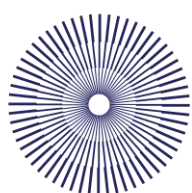




# 2027 Student Research Opportunities



**SAiGENCI**  
SOUTH AUSTRALIAN  
IMMUNOGENOMICS  
CANCER INSTITUTE

*an alliance of*





## About SAiGENCI

The South Australian immunoGENomics Cancer Institute (SAiGENCI) was established as an independent cancer-focused medical research institute located within Adelaide University.

The Institute was made possible by an \$80 million grant from the Commonwealth Government and is being jointly resourced by the Federal Department of Health, the Central Adelaide Local Health Network (CALHN) and Adelaide University.

*The overarching vision for SAiGENCI is to have a fundamentally positive impact on the conduct of cancer research in South Australia, so that fewer patients develop cancer, and the lives of those with cancer is improved.*

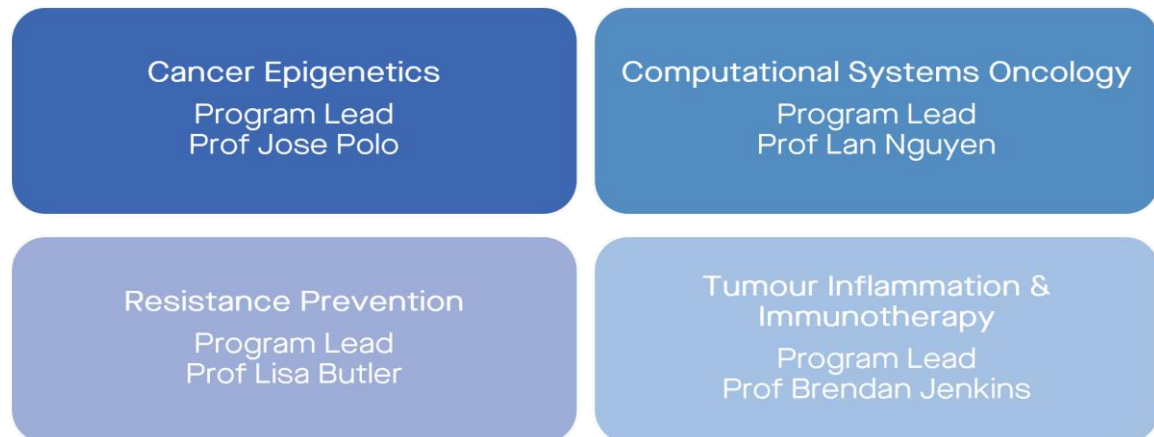
To achieve this vision, the Institute aims to be a hub for scientific discoveries and development of transformative technologies that will translate into improved clinical outcomes through:

- Forging strong research collaborations
- Developing and testing new technologies and discoveries
- Improving treatment and care options for people living with cancer
- Training South Australian clinicians
- Commercialising new discoveries

SAiGENCI's Director and Medical Oncologist, Professor Christopher Sweeney, formerly of the Dana-Faber Cancer Institute, Boston, Massachusetts, and Professor of Medicine at Harvard Medical School, leads a core of high performing groups across four scientific programs.



## SAiGENCI's Core Scientific Programs



SAiGENCI is comprised of a team of internationally leading cancer researchers and clinicians across these programs, who not only perform at an international level in their own right, but together are developing a distinct institutional culture focussed on excellence and clinical impact.

Our Institute members also take a lead role across the state in supporting networks with other cancer research groups in South Australia and support a highly collaborative culture across Australia and internationally.

Learn more about SAiGENCI, its research and people via our website:

<https://www.adelaide.edu.au/saigenci/>

## Training the Next Generation of Cancer Researchers

Are you looking for an opportunity to take the next step in your research career?

The Institute has a number of research projects on offer that are suitable for students at different stages of their scientific studies including; summer research projects for current undergraduate students (who have completed at least one year of study), Honours, Masters of Research (M Res), Masters of Philosophy (M Phil) and Doctor of Philosophy (PhD) candidates.

