Project title:	**Processing and analysis of MRI structural images in cohorts of older adults**
Project duration:	6 to 8 weeks
Description:	The research project involves processing and analysing the T1 structural images acquired as part of the OATS (Older Australian Twin Study: N~1200) and Lothian Birth Cohort (N~700). Similar processing has been performed on cohorts of younger adults and this processing will allow meta-analysing results across cohorts as well as investigating the replicability of results across different populations and age groups. Data analysis will consist in quantifying the variance explained by brain differences in the population.
Expected outcomes and deliverables:	Scholars will gain expertise in state-of-the-art processing of T1 images, using FreeSurfer 6.0. In addition, the scholars may gain skills in programming (bash, matlab, R) and data analysis (mixed models). Students will also be asked to produce a report or oral presentation at the end of their project.
Suitable for:	For example, this project is open to applications from students with an interest in brain imaging, big data, and statistical analyses. We expect motivated students, preferably with some experience or special interest in imaging or large datasets, programming and high performance computing.
Primary Supervisor:	Baptiste Couvy-Duchesne, Peter Visscher, Naomi Wray
Further info:	Do not hesitate to contact us directly for more information or expression of interest. Contact: Baptiste Couvy-Duchesne (Post-Doc), b.couvyduchesne@uq.edu.au

Project title:	**Identifying transcriptomic biomarkers of drug resistance in cancer cells using deep learning**
Project duration:	6 to 8 weeks
Description:	There has been substantial progress in identifying driver mutations for tumour initiation and development, and for identification of biomarkers which distinguish different types of cancer. However, there has been substantially less progress made on identification of genomic and transcriptomic biomarkers for development of drug resistance. Drug resistance mutations may only be present in a small proportion of tumour cells, making these mutations extremely challenging to detect. We hypothesise that by combining information about the transcriptome and drug resistance of cancer cell, it will be possible to identify drug resistance biomarkers, which can then be used to predict drug resistance from single-cell tumour transcriptome data. This project will use approaches from machine learning and statistics to build models predicting drug resistance from RNAseq data on approximately 100 cell lines. These cell lines have also been profiled for drug resistance against 265 compounds by the ' Genomics of Drug Sensitivity in Cancer' project.
Expected outcomes and deliverables:	Scholars will gain experience in high performance computing, analysis of RNAseq data, and development of predictive models using machine learning approaches, such as neural networks
Suitable for:	This project is open to applications from students with a background in mathematics or computer science.
Primary Supervisor:	Associate Professor Lachlan Coin
Further info:	Please contact Lachlan if interested in this project : l.coin@imb.uq.edu.au

Project title:	**Comparative genomics of coral reef symbionts**
Project duration:	Ten (10) weeks
Description:	*Symbiodinium* are a specialised group of dinoflagellate algae that grow symbiotically with diverse coral reef animals including corals and sponges. A modest, episodic increase in ocean water temperature can break down the coral-dinoflagellate symbiotic association (thus cause coral bleaching); unless this symbiosis is soon re-established, corals are at risk for starvation, disease and death. Our group is interested in the genome evolution of *Symbiodinium* and their closely related polar species, specifically related to their evolutionary transition from free-living to symbiotic lifestyles, and its functional implications for the coral host and the health of coral reefs in light of global climate change. This project aims to discover genes and functions in *Symbiodinium* that are specific and/or relevant to environmental adaptation using a comparative genomic approach, using newly sequenced and existing data.
Expected outcomes and deliverables:	This project is strictly computational based, with no wet-lab component. The researcher will acquire skills in genomics and bioinformatics of non-model systems, specifically in the analysis of high-throughput sequencing data, comparative analysis of large-genome-scale data, and functional annotation of genome sequences. The researcher will work as part of a team, and is expected to produce a report or oral presentation at the end of their project. Research outcomes may be included in a scholarly publication.
Suitable for:	Advanced undergraduate students (year 3+) or Masters students with a strong background in life sciences (i.e. biology and related subject areas), mathematics, and/or computer sciences. A background in genomics and/or bioinformatics is desirable but not essential. This project will require scripting (e.g. Python, PERL), high-performance computing in the UNIX environment, and/or R.
Primary Supervisor:	Dr Cheong Xin Chan
Further info:	Please contact Dr Chan at c.chan@imb.uq.edu.au prior to submitting an application.

