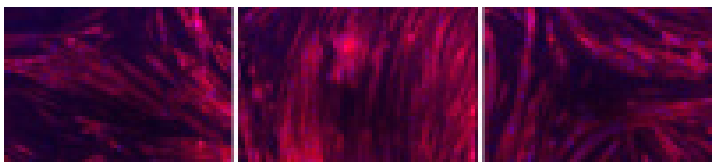
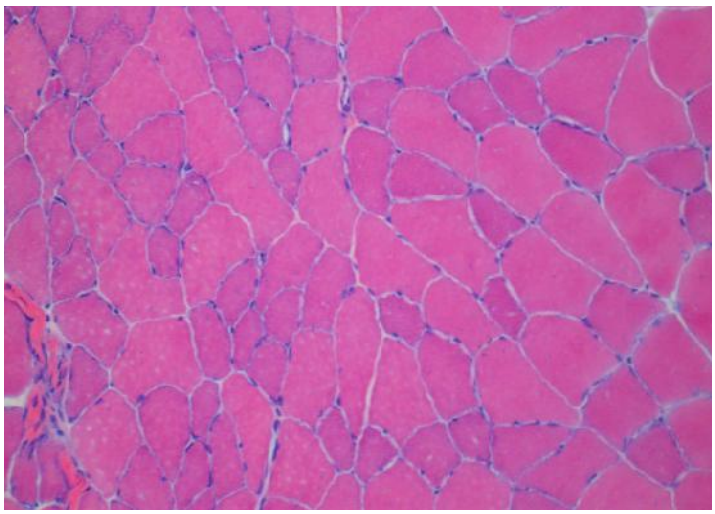
Website: click here

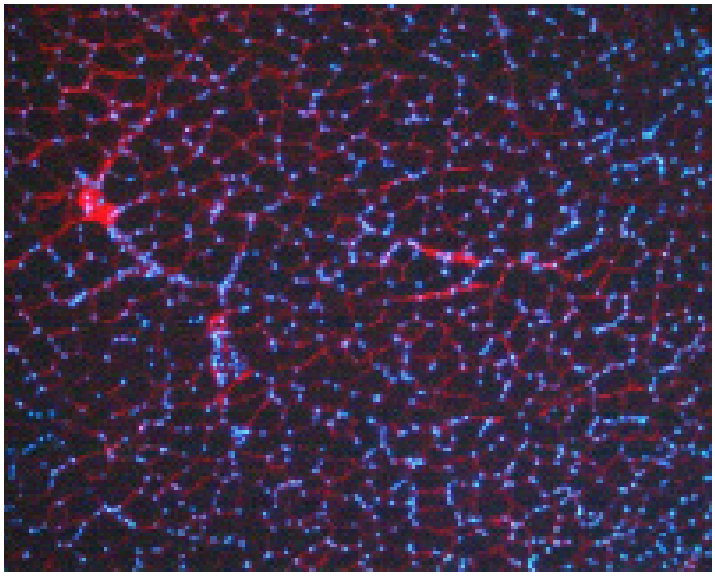
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Animal handling
- Animal models of disease
- Cell culture - eukaryotes incl. primary & cell lines
- Animal behaviour studies
- Human exercise trials
- Cell transfection

Our laboratory's research focusses on the comprehensive exploration of muscle function, repair mechanisms, and environmental stress responses to advance therapeutic interventions and rehabilitation strategies. Our multifaceted approach integrates basic muscle biology with applied therapeutic approaches to enhance muscle health and performance across diverse populations and challenging physiological conditions. Our research interest encompasses three interconnected research domains that collectively address muscle health from cellular to systemic levels. First, we focus on improving skeletal muscle regeneration processes post-injury, which is crucial for athletes, individuals in physically demanding professions, and patients suffering from muscle-related disorders such as muscular dystrophies and sarcopenia. Second, we investigate the impact of pharmacological and ergogenic aids on muscle contraction, adaptation to physical training, and post-injury recovery. Third, we examine how environmental stressors, particularly chronic heat stress, affecting muscle physiology and systemic adaptation responses. Our comprehensive research approach utilizes three complementary experimental platforms to investigate muscle function and adaptation across multiple biological scales. We employ cell culture systems to examine fundamental cellular mechanisms of muscle repair, contraction, and stress responses at the molecular level. Rodent models provide crucial insights into systemic physiological responses, tissue interactions, and the effects of interventions in controlled laboratory conditions. Human exercise trials allow us to translate our findings to real-world applications, testing therapeutic interventions and rehabilitation strategies in diverse populations under ecologically valid conditions. By bridging fundamental muscle biology with environmental physiology and applied therapeutic approaches, our research aims to enhance muscle health and performance across various populations and conditions, ultimately contributing to faster, more effective rehabilitation strategies and improved quality of life for individuals facing muscle-related challenges and environmental stressors.