Projects are based at SAiGENCI within the College of Health at [Adelaide University](#), in either the Adelaide Health & Medical Sciences (AHMS) building, the South Australian Health and Medical Research Institute (SAHMRI) and/or the Central Adelaide Local Health Network (CALHN), all co-located on North Terrace in the Adelaide CBD.

SAiGENCI and Adelaide University will provide researchers early in their career with a stimulating and supportive environment to achieve highly ambitious research goals and build connections for their future careers.

Read on for program specific details, research groups and available projects.



# Master of Philosophy and Doctor of Philosophy Research Opportunities

## Who are we looking for?

SAiGENCI is looking for talented, enthusiastic and dedicated individuals who have a shared vision to undertake research that will lead to fewer patients developing cancer and improving the lives of those with cancer.

Perhaps you have or will soon complete an Honours or Master's degree in a scientific field related to cancer research, or maybe you're a clinician looking to add a research component to your skillset.

If you are a high achieving individual who meets the eligibility criteria (see below) and are committed to a two-year Master of Philosophy (M Phil) or three to four-year Doctor of Philosophy (PhD) full-time research project (or part-time equivalent), we would like to hear from you!

## What we will offer – The SAiGENCI Graduate Program

The Institute will provide a unique training experience for its students including:

- Immersion in a community of Australia's leading cancer researchers with access to world class facilities and technologies
- Regular research forums and master classes from experts in the field
- Workshops for developing research and data analytical skills as well as career development
- Research funding to support candidates with project related expenses, including presenting their research at national and international conferences
- For those enrolled in a PhD, opportunity to participate in a paid 3-month industry internship with a partner organisation

## Eligibility Criteria for SAiGENCI Students

The Adelaide University [Graduate Research School](#) (AUGRS) administers all domestic and international postgraduate research degree applications. Positions are open to both domestic and international applicants who meet Adelaide University's entry requirements, including a minimum English language proficiency.

In addition to Adelaide University eligibility requirements, SAiGENCI M Phil and PhD applicants will need to have successfully completed an Honours degree (achieving a first-class final result), Master's coursework degree (achieving GPA > 6) that has

included a significant research component and thesis, or a Masters by Research degree. Individuals who have significant research experience and/or have contributed to peer-reviewed research publications will be viewed favourably.

Full details of the Adelaide University M Phil and PhD degrees, including eligibility details, can be found on the following AUGRS websites:

**Adelaide University Research Degree Opportunities**

<https://adelaide.edu.au/research/research-degrees/>

**Master of Philosophy**

<https://adelaide.edu.au/study/degrees/master-of-philosophy/>

**Doctor of Philosophy**

<https://adelaide.edu.au/study/degrees/doctor-of-philosophy/>

## **M Phil and PhD Scholarships**

### **Adelaide University and SAiGENCI major/base scholarships**

M Phil and PhD scholarships will be available for a period of two or three and a half years respectively with an indicative value of AUD \$36,500 per annum (2026 rate). Students who meet the Adelaide University eligibility requirements can apply for these scholarships with applications assessed on a competitive basis.

Tuition fee waivers will be available for international students who are offered admission and a major Adelaide University/SAiGENCI scholarship.

### **SAiGENCI top-up scholarships**

In addition to the major scholarship, all students selected for a M Phil or PhD research project with SAiGENCI will receive a \$5,000 per annum top-up scholarship and will be eligible to apply for other competitive scholarships.

## **Finding a Supervisor and Project**

### **Current or recently completed University of Adelaide, University of South Australia and Adelaide University students**

If you have previously studied with the University of Adelaide, University of South Australia or Adelaide University, contact the leader(s) of the project(s) or research areas listed below that excite you, to express your interest. Include in your email the level of

study you want to undertake (i.e. M Phil or PhD), a copy of your CV, academic transcript(s) and English language test results (if relevant).

The supervisor will review your documents and arrange a time to speak with you about the project if they believe you have the right background and experience for the project. If, after talking with the supervisor, you still wish to proceed and you have received the supervisors written support to apply for a position in their group and be considered for a SAiGENCI scholarship, you can begin your online application.