Project title:	**Strategies to Target Plasma Membrane Phospholipids of Bacteria**
Project duration:	*8-10 weeks*
Description:	Many of the antimicrobial agents developed in the Cooper group exert their action by targeting the fidelity of the bacterial membrane, either through physical disruption of membrane integrity or by impairment of the biosynthetic machinery required for the synthesis of critical membrane precursors. The unique lipid composition of Gram-positive bacterial membranes, which often contain an abundance of negatively charged phospholipids, provides an opportunity to rationally design antibiotic candidates that preferentially target bacterial membranes over eukaryotic membranes, which are essentially neutral. Indeed, our Vancapticin program is a successful example of this approach, where we restored the activity of vancomycin toward vancomycin-resistant bacteria using vancomycin-peptide conjugates. Cardiolipin is a unique phospholipid found in both Gram-positive and Gram-negative bacterial membranes, and constitutes an important component of the inner mitchondrial membrane of eukaryotes. Several recently discovered antibiotics have been proposed to target cardiolipin, suggesting it may be a new molecular target for antibiotics. This project will explore new strategies to target bacterial cardiolipin using short peptide sequences designed to interact with this unique phospholipid.
Expected outcomes and deliverables:	We have promising preliminary data for our compounds – they exhibit whole cell antibacterial activity and are able to synergistically restore the activity of several antibiotics that have been rendered ineffective due to resistance. At this stage, we seek to understand how our compounds interact with bacterial membranes, and use this information to synthesise additional analogues to explore structure-activity relationships. The intern will have the opportunity to understand the unique challenges of antibiotic discovery and development in a globally recognised research group, and contribute to a high impact research area. Importantly, projects are designed to challenge the intern, and will NOT involve routine repetitive analysis. As such, it will require the intern to think beyond the usual "laboratory practical manual", where an analytical mind and attention to detail is an asset for identifying and overcoming unforeseen difficulties. The intern will have a clear set objectives and will receive continual guidance during the course of the project.
Suitable for:	This project is open to applications from students with a background in chemistry (second/third year chemistry) and a keen interest in medicinal chemistry, drug discovery and design, and the interplay between biology and chemistry.
Primary Supervisor:	Dr Karl Hansford
Further info:	For additional information, contact Karl directly: k.hansford@imb.uq.edu.au

Project title:	**Visualization of neuronal protein sorting events by high-resolution structural biology methods.**
Project duration:	6-8 weeks
Description:	**Summary of research interests:** We are focused on understanding the fundamental cellular process of intracellular protein sorting in human neuronal cells. Specifically, we study protein machineries that operate as cargo vans within the cell. These protein complexes direct the cargo (cell surface receptors) either to recycling or degradative sorting routes thereby maintaining the overall cellular homeostasis. Defects in these protein machineries result in abnormal trafficking of cell surface receptors that has implications in several neurodegenerative diseases including Parkinson's, amyotrophic lateral sclerosis. We take advantage of hybrid structural biology approaches to obtain an overall three-dimensional map of these trafficking protein complexes. We also employ biophysical, biochemical and molecular biology methods to decipher how these protein assemblies (cargo vans) engage their cargo (cell surface receptors). We adopt multidisciplinary approach and together with our cell biology collaborators we aim to construct atomic resolution maps of cellular sorting events.
Expected outcomes and deliverables:	*Students will get hands on training in molecular cloning, recombinant protein expression and purification. They will also be able to learn protein characterisation techniques such as size exclusion chromatography, multi angle laser light scattering. The student will also study protein-protein, protein-lipid and protein-ligand interactions using pull-down assays, Isothermal titration calorimetry and* optical interferometry. Finally, if time permits, training will be given to grow protein crystals for protein atomic structure determination.
Suitable for:	*This project is open to applications from students with a background in biochemistry or cell biology 3-4 year students.*
Primary Supervisor:	Dr. Rajesh Ghai and A/Prof. Brett Collins
Further info:	r.ghai@uq.edu.au