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Dr. Maria Jelinic
Bundoora

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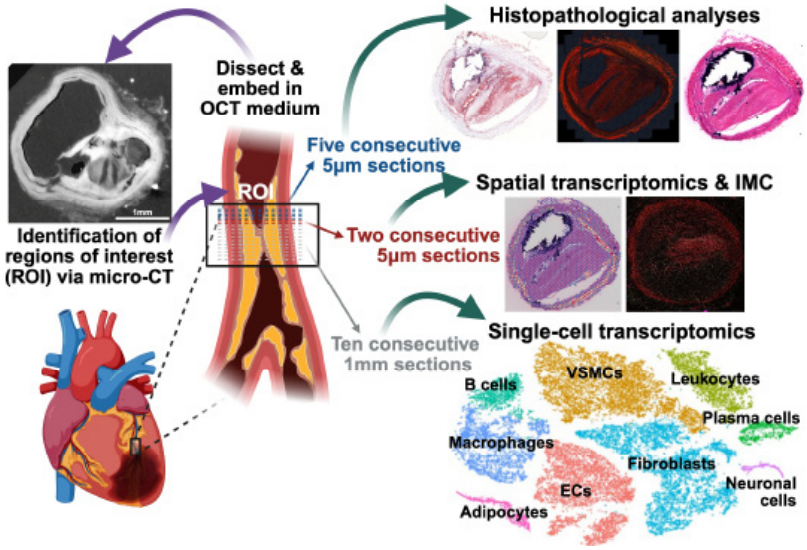
Website: click here

Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Animal handling
- Animal models of disease
- Flow cytometry
- Histology
- Immunoassays
- PCR assays
- Light microscopy

The Obesity and Diabetes Research Group investigates the mechanisms that drive cardiac, vascular and renal complications in cardiometabolic disease using clinically-relevant rodent models. One limitation the group recently addressed is the sex bias in preclinical studies of cardiometabolic disease. It is well-established that an overwhelming majority of rodent studies in cardiometabolic disease are in males. This is at least partly due to female rodents being highly resistant to weight gain and the development of metabolic disturbances in response to traditional models of cardiometabolic disease. Recently, the Obesity and Diabetes Research group developed a new mouse model of diet-induced metabolic syndrome where weight gain and glycaemic dysregulation are comparable between sexes. This model is now being used by the group (and by collaborators) in several research projects (described next).



Project 1. Characterising a new mouse model of atherosclerosis. Atherosclerosis is one of the leading causes of death worldwide, but is difficult to treat pharmacologically due to a poor understanding of the molecular mechanisms that contribute to disease progression. One factor that has limited our progress in understanding is that many of the animal models to date do not accurately reflect the clinical presentation of patients. This honours project would directly address this gap in the field by characterising a new clinically-relevant mouse model of atherosclerosis that my research group is developing.

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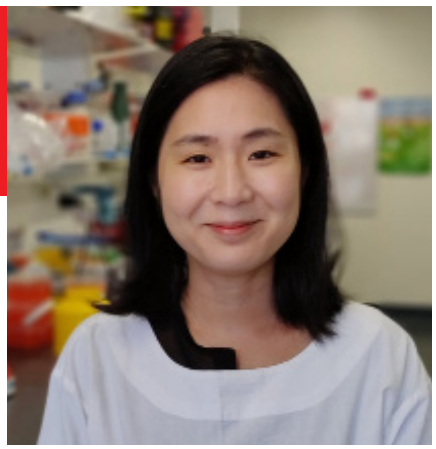
Dr. Helena Kim
Bundoora