### **All other applicants**

If you have not previously studied with the University of Adelaide, University of South Australia or Adelaide University, visit the AUGRS website (<https://adelaide.edu.au/research/research-degrees/find-a-supervisor/>) and follow the instructions to identify your Adelaide University research supervisor. This will involve a pre-assessment process where you can nominate up to three supervisors and upload a portfolio of documents. The AUGRS will review your enquiry for completeness, quality and eligibility before providing them to the nominated supervisors.

The supervisor(s) will review your documents and arrange a time to speak with you about the project if they believe you have the right background and experience for the project. If, after talking with the supervisor, you still wish to proceed and you have received the supervisors written support to apply for a position in their group and be considered for a SAiGENCI scholarship, you can begin your online application.

### **Applying Online for Graduate Research Admission and Major Scholarship**

All applicants will need to apply online through Adelaide University as outlined on the Apply for a Research Degree webpage at <https://adelaide.edu.au/study/how-to-apply/research/>.

We strongly encourage you to apply during one of Adelaide University's main application rounds as shown on the [Research Scholarships](https://adelaide.edu.au/research/research-degrees/research-scholarships/) webpage at <https://adelaide.edu.au/research/research-degrees/research-scholarships/>.

Follow the AUGRS instructions to create an account to complete your online application. You can save your application at any stage and do not need to complete it in one session. **We encourage you to begin your application well in advance of the application deadline.**

When applying for a SAiGENCI research project and scholarship, enter the details below that are relevant to your situation at the application headings shown.

Once all sections of the application are complete, review your details carefully before submitting.

### Domestic applicants

**Application Type:** Select Admission and Scholarship.

**Study Preferences:** Enter the relevant details from the table below.

|               | M Phil Applicants               | PhD Applicants                 |
|---------------|---------------------------------|--------------------------------|
| Study Type    | Masters by Research             | Doctor of Philosophy           |
| Award         | Master of Philosophy in Health  | Doctor of Philosophy in Health |
| School        | Pharmacy and Biomedical Science |                                |
| Research Area | Biomedical Sciences             |                                |

**Scholarship Selection:** Select the relevant Adelaide University Research Scholarship based on whether you are applying for an M Phil or PhD.

**Research Interests:** You will need to complete a short (500-800 word) research proposal on the Adelaide University Graduate Research Proposal form available within the application. The research proposal will include a title, project summary, project details, research methods and references. Enter “School of Pharmacy & Biomedical Science (SAiGENCI)” as the proposed School/Discipline.

**Structured Curriculum Vitae:** You will also be required to provide your curriculum vitae on the Adelaide University Structured CV Template available within the application.

### International applicants

**Financial Support:** Select seeking a scholarship from Adelaide University.

**Study Preferences:** Enter the relevant details from the table below.

|               | M Phil Applicants    | PhD Applicants       |
|---------------|----------------------|----------------------|
| Study Type    | Masters by Research  | Doctorate            |
| Award Sought  | Master of Philosophy | Doctor of Philosophy |
| Research Area | Biomedical Sciences  |                      |

**Research Interests & Proposal:** You will need to complete a short (500-800 word) research proposal on the Adelaide University Graduate Research Proposal form available within the application. The research proposal will include a title, project summary, project details, research methods and references. Enter “School of Pharmacy & Biomedical Science (SAiGENCI)” as the proposed School/Discipline.

**Structured Curriculum Vitae:** You will also be required to provide your curriculum vitae on the Adelaide University Structured CV Template available within the application.

SAiGENCI specific Graduate Research application queries can be directed to:

Joanna Sundstrom

SAiGENCI Graduate Program

[saigenci@adelaide.edu.au](mailto:saigenci@adelaide.edu.au)

Please include “SAiGENCI Graduate Research enquiry” in the email subject heading.

All other queries should be directed to the AUGRS using the online enquiry form

available at <https://adelaide.edu.au/study/enquire/> or via email to

[graduate.research@adelaide.edu.au](mailto:graduate.research@adelaide.edu.au).



## One Year Research Project Opportunities

SAiGENCI offers eligible students who have completed a three-year undergraduate degree the opportunity to work on a one-year research project through the degrees shown below.