Project title:	**New paradigm for discovering antibiotics**
Project duration:	The timeline for the project is 6-10 weeks
Description:	**Background:** Natural products possess enormous structural and chemical diversity that is unsurpassed by any synthetic libraries. About 40% of the chemical scaffolds found in natural products are absent in today's medicinal chemistry repertoire. Based on various chemical properties, combinatorial compounds occupy a much smaller area in molecular space than natural products. Although combinatorial compounds occupy a well-defined area, natural products and drugs occupy all of this space as well as additional volumes. Most importantly, natural products are evolutionarily optimized as drug-like molecules. This is evident upon realization that natural products and drugs occupy approximately the same molecular space. The discovery of antibiotics more than 70 years ago initiated an era of drug innovation in human and animal health. Microbes have demonstrated their capacity to produce valuable bioactive metabolites. For example, actinomycetes supply >50% of all antibiotics in use today, including glycopeptides (e.g. vancomycin), aminoglycosides (e.g. streptomycin), anthracyclines (e.g. tetracyclines) and important anticancer (e.g. doxorubicin) and anthelmintics (e.g. ivermectins) agents. In addition, fungi have also been significant producers of important drugs with well-recognised antibiotic such as penicillins. The history of natural product discovery is full of remarkable stories. *Therefore, the historic impact of microbial metabolites on human health has been profound*. However, these discoveries were interrupted by the emergence of drug resistance pathogens such as *Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumanii, Pseudomonas aeruginosa* and *Enterobacter* species (the so-called ESKAPE pathogens). As a result there is an ever increase in the demands for new discoveries to overcome the threat from these pathogens. **Hypothesis:** Microbial biodiscovery from new sources will deliver valuable knowledge and new chemistry that will inform basic and applied science against multi-drug resistance bacteria **Aims:** 1. Cultivate a library of Australian microbes isolated from different sources such as soil from caves and mangroves. 2. Chemical and biological profiling for the crude extracts from microbes. **Approaches:** This project will deliver a new microbial biodiscovery paradigm, better suited to discover new antibiotics effective against clinically relevant pathogens such as *Mycobacterium tuberculosis* and other drug resistant bacteria.
Expected outcomes and deliverables:	The scholar will gain skills in cultivating microbes using micro-bioreactors and extraction of microbial crude extracts. In addition, the scholar will gain skills in using high-performance liquid chromatograph (HPLC-DAD-MS) and ultra high performance liquid chromatography (UPLC-DAD). They will also have the chance to run antimicrobial and anticancer assays. All these skills will enable to scholar to present an oral presentation and write a comprehensive report.
Suitable for:	This project requires 3 students to work on different samples for microbial isolation and purification. It is highly recommend that the student(s) have a good chemistry and microbiology background and are familiar with microbial cultivation traditional techniques.
Primary Supervisor:	Prof. Robert J. Capon Dr Zeinab Khalil
Further info:	If you have any enquires or interested, please feel free to email me on z.khalil@uq.edu.au

Project title:	**NMR Spectroscopy**
Project duration:	6 – 10 weeks
Description:	Our work focuses on applying NMR spectroscopy in drug design and development. By determining the structures of biologically active molecules and thus design novel drugs. We have a particular interest in stabilising proteins by joining their ends to make circular molecules.
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Professor David Craik
Further info:	Please contact David Craik before at d.craik@imb.uq.edu.au

Project title:	**Chemistry and Human Therapeutics**
Project duration:	6 – 10 weeks
Description:	Our group seeks to understand molecular mechanisms of chemical reactions, biological processes, disease development and drug action. Understanding how molecules interact, how chemical and biological reactions work, and how structure influences activity enables us to design, synthesize and evaluate enzyme inhibitors, receptor antagonists and protein-binding ligands as new drugs for cancer, infections diseases, inflammatory disorders, diabetes and obesity, and Alzheimer's disease. New drugs discovered by our chemists are studied by biochemists, cell biologists and pharmacologists in our group for their effects on human cells and in animal models of human diseases.
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Professor David Fairlie
Further info:	Please contact David Fairlie before at d.fairlie@imb.uq.edu.au

Project title:	**Microbial structural biology and solar biofuels from algal cells**
Project duration:	6 – 10 weeks
Description:	Our research focuses on the use of microalgae for the development of clean fuels to reduce CO2 emissions, increase energy security and enable sustainable economic development.
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Professor Ben Hankamer
Further info:	Please contact Ben Hankamer at b.hankamer@imb.uq.edu.au

Project title:	**Neuropharmacology and Pain**
Project duration:	6 – 10 weeks
Description:	Sensory neurons are fundamental for our interaction with the external world by detecting stimuli including cold, heat, touch, pressure, vibration and tissue injury. These external stimuli are then transformed to electrical signals through specialised molecules, which detect temperature, mechanical stimulation and various chemicals. Although significant progress has been made towards determining the molecular identity of selected receptors and ion channels involved in sensory perception, our understanding of how these contribute to sensory perception and in particular pain is limited. Toxins from plants and animal venoms have provided highly specific tools, which allow dissection of the mechanisms of sensory perception and pain and may provide novel molecules with analgesic potential.
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Dr Irina Vetter
Further info:	Please contact Irina Vetter at i.vetter@imb.uq.edu.au