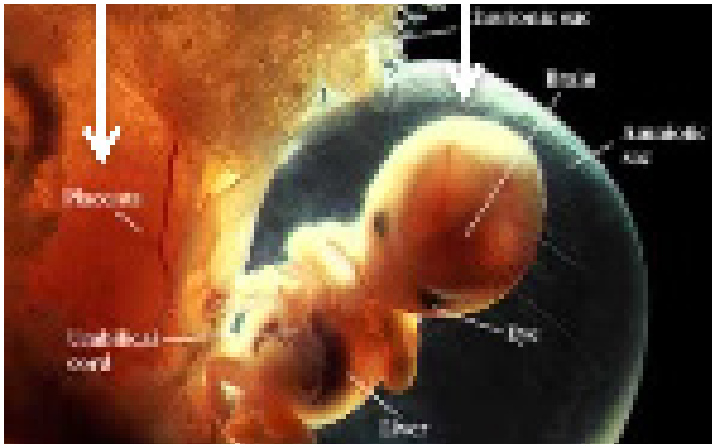


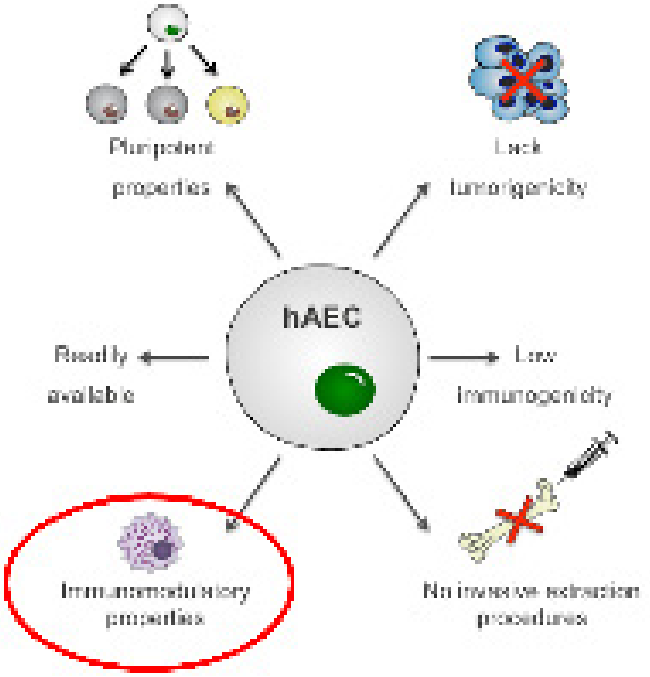
E-mail: h.kim2@latrobe.edu.au
Website: click here

Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

- Experimental stroke surgery & treatment
- Animal behaviour studies
- Animal handling
- Flow cytometry
- Gene expression assays
- Histology
- Light microscopy

Our Centre for Cardiovascular Biology and Disease Research is investigating mechanisms that cause heart attacks and strokes, with a specific focus on discovering new therapies that can prevent them. Heart attacks and strokes occur when cardiac or brain tissue is deprived of blood due to the blockage of a coronary or cerebral artery, respectively. Our research is generally aimed at identifying the disease pathways within the blood vessel wall that lead to arterial blockages, as well as the inflammatory mechanisms in the ischaemic organs that eventually lead to cell death. This project would be a part of the work being done in the Stroke Division of our Centre, that is led by Drs Helena Kim and Richard Zhang together with Prof Sobey. We are particularly interested in determining whether cell therapies can effectively treat stroke.





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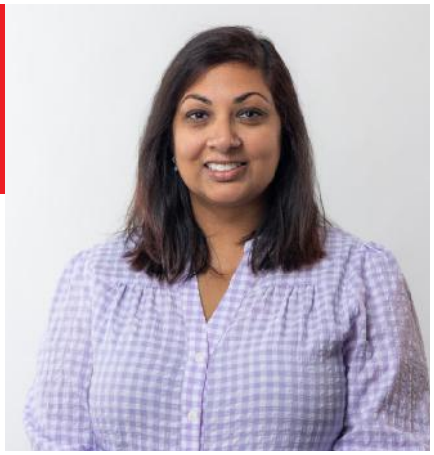
Dr. Rahini Ragavan
Bundoora



E-mail: r.ragavan@latrobe.edu.au
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Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

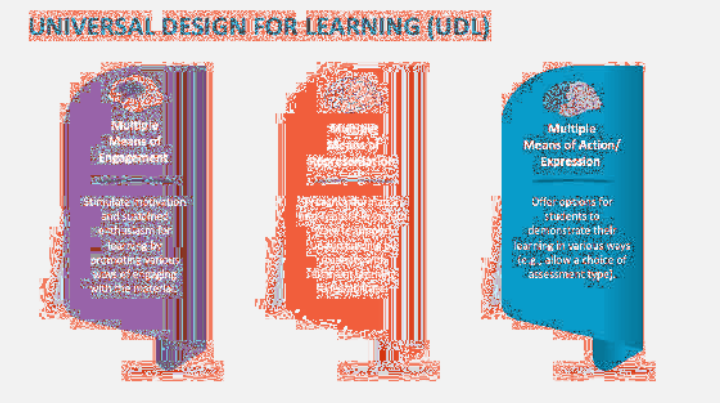
- Pedagogy
- Thematic analysis
- Student engagement and experience
- EDU2030

Student engagement is widely recognized as a key determinant of academic success, yet engagement levels often vary across subjects and majors. I'm really interested in investigating how student engagement and experience differ across disciplines within MAPP, with a particular focus on the strategies that appear to be effective in promoting participation, motivation, and learning. I'm also interested in identifying what teaching modalities (ie online lecture videos, H5P activities, f2f workshops, gamification etc) students find engaging and whether higher engagement corelates to higher academic success.