Interested students should get in touch with a supervisor who works on a project or research area of interest (see projects below) to see if they have the capacity to take on a student. Please include a copy of your CV, academic transcript and a brief description of why you are interested in doing a one-year research project with the supervisor/in the area of research you have chosen.

### Honours

Honours is a one-year qualification studied as an addition to an undergraduate degree. Completing an Honours degree provides an opportunity to investigate an area of interest in greater detail whilst gaining hands on research experience.

The one-year legacy Honours degree is available to students who began their bachelor degree at the University of Adelaide or the University of South Australia who satisfy certain requirements. Further information is available at

<https://students.adelaide.edu.au/graduate-research/one-year-honours-at-adelaide-university>.

### Master of Research

The Adelaide University Master of Research is a 1.5 year postgraduate research degree which incorporates coursework exploring a range of topics including research methodologies and research skills. You will then use these skills to help plan and execute your own one-year independent research project. Domestic students pay no tuition fees for this program.

Full details of the Adelaide University Master of Research degree, including eligibility and how to apply, can be found on the following AUGRS website:

**Adelaide University Masters of Research**

<https://adelaide.edu.au/study/degrees/master-of-research/>

## Summer Research Opportunities

A summer research project is a great opportunity for undergraduate students to get a taste of what it is like to work in a research lab.

Information about the 2026/2027 Adelaide University Summer Research Scholarship scheme will be advertised later in 2026.

## Summary of Available Research Projects

| Program                        | Project Title                                                                                                                    | Supervisor(s)                                              | Page |
|--------------------------------|----------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------|------|
| Cancer Epigenetics             | Pluripotency factors and cancer                                                                                                  | Dr Jose Polo, Dr Nora Liu, Dr Ning Liu & Dr Clara Blotas   | 14   |
|                                | Uncovering the regulatory complex of transcription factors in different cancers                                                  | Prof Jose Polo, Dr Nora Liu, Dr Ning Liu & Dr Clara Blotas | 16   |
|                                | From endometriosis to ovarian cancer: modelling malignant transformation using organoids and multi-omics                         | Prof Jose Polo & Dr Nora Liu                               | 18   |
|                                | Establishing the transcriptional and epigenetic programs that drive stem cell fate in normal haematopoiesis and blood cancers    | Prof Jose Polo, Dr Nora Liu & Dr Winne Kan                 | 19   |
|                                | Developing an epigenetic foundational model                                                                                      | Prof Jose Polo & Dr Ning Liu                               | 20   |
|                                | Understanding cellular identity using partial reprogramming                                                                      | Prof Jose Polo & Dr Clara Blotas                           | 21   |
|                                | Enquire directly to discuss potential projects with the Molecular Epigenetics Research Group in 2027                             | Dr Luke Isbel                                              | 22   |
|                                | Modulation of hormone receptor activity by mutant GATA3 in breast cancer                                                         | Dr Adrienne Sullivan & Dr Ashleigh Geiger                  | 23   |
|                                | An epigenetic roadmap to silencing: the molecular events of enhancer remodelling in stem cell differentiation                    | Dr Adrienne Sullivan, Dr Ning Liu & Dr Kate Dredge         | 24   |
|                                | Chromatin-modifying enzymes and cancer                                                                                           | Dr Qi Zhang                                                | 27   |
| Computational Systems Oncology | Cracking cancer's code: Modelling how cells outsmart drugs                                                                       | Prof Lan Nguyen & Dr Sungyoung Shin                        | 30   |
|                                | Designing smarter drug combinations against cancer                                                                               | Prof Lan Nguyen, Dr Sungyoung Shin & Dr Anthony Hart       | 30   |
|                                | AI meets biology: Network-guided machine learning for cancer biomarkers                                                          | Prof Lan Nguyen & Dr Sungyoung Shin                        | 31   |
|                                | Discovering synthetic lethal interactions for cancer therapy                                                                     | Prof Lan Nguyen                                            | 31   |
|                                | Decoding cellular decision-making: Building multi-pathway models                                                                 | Prof Lan Nguyen                                            | 32   |
|                                | Identifying prostate cancer susceptibility through HLA haplotypes                                                                | Dr Simran Kaur, Prof Christopher Sweeney & Dr Fuyi Li      | 33   |
|                                | Dissecting HLA-mediated genetic pleiotropy across immune-mediated diseases and cancer                                            | Dr Simran Kaur & Dr Kristen Feher                          | 34   |
|                                | Robust multimodal learning for cancer prognosis analysis                                                                         | Dr Fuyi Li                                                 | 37   |
|                                | AI-driven drug-target interaction prediction                                                                                     | Dr Fuyi Li                                                 | 38   |
|                                | Large-language AI models to study the immune system                                                                              | Dr Stefano Mangiola                                        | 40   |
|                                | Build large-scale and scalable computational infrastructure for analysis, deployment and exploration of the single-cell universe | Dr Stefano Mangiola                                        | 41   |
|                                | Developing the Tidyomics ecosystem                                                                                               | Dr Stefano Mangiola                                        | 42   |