Project title:	**Vascular biology and development**
Project duration:	6 - 10 weeks
Description:	Our research investigates how blood and lymphatic vessels form from pre-existing vessels. We aim to discover new genes and molecular pathways that regulate vascular growth during the development of the embryo and in disease. To do this, we use the zebrafish embryo as a model biological system as it is similar to mammalian models and humans, and offers a unique combination of direct imaging techniques, embryological tools and genetic tools for the study of developmental processes.
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Dr Ben Hogan
Further info:	Please contact Ben Hogan at b.hogan@imb.uq.edu.au

Project title:	**Genetics and cell biology of cardiac development**
Project duration:	6 – 10 weeks
Description:	The heart is essential for life support and any defects that alter its structure or function can be fatal. Our laboratory, investigates how the heart forms by using forward genetics to identify new, previously unidentified genes that regulate cardiac development. My research aims to understand how to build a heart
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Dr Kelly Smith
Further info:	Please contact Kelly Smith at k.smith@imb.uq.edu.au

Project title:	**Nuclear receptors and Metabolism**
Project duration:	6 – 10 weeks
Description:	Our research focuses on elucidating the functional role of nuclear hormone receptors in the regulation of metabolism in the context of metabolic disease (eg. Dyslipidaemia, diabetes and obesity) and breast cancer. The nuclear hormone receptors (NR) belong to a superfamily of hormone-dependent DNA binding factors that translate pathophysiological, metabolic, and nutritional signals into gene regulation. Dysfunctional NR signalling results in obesity, type 2 diabetes and cancer. Metabolic disease increases the risk and incidence of cancer. The majority of our research is focused on skeletal muscle, because NRs are expressed in skeletal muscle, which is a peripheral tissue that accounts for ~40 percent of the total body mass and energy expenditure, and is a major site of fatty acid and glucose oxidation. Consequently, muscle has a significant role in insulin sensitivity, the blood lipid profile, and energy balance. The objective of our current research is to examine the role of 'orphan' NRs in metabolic disease, and breast cancer. We are testing the hypothesis that the orphan NRs, for example RORs and NR4As, control pathophysiological the process in metabolic disease and cancer
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Professor George Muscat
Further info:	Please contact George Muscat at g.muscat@imb.uq.edu.au

Project title:	**Inflammasomes in infection and inflammatory disease**
Project duration:	6 – 10 weeks
Description:	The innate immune system is critical to defence against infection, but also drives unhealthy processes in inflammatory disease. An important emerging player in innate immunity in both of these settings is the 'inflammasome' pathway. Inflammasomes are molecular machines that trigger cytokine maturation and immune system activation in response to signals indicating cellular 'danger'. While the inflammasome pathway is critical for host defence against infection, it is also a key driver of unhealthy inflammation in many human diseases. We use a wide variety of molecular and cell biology techniques, in conjunction with animal models and human clinical samples, to investigate the biology of inflammasomes in host defence and inflammatory disease at the molecular, cellular and organismal levels.
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Dr Kate Schroder
Further info:	Please contact Kate Schroder at k.schroder@imb.uq.edu.au

Project title:	**Stop gulping! A new way to kill cancer cells.**
Project duration:	6 weeks but ideally used as an introduction to Masters/Honours or 3rd year research subject since a longer immersion in this project is required to acquire the necessary skill set.
Description:	Mammalian cells use macropinocytosis – a pathway for **gulping** fluid and particles – to ingest many things from pathogens to nutrients. Cells in low nutrient environments, like at the middle of a tumour or at sites of infection – need to upregulate macropinocytosis to ingest protein as an extra energy source for their survival and growth. Aggressive cancer cells cannot grow without macropinocytosis and blocking this gulping pathway is now being investigated as a target for new cancer drugs. This project will use cancer cells expressing fluorescently tagged proteins to image macropinocytosis in live cells to document (visualize in 3D) macropinosome molecular landscapes and functions. This information will allow us to choose specific macropinosome proteins to target with drugs in order to stop/control gulping and growth in cancer cells and immune cells.
Expected outcomes and deliverables:	Students will get to work with experts at the cutting edge of cell imaging using some of the most sophisticated microscopes in the world. You will acquire career skills in imaging, image analysis and visualization techniques. You will work with cancer cells in the lab. Students will be asked to produce a report or oral presentation to the lab at the end of their project. This work is being conducted with other labs as part of an international collaboration.
Suitable for:	Those who understand some cell biology and share our desire to understand and treat disease. Those with a keen interest in learning microscopy and cell imaging as a future career skill, with or without serious computing/programming /visualization. Those willing to work hard and learn lots. AI, VR, a bonus.
Primary Supervisor:	Professor Jenny Stow, IMB
Further info:	Please submit your application. You can email me with the title 'summer student' if you have urgent questions. J.stow@imb.uq.edu.au