This study will include both quantitative and qualitative (thematic) approaches. LMS analytics, attendance records, and assessment outcomes may be examined to provide measurable indicators of engagement, while student surveys and focus groups will capture perceptions, experiences, and suggestions for improvement. This mixed-methods approach will provide both breadth and depth in understanding the complex factors that influence engagement. A central component of this investigation will be the lens of Universal Design for Learning (UDL). UDL provides a framework for creating inclusive learning environments by offering multiple means of engagement, representation, and expression.

Rather than assuming a "one-size-fits-all" approach, UDL encourages flexible teaching practices that account for diverse learner needs, abilities, and preferences. Applying this framework to the analysis of student engagement will allow for an exploration of how different teaching strategies—whether lecture-based, workshop-driven, or LMS-supported—impact students with varying learning styles, backgrounds, and levels of confidence.

Ultimately, the aim of this project is to identify effective, inclusive, and sustainable practices that can be adapted across different subjects and majors. By highlighting strategies aligned with UDL and inclusive education principles, the findings have the potential to inform curriculum design, support student success, and foster more equitable learning experiences within higher education.



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A/Prof. Antony (Bill) Vinh
Bundoora

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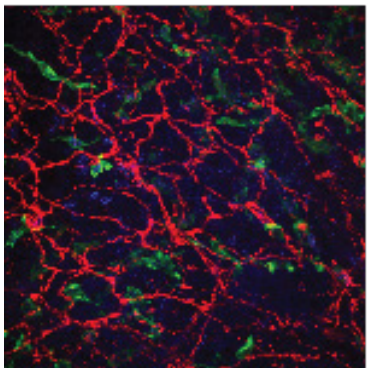
Website: click here

Number of projects: **1-2**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

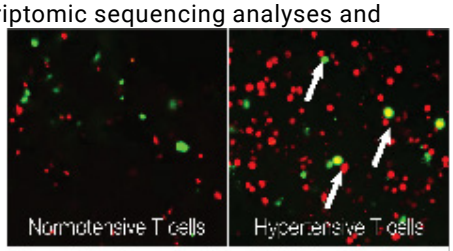
- Animal handling
- Histology
- Animal models of disease
- Genetic expression analyses
- Flow cytometry
- Immunoassays
- Bioinformatics

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.

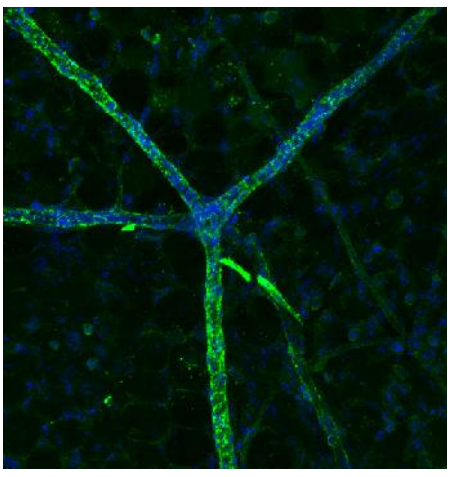


Project 1. B and T lymphocytes/cells in hypertension. Primary supervisor: Dr Hericka Figueiredo Galvao, A/Prof Bill Vinh. B and T cells have been shown to be required for the full development of hypertension. However, the precise mechanisms remain understudied. This project will combine pre-clinical 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 (Red: 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 a world-first lytic bacteriophage that targets one of the most abundant gut commensal bacteria. This projects 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.



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Cardiovascular Research (Baker Institute)

A/Prof. David Greening
Baker Heart & Diabetes Institute

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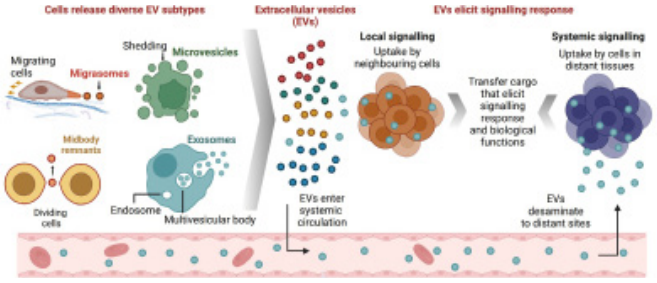
Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

- 3D cell culture
- Proteomics
- Cell culture - eukaryotes incl. primary & cell lines
- Multi-omics
- Bioinformatics
- Light microscopy