| Program                             | Project Title                                                                                               | Supervisor(s)                                                       | Page |
|-------------------------------------|-------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|------|
| Resistance Prevention               | Enquire directly to discuss potential projects with the Prostate Cancer Research Group in 2027              | Prof Lisa Butler                                                    | 45   |
|                                     | Establishing the regulatory function of transposable elements in cancer (Bioinformatics)                    | Dr Joanna Achinger-Kawecka, & Dr Daniel Thomson                     | 46   |
|                                     | Dissecting transposable elements contribution to cancer                                                     | Dr Joanna Achinger-Kawecka, Dr Daniel Thomson & Geraldine Lavel-Law | 47   |
|                                     | Metabolic biomarkers for patient stratification and targeted therapy in prostate cancer                     | Dr Zeyad Nassar & Prof Lisa Butler                                  | 49   |
|                                     | Enquire directly to discuss potential projects with the Molecular & Proximity Discovery Laboratory for 2027 | Dr Michael Roy                                                      | 51   |
|                                     | Modulating oxidative stress responses to augment radiation therapy efficacy in prostate cancer              | Dr Katherine Morel & Prof Christopher Sweeney                       | 54   |
| Tumour Inflammation & Immunotherapy | Identification of novel immune regulators in stomach (gastric) cancer                                       | Dr Ruby Dawson & Prof Brendan Jenkins                               | 57   |
|                                     | The role of innate immune regulators in pancreatitis and pancreatic cancer                                  | Prof Brendan Jenkins, Dr Mohamed Saad & Dr Joshua Chey              | 58   |
|                                     | Identification of immune system regulators as therapeutic targets in lung cancer                            | Prof Brendan Jenkins & Dr Mohamed Saad                              | 60   |
|                                     | Nanotechnology-based in situ vaccines for cancer immunotherapy                                              | Dr Yannan Yang, Dr Moustafa Mabrouk & Dr Than Loc Nguyen            | 62   |
|                                     | Boosting response to immunotherapy in lung and pancreatic cancers                                           | Dr Mara Zeissig & Dr Charlotte Toomes                               | 65   |
|                                     | KRAS inhibitors for the treatment of pancreatic cancer                                                      | Dr Mara Zeissig & Dr Tamsin Lannagan                                | 66   |

## Projects in Cancer Epigenetics

### Epigenetic Processes in Pluripotency and Reprogramming Laboratory



Prof Jose Polo  
Group Leader



Dr Nora Liu  
Research Fellow



Dr Ning Liu  
Research Fellow



Dr Clara Blotas  
Research Fellow

The relationship between epigenetics and cancer is well established.

The Polo Research Group is interested in understanding transcriptional and epigenetic mechanisms that govern cell identity.

We particularly focus on factors that regulate pluripotency of stem cells, reprogramming of somatic cells into induced pluripotent stem (iPS) cells and other cells, and regulate cancer growth and development.