Project title:	**Pathogen surveillance, innate immunity and inflammation**
Project duration:	6 – 10 weeks
Description:	My group studies the innate immune system. Innate immune cells, such as macrophages, express a broad repertoire of pattern recognition receptors that act as danger sensors. For example, members of the Toll-like Receptor (TLR) family detect a number of pathogen-associated molecular patterns such as LPS from Gram-negative bacteria. Macrophage activation through TLRs regulations expression of genes involved in antimicrobial responses and inflammation. Thus, TLR signalling is required for effective control of invading microorganisms, but if dysregulated, contributes to acute and chronic inflammatory diseases. We study TLR signalling pathways and the function of the novel TLR-regulated genes in inflammation and in responses to bacterial pathogens (e.g *Salmonella*, uropathogenic *E. coli*).
Suitable for:	This project would be suitable for candidates looking to progress to honours and/or a PhD
Primary Supervisors:	Prof Matt Sweet
Further info:	Please contact Matt Sweet at m.sweet@imb.uq.edu.au

Project title:	**Cytoskeletal crosstalk at cell-cell junctions**
Project duration:	10 weeks
Description:	Cell-cell junctions are essential mechanical and signaling hubs with a wide diversity of molecules involved. Among these molecules are cortical signaling and cytoskeletal regulators which together strongly influence micro- and macro-morphology via downstream signaling pathways. Despite our increasing knowledge of the role of individual cytoskeletal filaments at cell-cell junctions, the crosstalk between different filaments is largely understudied. In this project we will focus on the interplay between actin filaments and microtubules, and aim to elucidate the molecules and mechanisms that maintain the tightly controlled functions of cell-cell junctions. To do so, we will combine super resolution microscopy techniques with in vitro and cellular experiments, and analyse obtained images with sophisticated image analysis tools.
Expected outcomes and deliverables:	Students will gain experience in general molecular laboratory work, microscopy sample preparation, fluorescence imaging using state-of-the-art microscopy systems and image analysis. In addition, they will read literature, write a report and present in departmental subgroup meetings.
Suitable for:	This project is open to applications from students with a background in biomedical sciences who have hands-on laboratory experience.
Primary Supervisor:	Dr. Ivar Noordstra and Prof. Alpha Yap
Further info:	For further information please contact Ivar Noordstra i.noordstra@imb.uq.edu.au or Alpha Yap a.yap@uq.edu.au

Project title:	**The non-coding transcriptome in stem cell differentiation**
Project duration:	Summer term
Description:	The non-coding transcriptome remains one of the least understood components of the genome. We have identified more than 2000 unannotated non-coding RNAs during cardiac differentiation of human stem cells. This project will use computational strategies to identify the species, map them to the genome, and understand their biology in regulating the protein coding transcriptome. The project will have a close interface with cell biologists in the lab for functional testing of candidate non-coding RNAs *in vitro.*
Expected outcomes and deliverables:	This project will contribute to work that may result in a publication depending on the quality of outcomes.
Suitable for:	The project is open to students with training in bioinformatics with familiarity using R, ~~Pytho~~n and Linux commands. Familiarity with genetics, managing large genomics data sets, and non-coding RNA biology is desirable but not required.
Primary Supervisor:	Co-supervised by Nathan Palpant and Quan Nguyen, Institute for Molecular Bioscience
Further info:	If you have questions please email us n.palpant@uq.edu.au and quan.nguyen@imb.uq.edu.au

Project title:	**Implementing machine learning to find disease markers from single cell and population genomics data**
Project duration:	Summer term
Description:	Genomics data are being generated at an unprecedented speed, both in scale (hundreds of thousands of samples) and resolution (single cell). Machine learning in human genomics is an emerging field, which uses the power of statistics and high-performance computers in combination with biological knowledge to extract new information relevant to disease diagnosis and treatment. This project will implement current methods to combine existing single-cell RNA sequencing data with public Cancer Cell Atlas data to find gene markers for cancer diseases.
Expected outcomes and deliverables:	This project will contribute to work that may result in a publication depending on the quality of outcomes. The student will strengthen multidisciplinary skills, including writing R/Python scripts, applying statistical models, and understanding biological pathways implicated in cancer diseases.
Suitable for:	The project is open to students with training in bioinformatics with familiarity using R/Python and Linux commands.
Primary Supervisor:	Supervised by Dr Quan Nguyen
Further info:	If you have questions please email quan.nguyen@uq.edu.au