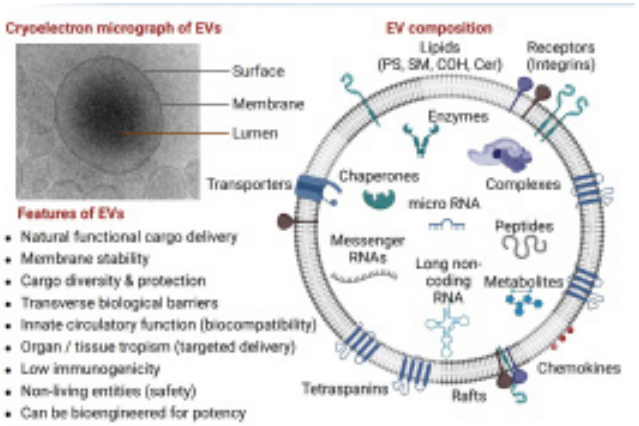
The Molecular Proteomics laboratory explores intercellular signalling and apply advanced omics in the context of the heart and circulation. Our research program seeks to understand cell signalling through nanovesicles as a therapeutic strategy and integrate multi-disciplinary technologies to understand 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



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Prof. Peter Meikle
Baker Heart & Diabetes Institute

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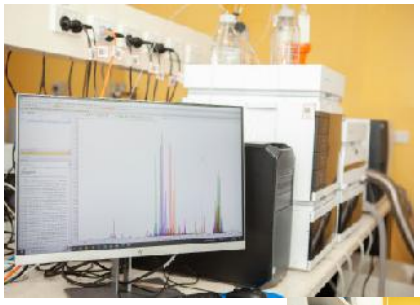
Number of projects: **2**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

- Animal models of disease
- Cell culture - eukaryotes, incl. primary & cell lines
- Metabolomics (incl. lipidomics)
- Bioinformatics
- Flow cytometry

Dysregulation of lipid metabolism underpins multiple diseases including obesity, type 2 diabetes, cardiovascular disease and age related dementia. While lipid metabolic pathways are well characterised, their dysregulation resulting from environmental and genetic influences are less well understood, particularly in a setting of chronic disease. The Metabolomics laboratory has utilised tandem mass spectrometry to developed the only high-throughput lipidomics platform in Australia and has performed some of the largest clinical and population lipidomic studies reported. These have enabled the characterisation of metabolic pathways and identified lipidomic biomarker profiles that are able to better predict disease risk and therapeutic efficacy. Modulation of the same pathways now holds potential as an interventional strategy to prevent, attenuate or treat the major chronic diseases. We are applying our state of the art lipidomic capabilities to characterise the relationship between lipid metabolism and cardiometabolic disease. Clinical translation of the outcomes from these studies will deliver new diagnostic/risk assessment/monitoring tests and therapeutic interventions for chronic disease.



We have a number of Honours/Masters/PhD projects available for 2024 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. *Co-supervisor Dr Thomas Meikle*
3. Revolutionising disease prediction and management through plasma lipidomic profiling. *Co-supervisor Dr Corey Giles*
4. Unlocking the secrets of cardiometabolic diseases through multi-omic integration. *Co-supervisor Dr Corey Giles*

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Cancer Medicine (Olivia Newton-John Cancer Research Institute)

Dr. Quentin Gouil
ONJCRI

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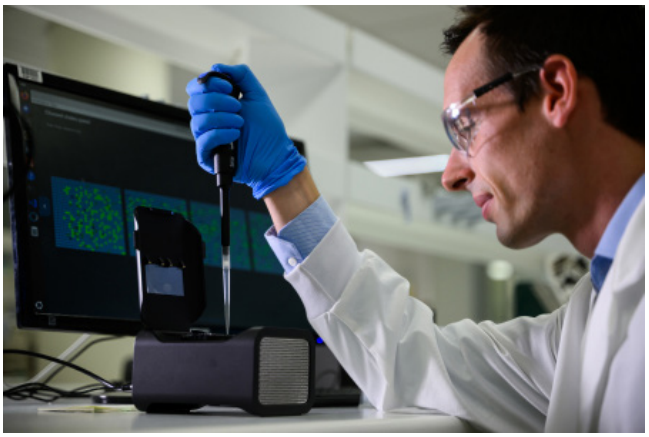
Number of projects: **2**
Full-time or part-time: **Either**
Feb or July start: **Both**
Masters conversion: **Yes**

- Bioinformatics
- Chromosomal and/or nucleotide extraction assays
- Cell culture - eukaryotes incl. primary & cell lines
- Genetic sequencing

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.

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Dr. Andrew Guirguis
ONJCRI

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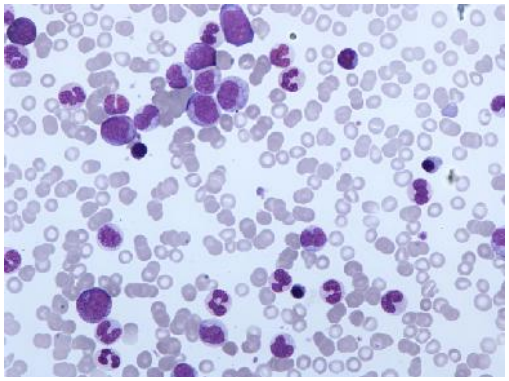
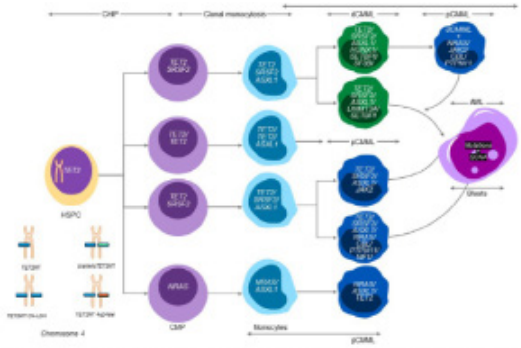
Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **No**