### Projects Available in the Epigenetic Processes in Pluripotency and Reprogramming Laboratory

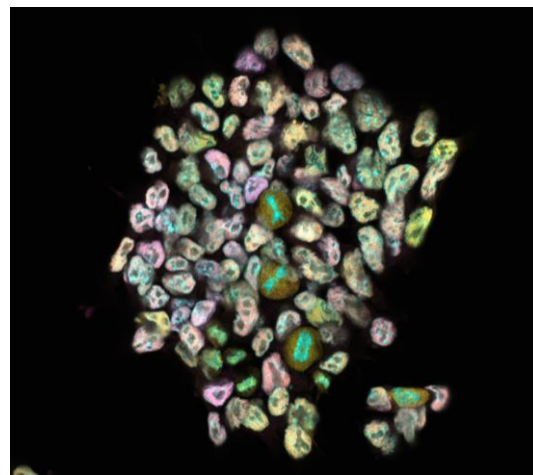
|                               |                                                                                                                              |
|-------------------------------|------------------------------------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Pluripotency factors and cancer                                                                                              |
| <b>Project Supervisor(s):</b> | <a href="#">Prof Jose Polo</a> , <a href="#">Dr Nora Liu</a> , <a href="#">Dr Ning Liu</a> , <a href="#">Dr Clara Blotas</a> |
| <b>Suitable for:</b>          | M Res, M Phil, PhD                                                                                                           |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                                                         |

## Project outline

Pluripotent stem cells can self-renew indefinitely and give rise to all cells of the adult organism. These remarkable capacities are the result of a core transcriptional network controlled by OCT4, SOX2 and NANOG, whose expression is lost upon differentiation. Several cancers have been shown to reactivate OCT4, SOX2 and/or NANOG, with high expression levels positively correlating with cancer progression and severity. Since they are linked to proliferative and multi-lineage differentiation capacity of cancer cells, they present attractive anticancer targets. However, they are considered “undruggable” since they lack catalytic active sites for molecules to bind.

To provide therapeutic alternatives, the Polo research group has adapted and developed various novel techniques to determine how expression and function of the pluripotency factors OCT4, SOX2 and NANOG are controlled in various physiological and pathological cell types, including embryonic stem cells and cancer respectively.

The candidate will develop skills/techniques in a combination of different molecular, biochemical, cellular techniques and genome wide approaches (RNA-seq, MS-MS, ATAC-seq, ChIP-seq, SC-RNA-seq, etc.) to dissect the nature and dynamics of such events.



Mouse embryonic stem cells stained for OCT4 (yellow), NANOG (magenta) and DNA (cyan).

Our ideal candidate will have high academic achievement and relevant experience and interest in stem cell and/or epigenetic and biochemical techniques.

This project encompasses both wet laboratory and bioinformatic components, making it suitable for students interested in cell-based and molecular biochemical wet lab techniques or bioinformatics and computational analysis, or a combination thereof.

## For more information about this project contact:

Prof Jose Polo

Email: [jose.polo@adelaide.edu.au](mailto:jose.polo@adelaide.edu.au)

Ms Suzanne Maiolo

Email: [suzanne.maiolo@adelaide.edu.au](mailto:suzanne.maiolo@adelaide.edu.au)

## Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/jose.polo>

<https://researchers.adelaide.edu.au/profile/nora.liu>

<https://researchers.adelaide.edu.au/profile/ning.liu>

<https://researchers.adelaide.edu.au/profile/clara.blotas>

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**Project Title:** Uncovering the regulatory complex of transcription factors in different cancers