Project title:	**Discovery and characterisation of novel conotoxins from fish hunting cone snail venom.**
Project duration:	6-10 weeks
Description:	Venomous marine cone snails have evolved with one of the most sophisticated envenomation strategies that serve both predatory and defensive roles. Their venom typically comprises a complex cocktail of potent peptides known as conotoxins or conopeptides. These peptides are regarded as true pharmaceutical treasure, with one marketed drug and many more original molecules to be discovered. In this project, we propose to isolate and characterise a two specific groups of peptides (kappaA peptides) used by fish hunting cone snails to cause immediate rigid paralysis with stiff fibrillating fins. Despite their important role in prey capture the pharmacological target of these peptides are not yet identified. Therefore, first phase of this project will focus on purification of these peptides from collected venom samples (from *C. magus* and *C. striatus*). The second phase involves in developing a behavioural assay using Zebrabox to determine the behavioural changes upon administration of the peptides. Along with kappaA peptides, few other characterised peptides groups (calcium channel blockers, nicotinic receptor blockers etc) will also be tested using the developed assay.
Expected outcomes and deliverables:	The scholar is expected to gain skills in peptide purification using HPLC, peptide identification using several mass spectrometric methods (MALDI, LC-MS/MS), behavioural assays with Zebra fish models, human cell culture and performance of FLIPR based assays. Students may also be asked to produce a report or oral presentation at the end of their project and may have an opportunity to generate publications from their research depending on the results.
Suitable for:	Students with brief background in biochemistry or Molecular biology are preferred. 2-4 year students are eligible to apply. Previous lab experience is preferred.
Primary Supervisor:	Himaya Siddhihalu Wickrama Hewage
Further info:	S.W.A. Himaya IMB, Level 6, Room 6.077 Email: h.siddhihalu@imb.uq.edu.au Phone: 033462722 If needed I am available to be contacted by students prior to submitting an application.

Project title:	**Investigating Disease Mechanisms using Cell-free DNA**
Project duration:	6 to 8 weeks
Description:	The aim of this project is to investigate cell-free DNA in motor neuron disease (MND). We hypothesise that cell-free DNA (abundance and cell-of-origin) will differ in MND patients compared to controls, to be used as a biomarker of disease.
Expected outcomes and deliverables:	In this project, you will have the opportunity to work with a multi-disciplinary team focussed on understanding the genetic and environmental mechanisms contributing to motor neuron disease (MND). You will be exposed to both clinical research and scientific research programs allowing you to be involved in both laboratory (bench) work and dry-lab (computer) analyses, which may result in the generation of research publications.
Suitable for:	This project is open to applications from all students, with clinical focus it may interest pre-medical provisional students interested in MD-HDR pathway.
Primary Supervisor:	Dr Fleur Garton
Further info:	Do not hesitate to contact me directly for more information or expression of interest. Contact: f.garton@imb.uq.edu.au 3346 2626

Project title:	**Using genetic data to inform the potential for cardiovascular drugs in treatment of neurological disorders**
Project duration:	10 weeks
Description:	Aim: Determine if a gene whose protein product is targeted by cardiovascular drugs is in the causal pathway for neurological disorders such as Alzheimer's, Parkinson's, Major Depression and schizophrenia. Approach: The project will use large-scale genetic and genomic data to perform Mendelian randomisation analyses to determine if there is a causal role of proteins targeted by cardiovascular drugs in neurological disorders. Importance: If a causal role is supported by the analysis, this would provide evidence to use such drugs or modified versions of the drugs for a different disease than it was originally intended.
Expected outcomes and deliverables:	They will apply statistical genetic approaches to answer questions that have real translational potential to clinic. The project may lead to publication as a first author. They will also be asked to give an oral presentation to the group.
Suitable for:	The project is open to students who have completed the **Statistical Analysis of Genetic Data (STAT7306) at UQ (https://my.uq.edu.au/programs-courses/course.html?course_code=STAT7306)** They would need to be familiar with using R programming. A background in genetics/bioinformatics would be favoured.
Primary Supervisor:	Sonia Shah
Further info:	sonia.shah@imb.uq.edu.au Please contact me for an informal discussion prior to submitting an application.