- Bioinformatics
- Cell culture - eukaryotes, prokaryotes
- Histology
- Cell transfection
- CRISR-Cas9 gene editing of cells
- Genetic sequencing
- Flow cytometry
- Molecular cloning

The Blood Cancer Drivers and Therapeutics (BCDT) Lab is dedicated to understanding and preventing the transformation of chronic bone marrow disorders into aggressive secondary acute myeloid leukaemia (sAML). Many older adults develop "pre-leukaemic" syndromes such as chronic myelomonocytic leukaemia (CMML), myelodysplastic syndromes (MDS), or clonal haematopoiesis (CH). While some patients remain stable for years, many progress rapidly to sAML, which has a very poor prognosis. Our lab aims to understand what drives this transformation and how to prevent it. We use cutting-edge tools including CRISPR gene editing, single-cell sequencing, and a powerful barcoding system (SPLINTR) to track how individual cells evolve over time. We also study the bone marrow environment that supports cancer growth and explore how to re-activate the immune system to stop disease progression. Through mouse models, patient-derived samples, and high-throughput screening, we identify molecular changes that increase risk of transformation. The goal is to intervene early and design therapies that block progression. Students joining our lab will contribute to translational research with the potential to transform how pre-leukaemic diseases are detected and treated.

Project 1. Modelling CMML through gene editing to mimic high-risk leukaemia. This project focuses on understanding how genetic mutations contribute to CMML by using CRISPR/Cas9 gene editing to recreate these mutations in the lab. The most frequently mutated genes in CMML include TET2, SRSF2 and ASXL1. When mutated, these aberrant genes disrupt regulation, pushing blood stem cells towards abnormal development and cancer. Starting with cells engineered for a human-like SRSF2 mutation and null for TET2, we will introduce additional CMML-relevant mutations to mimic the disease. We will investigate mutations in ASXL1 and other genes involved in disease progression, such as those in DNMT3A, RUNX1, SETBP1 or CBL. The efficacy of lenzilumab, a targeted therapeutic, will be tested in these compound mutants and treated cells will undergo a CRISPR screen to discover novel drivers of drug resistance and progression. Students will learn to grow and manipulate cells, design and validate genome editing tools, and study how these changes affect cell growth and gene expression. This project will assess how these mutant cells respond to standard therapies and may uncover new genetic factors that drive treatment resistance and disease progression, providing insights into why some patients fail to respond. This is a hands-on opportunity to explore gene editing, genomics and cancer biology while contributing to the future of personalised therapies for blood cancers.





Schematic representation of patterns of clonal evolution in CMML.

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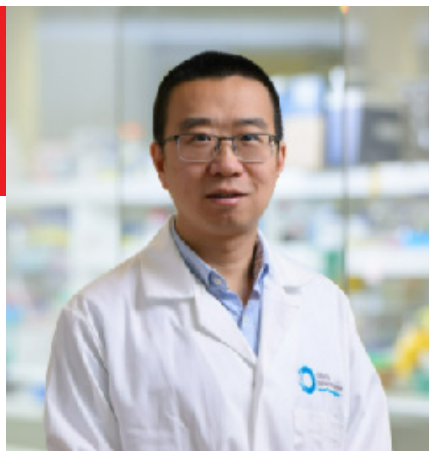
Dr. Yi (David) Ju
ONJCRI



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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: **No**

- Animal handling
- Cell culture - eukaryotes incl. primary & cell lines
- Cell transfection
- Flow cytometry
- Gene expression analysis
- Immunoassays
- mRNA-lipid Nanoparticle formulation

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.