**Project Supervisor(s):** [Prof Jose Polo](#), [Dr Nora Liu](#), [Dr Ning Liu](#), [Dr Clara Blotas](#)

**Suitable for:** M Res, M Phil, PhD

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

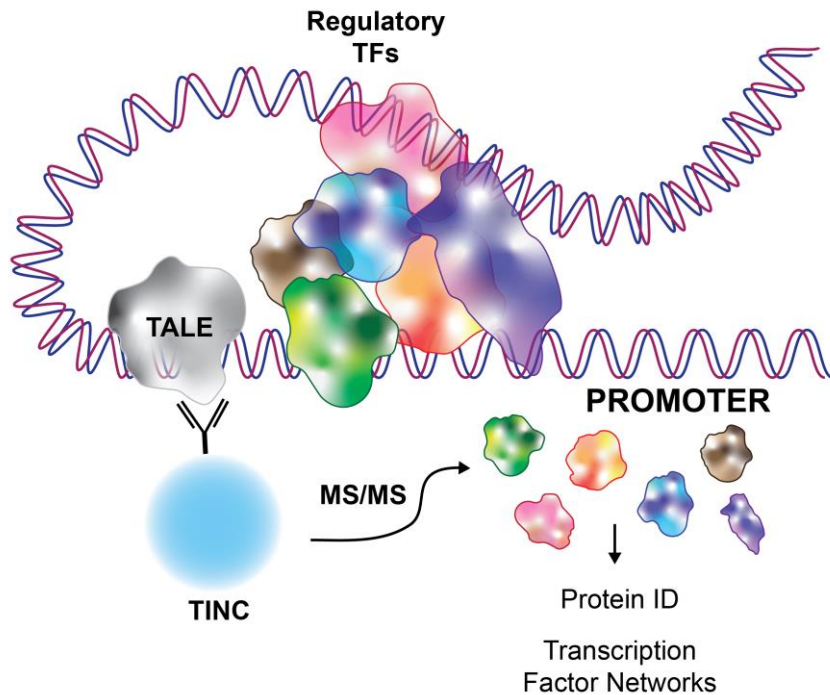
### Project outline

Cellular identity is controlled by transcription factors (TFs), which bind to specific regulatory elements (REs) within the genome to regulate gene expression and cell fate changes. Recent advances in epigenome profiling techniques have significantly increased our understanding of which REs are utilised in which cell type, however, which factors interact with these REs remains largely elusive.

A major impediment to dissecting protein complexes at specific genomic loci is the shortage of appropriate techniques. The most common technique to assess TF binding is chromatin immunoprecipitation (ChIP), which relies on antibodies to interrogate the binding sites of a single TF. Yet, ChIP does not allow dissection of the composition of a multi-protein complex at a specific locus.

Importantly, the Polo research group has developed a novel epigenetic technique termed TINC (TALE-mediated Isolation of Native Chromatin), which allows us to do exactly that (Knaupp et al., Stem Cell Reports 2020). TINC relies on epitope-tagged TALEs, which are DNA-binding proteins engineerable to target specific genomic regions. Upon cross-linking of the cells, the target regions are isolated based on affinity purification of the TALE and associated nucleic acid and protein molecules are analysed by next generation sequencing and mass spectrometry, respectively. In our proof-of-concept experiments, we dissected the protein complex formed at the Nanog promoter, a key pluripotency RE. We identified TFs previously known to bind to this locus as well as novel proteins whose role in pluripotency we further validated (Knaupp et al., Stem Cell Reports 2020). Consequently, with this valuable technique at hand, this PhD project aims at deciphering how the key TFs drive and regulate different cancers, which in turn has major potential in identifying novel therapeutic targets.





Graphical representation of TINC: TALE-mediated isolation of nuclear chromatin.

The candidate will develop skills/techniques in a combination of different molecular, biochemical, cellular techniques and genome wide approaches (RNA-seq, MS-MS, ATAC-seq, ChIP-seq, SC-RNA-seq, etc.) to dissect the nature and dynamics of such events. Our ideal candidate will have high academic achievement and relevant experience and interest in stem cell and/or epigenetic and biochemical techniques.

This project encompasses both wet laboratory and bioinformatic components, making it suitable for students interested in cell-based and molecular biochemical wet lab techniques or bioinformatics and computational analysis, or a combination thereof.

#### For more information about this project contact:

Prof Jose Polo

Email: [jose.polo@adelaide.edu.au](mailto:jose.polo@adelaide.edu.au)

Ms Suzanne Maiolo

Email: [suzanne.maiolo@adelaide.edu.au](mailto:suzanne.maiolo@adelaide.edu.au)

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<https://researchers.adelaide.edu.au/profile/ning.liu>

<https://researchers.adelaide.edu.au/profile/clara.blotas>

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**Project Title:** From endometriosis to ovarian cancer: modelling malignant transformation using organoids and multi-omics

**Project Supervisor(s):** [Prof Jose Polo](#), [Dr Nora Liu](#)

**Suitable for:** M Res, M Phil, PhD

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### **Project outline**

Endometriosis-associated ovarian cancers, including ovarian clear cell carcinoma and endometrioid ovarian carcinoma, frequently co-occur with endometriosis, a condition affecting approximately 10% of reproductive aged women worldwide. Women with endometriosis have a two-to-three-fold increased risk of developing these cancers, yet the molecular mechanisms underlying this transition remain poorly understood.