Project title:	**Visualisation of multi-omic datasets for endometrium**
Project duration:	10 weeks
Description:	Human endometrium is a highly specialised and complex tissue that plays a vital role in female fertility, embryo implantation and pregnancy. Our group is focused on using genetics and genomics to increase our knowledge of the factors affecting endometrial biology and contributing to endometrial diseases such as endometriosis. We have produced multiple omic datasets in our research including the largest expression and methylation datasets for endometrium. The aim of this project is to design and create a computer/web based interactive visualisation tools that will allow members of our group and our collaborators to access information from, and integrate results across our datasets. This resource would allow researchers to interrogate various aspects of our data to answer research questions and ultimately increase our understanding of genetic and epigenetic mechanisms affecting the endometrium and endometrial disease biology.
Expected outcomes and deliverables:	The student will gain skills in handling and interpreting various omic datasets including expression array data, methylation array data, RNA-seq data and genotype data. They will also develop skills in data visualisation and integration, programing and webpage/app development. The student will also be a part of manuscript preparation to generate publications from their work.
Suitable for:	This project is open to applications from students with a basic background in computing, data visualisation, statistics and/or bioinformatics. Any experience in statistical computing software (eg. R) and data visualisation software (eg. Shiny, UCSC genome browser, IGV) is also preferred but not mandatory.
Primary Supervisor:	Professor Grant Montgomery
Further info:	Professor Grant Montgomery Ph: +61 7 3346 2612 Email: g.montgomery1@uq.edu.au Dr Sally Mortlock Ph: +61 7 3346 2077 Email: s.mortlock@imb.uq.edu.au

Project title:	**Integrating omic data to identify target genes for endometriosis**
Project duration:	10 weeks
Description:	Endometriosis is a disease occurring in 7-10% of women whereby tissue similar to that of the endometrium grows outside the uterus. Large scale genetic studies have identified 14 genomic regions associated with endometriosis. Recent investigations have also found associations between genetic variants and gene expression and methylation in the endometrium. The aim of this project is to integrate genetic, expression and methylation data with transcript level data from >300 endometrial samples to investigate genetic and epigenetic mechanisms regulating genes in endometriosis risk regions. Data from publically available databases such as ENCODE and Roadmap will also be downloaded to functionally annotate regions. Mapping out regulatory mechanisms in these risk regions will help prioritise target genes for functional analysis.
Expected outcomes and deliverables:	The student will gain skills in analysis of multiple omic datasets including, gene expression array data, methylation array data, RNA-seq data and genotype data. They will also develop skills in data visualisation and integrating and interrogating publically available datasets. The student will also be a part of manuscript preparation to generate publications from their research.
Suitable for:	This project is open to applications from students with a basic background in genetics, statistics and/or bioinformatics. Any experience in statistical computing software (eg. R) and data visualisation (eg. UCSC genome browser, IGV) is also preferred but not mandatory.
Primary Supervisor:	Professor Grant Montgomery
Further info:	Professor Grant Montgomery Ph: +61 7 3346 2612 Email: g.montgomery1@uq.edu.au Dr Sally Mortlock Ph: +61 7 3346 2077 Email: s.mortlock@imb.uq.edu.au

Project title:	**Towards the synthesis of potent small molecule immunostimulants**
Project duration:	10 weeks
Description:	Mucosal associated invariant T cells (MAIT) cells are important immune T cells that protect humans against many bacteria, fungi and viruses. In 2014, we found that a bacterial compound related to riboflavin potently activated MAIT cells (EC_{50} 2 pM). This compound, known as 5-OP-RU, is a critical reagent in MAIT cell immunological research. We currently synthesise 5-OP-RU and analogues, and distribute these to national and international collaborators, leading to other recent key discoveries. *Aim: Synthesise advanced intermediates of 5-OP-RU and/or related immunostimulants to enable Australian and international MAIT cell research.*
Expected outcomes and deliverables:	The research student will gain experience in carrying out complex multistep synthesis towards biologically active compounds. This includes the use of NMR spectroscopy, automated flash chromatography, and advanced anhydrous reaction manipulation skills. The research will be conducted Prof. David Fairlie's laboratory at the Institute for Molecular Bioscience. The student will be exposed to a multidisciplinary research environment, consisting of computational, small molecule and peptide chemists, as well as molecular biologists and experimental pharmacologists. The group is also the QLD node of the ARC Centre of Excellence in Advanced Molecular Imaging. This is a very exciting immunology field, and this chemistry project will be expected to produce advanced intermediates of potent immunostimulants to enable MAIT cell research worldwide.
Suitable for:	The project is open to 3rd to 4th year applicants with a strong background in organic chemistry. Experience in a synthetic chemistry lab is highly desirable.
Primary Supervisor:	Dr Jeffrey Mak
Further info:	Please contact Dr Mak (j.mak@uq.edu.au) prior to submitting an application, or for further information.