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Prof. John Mariadason
ONJCRI

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

- Cancer
- Cell culture - eukaryotes incl. primary & cell lines
- 3D cell culture
- Molecular cloning & CRISPR-Cas9 gene editing
- Gene expression analysis (sequencing & PCR)
- Protein biochemistry
- Histology (incl. immunohistochemistry)
- Flow cytometry

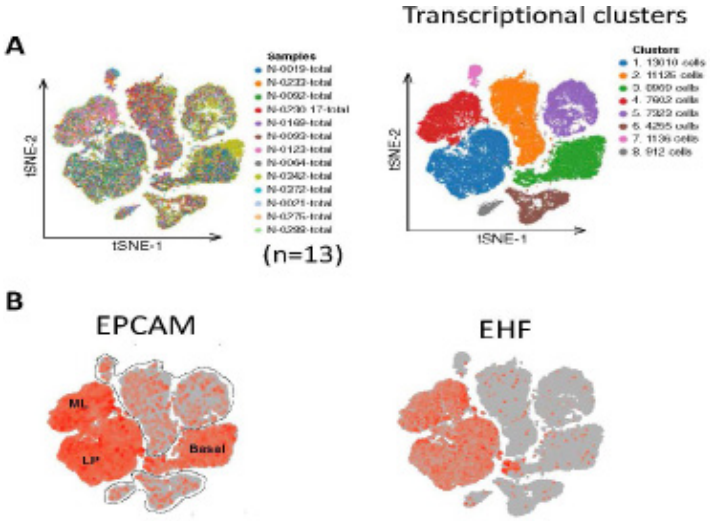
Our team is looking for new ways to treat colon (bowel), breast and liver cancers. We are particularly focused on identifying and targeting major proteins that enable tumour cells to survive in the body, and are testing whether drugs which work in other cancers can be re-purposed for treatment of gastrointestinal cancers.

Project 1. Role of the EHF transcription factor in breast cancer. We recently generated an Ehf knockout mouse, and found that female mice are unable to feed their pups. Examination of the mammary glands of Ehf KO mice revealed a pronounced defect in the development of this tissue during pregnancy. Expression of EHF is also downregulated in human breast cancers, particularly the triple negative subtype, where tumours with low EHF expression have a poorer outcome. Triple negative breast cancers (TNBC's) comprise ~20% of all breast cancers, and have limited treatment options. There is therefore an urgent need to identify the driver genes which give rise of this subtype so that new treatments can be developed.

The goal of this Honours project is to determine the role of EHF in the growth, survival, migration and chemotherapy response in triple negative breast cancer cells. We will achieve this as follows:

1. Determine the level of EHF mRNA and protein expression in 20 breast cancer cell lines, including 5 TNBC cell lines.
2. Determine the effect of EHF re-expression on cell proliferation, survival, migration and response to chemotherapy in TNBC cells.
3. Determine the effect of EHF knockdown in TNBC cells which express EHF on cell proliferation, survival, migration and response to chemotherapy.
4. Identify the target genes of EHF in TNBC cells following EHF knockdown or overexpression.

The student undertaking this project will learn the fundamental concepts of cancer biology, and use a variety of techniques including working with cell line models of breast cancer, western blotting, immunohistochemistry, transfections and assessing response to drug treatment.



EHF expression in total cells from human breast tissue

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Prof. Delphine Merino
ONJCRI

- Cancer
- Cell culture - eukaryotes incl. primary & cell lines
- Confocal fluorescence microscopy
- Molecular cloning & cell transfection
- Animal models of disease
- Flow cytometry
- Genetic sequencing
- Drug assays

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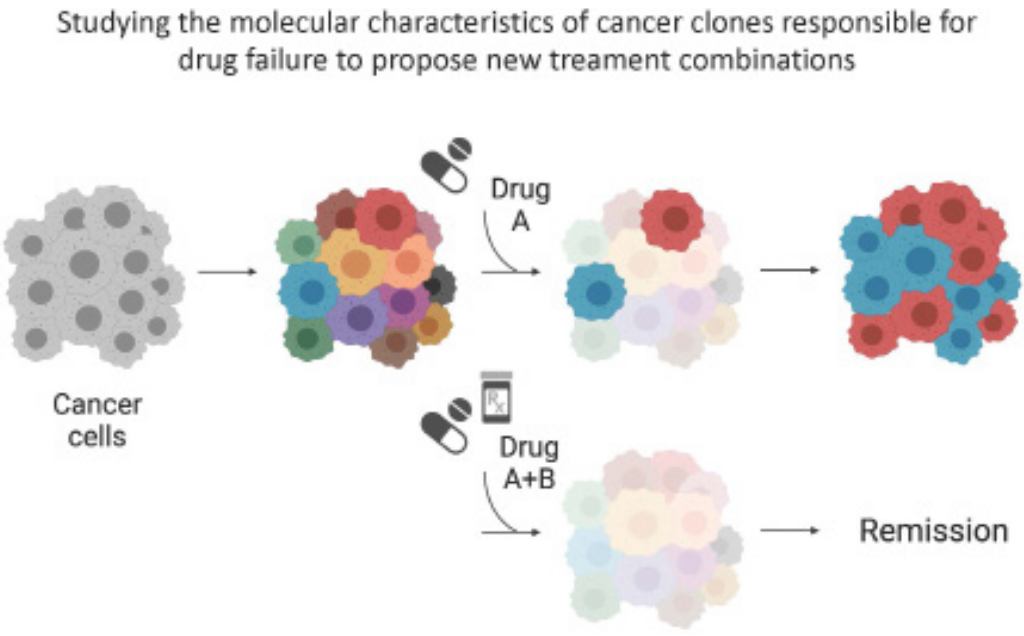
Website: click here

Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Feb only**
Masters conversion: **Yes**

Glioblastoma is the most aggressive form of brain cancer. The lack of improvement for patients with glioblastoma in the last 30 years is multifactorial, including widespread cellular differences between cells in any one cancer mass (tumour heterogeneity), lack of adequate laboratory models and the lack of combinatorial approaches in the clinic.