Project title:	**Searching for Sortase A inhibitors with antimicrobial potency**
Project duration:	10 weeks as a UQ Summer project with the possibility to extend it as a Master Research Project
Description:	The project is aims to utilise the activity of the enzyme, Sortase, within Gram positive bacteria, to act on an engineer peptidic compound with antibiotic activity. Cleavage of the peptide by Sortase will result in one part of the peptidic compound being covalently incorporated to the peptidoglycan at the surface of the bacteria, such that it can act to potentially inhibit the bacteria membrane maturation process, while bound to the bacterial cell surface. A second fragment is released and then may non-covalently interact with the surface of the cell wall to have additional inhibitory actions. Applying the bacterial enzyme to incorporate the antibiotic close to the bacteria membrane can improve its clinical performance by increasing the local drug concentration and at the same time reduce the side effects caused by high dosing. To monitor the second fragment release by the action of Sortase, a specific analytical assay will be developed.
Expected outcomes and deliverables:	This project will suit students who are interested in chemistry and analytical chemistry and will enable the students to get hands on experience with analytical chemistry equipment and techniques, as well as undertake preparative scale compound isolation and structure elucidation with NMR and MS.
Suitable for:	This project is open to applications from students with a background in (bio)chemistry, 3-4 year students.
Primary Supervisor:	Dr Zyta Ziora
Further info:	Zyta Ziora <z.ziora@imb.uq.edu.au Mark Blaskovich <m.blaskovich@imb.uq.edu.au

Project title:	**Molecular mechanisms involved in liver fibrosis**
Project duration:	6 – 8 weeks.
Description:	Chronic liver disease (CLD) can be caused by viral hepatitis, alcohol and/or fatty liver disease. In CLD, repeated bouts of cellular injury and damage drives inflammation, leading to hepatic stellate cell activation and tissue-destructive fibrosis. This project will investigate molecular mechanisms involved in hepatic stellate cell activation, including in response to inflammation-associated stimuli. The project will employ molecular and cell-based approaches to do so.
Expected outcomes and deliverables:	Successful applicant(s) should gain knowledge and skills in standard cellular and molecular techniques (e.g. cell culture, cloning/sub-cloning, gene expression analyses such as qPCR and immunoblotting), as well as in data analysis and presentation. Students may be asked to produce a short report and/or deliver a short oral presentation at the end of their project.
Suitable for:	This project is open to UQ-enrolled students only. Applicants should have a background in cell biology, immunology and/or biochemistry at Undergraduate level. This project would be suitable for candidates looking to progress to honours and/or a PhD.
Primary Supervisor:	Prof Matthew Sweet
Further info:	Please contact Matt Sweet (m.sweet@imb.uq.edu.au) before submitting an application.

Project title:	Integrative data analysis of the roles of noncoding RNAs in transcriptional regulation in cardiac differentiation
Project duration:	Summer term
Description:	This project aims at investigating the transcriptional regulation roles of noncoding RNAs in cardiac differentiation by integrating multiple data types. The data represent transcriptional states at multiple time-points of a cell line undergoing differentiation from induced pluripotency state to mature cardiomyocytes. We have generated RNA-seq and sRNA-seq data and have collected relevant ChiP-seq data. We will generate in-house CAGE (Cap Analysis of Gene Expression) data and will obtain HiC data from collaborators. CAGE sequencing detects the expression of protein-coding genes (mRNA), long non-protein coding genes (lncRNA), as well as the activity of active promoters and enhancers. HiC data provides genome-wide chromatin looping information for inferring enhancer-promoter-gene interactions. Using sRNA, RNA-seq and CAGE we comprehensively quantify, at the genome-wide scale, multiple snapshots of the transcriptome, including the expression levels of mRNA, lncRNA and small RNA. Combining CAGE, HiC data, and ChiP-seq data we will infer genome-wide regulation pattern via DNA-Protein and DNA-DNA interactions. The regulatory information includes activities of enhancers and promoters, and interaction between enhancers/promoters with possible gene targets, and binding activities of relevant transcription factors. Furthermore, network correlation analysis between ncRNA and mRNA would reveal potential underlying molecular mechanisms of how the identified ncRNA may act on regulating the cellular processes. Together, the five datatypes will allow the detection and in silico validation of novel noncoding RNAs important for differentiating induced pluripotent stem cells into mature cardiomyocytes.
Expected outcomes and deliverables:	The student will learn computational methods to integrate multiple types of transcriptomics and chromatin interaction data, including CAGE, small RNA (sRNA), total RNA (RNA-seq), ChiP-seq and HiC sequencing data.
Suitable for:	The project is open to students with training in bioinformatics with familiarity using R/Python and Linux commands.
Primary Supervisor:	Supervised by Dr Quan Nguyen and Dr Nathan Palpant
Further info:	If you have questions please email quan.nguyen@uq.edu.au and n.palpant@uq.edu.au