This project will address all these issues by using new cell lines that have been labelled with fluorescent barcodes, a process called optical barcoding. This technology allows individual cancer cells to be tagged with fluorescent proteins, enabling the identification, quantification and characterisation by imaging, flow cytometry and single cell sequencing. The cell lines have been chosen to include the three common molecular subtypes of glioblastoma (EGFR normal levels in 50%, EGFR high levels in 25% and EGFRvIII mutated in 25%).

The objective of this project is to treat these barcoded cell lines in the lab, using realistic treatment approaches that mirror that used in the clinic. In addition, we will also test novel drugs, especially in combination with chemo-radiation. Using the barcoding tags, we can now identify the individual cells that respond or don't respond, and then analyse these by sequencing to understand what underlies their drug sensitivity. In this way, we will make novel discoveries, identify newer treatment approaches, and identify new ways of determining which patients will benefit best from different therapies.



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Dr. Bhupinder Pal
ONJCRI

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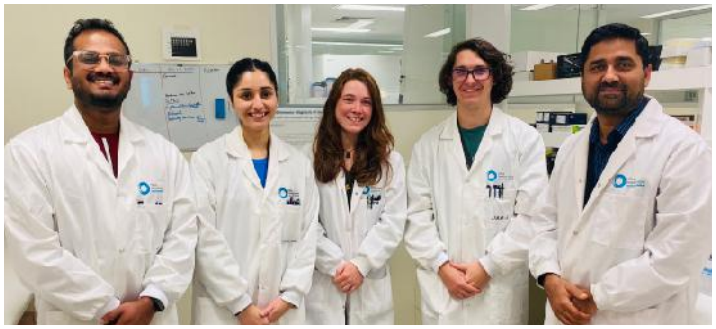
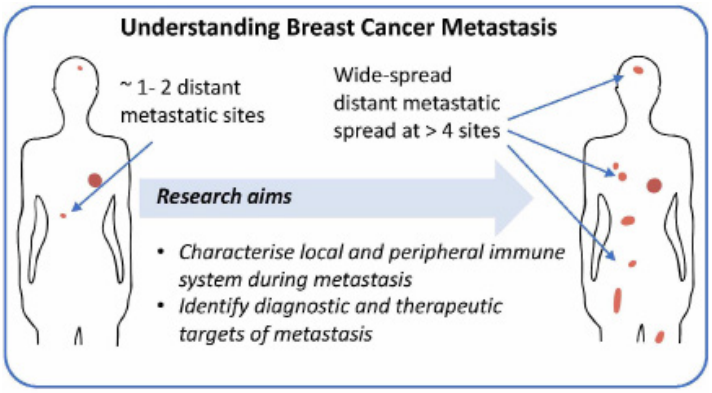
Number of projects: **1**
Full-time or part-time: **Full-time**
Feb or July start: **Both**
Masters conversion: **Yes**

- Cancer
- Animal handling & models of disease
- Single-cell genomics & spatial transcriptomics
- 3D cell culture
- Mammalian cell culture
- Flow cytometry
- Histology & immunoassays
- Bioinformatics

We apply new molecular techniques that allow epigenetic, transcriptomic and spatial gene analysis at the single-cell level. The Cancer Single Cell Genomics Laboratory is embedded within La Trobe University's School of Cancer Medicine at ONJCRI. The lab provides a unique scientific environment that enables students to gain research experience in cancer biology, genomics and development biology. We utilises mouse models and patient samples to gain novel molecular insights during normal mammary gland development and understand the role of tissue heterogeneity during cancer progression.





Project 1. Understanding breast cancer metastatic disease to design new and improved diagnostic and treatment strategies. Majority of breast cancer related deaths are due to metastasis, where cancer spreads to multiple organs including the lung, liver, bone and brain. Our goal is to find a cure for metastatic disease and detect it at an early, treatable stage. The proposed project is built on exciting discoveries made by our lab and is designed to study the role of circulating immune cells in blood and tumour microenvironment during metastasis. Our project offers the opportunity to learn various cutting-edge molecular techniques (Single-cell RNAseq/Spatial transcriptomics) and utilise mouse mammary tumour models to test candidate immunotherapy targets.

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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!

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