This project will use advanced 3D patient-derived organoid models and next generation sequencing approaches, including single cell RNA sequencing, spatial transcriptomics, ATAC seq, and ChIP seq, to investigate the transcriptional and epigenetic changes that drive disease progression. Both experimental and computational components are involved, making the project suitable for students interested in wet lab or bioinformatics.

Ideal candidates should be highly motivated with a strong academic record and interest in organoids and/or epigenetic and biochemical techniques and bioinformatics.

### **For more information about this project contact:**

Prof Jose Polo

Email: [jose.polo@adelaide.edu.au](mailto:jose.polo@adelaide.edu.au)

Dr Nora Liu

Email: [nora.liu@adelaide.edu.au](mailto:nora.liu@adelaide.edu.au)

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|                               |                                                                                                                               |
|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Establishing the transcriptional and epigenetic programs that drive stem cell fate in normal haematopoiesis and blood cancers |
| <b>Project Supervisor(s):</b> | <a href="#">Prof Jose Polo</a> , <a href="#">Dr Nora Liu</a> , Dr Winne Kan                                                   |
| <b>Suitable for:</b>          | M Res, M Phil, PhD                                                                                                            |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                                                          |

### Project outline

Normal haematopoiesis stem cells give rise to all types of blood cells. This process is under the control of cytokines such as IL-3 that regulate the self-renewal and the differentiation of the stem cells into all the cells that we find in peripheral blood. In leukaemia, however, the stem cells are dysregulated. There is abnormal self-renewal and impaired differentiation of stem and progenitor cells, major dysfunctions that are responsible for the aggressive nature of some leukemias and for the relapse of patients after treatment. The Cytokine Receptor Lab has recently discovered that IL-3 controls stem cell fate and that this is determined by the type of assembly of the IL-3 receptor that is expressed on the cell surface. In its hexameric form, the IL-3 receptor promotes stemness while the dodecameric form induces cell differentiation (Kan et al., Cancer Discovery). Importantly, leukaemia stem cells preferentially activate hexamer signalling to maintain their stemness and self-renewal properties.

In this project, working together with the Cytokine Receptor Lab, we will perform bioinformatic analyses to: i) dissect the gene expression programs induced by different IL-3 receptor assemblies that drive cell fate decisions in normal haematopoiesis and in leukaemia.

Ideal candidates should be highly motivated with a strong academic record and interest in cytokines, leukaemia and/or epigenetic and biochemical techniques and bioinformatics.

### For more information about this project contact:

Prof Jose Polo

Email: [jose.polo@adelaide.edu.au](mailto:jose.polo@adelaide.edu.au)

Dr Nora Liu

Email: [nora.liu@adelaide.edu.au](mailto:nora.liu@adelaide.edu.au)

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### Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/jose.polo>

<https://researchers.adelaide.edu.au/profile/nora.liu>

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**Project Title:** Developing an epigenetic foundational model  
**Project Supervisor(s):** [Prof Jose Polo](#), [Dr Ning Liu](#)  
**Suitable for:** M Res, M Phil, PhD  
**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### **Project outline**

We are developing an epigenetics-focused foundation model that learns how multiple layers of epigenomic regulation, including chromatin accessibility, histone modifications, DNA methylation, and gene expression, work together to define cell identity across tissues, developmental time, and disease systems. This project aims to build a pre-trained AI model, which allows further fine-tuning tasks. Tasks will include predicting and interpreting regulatory programs, so that researchers can better understand how cells change in development and complex diseases such as cancers and developmental disorders.

As a student on this project, you would work at the intersection of AI and biology, gaining hands-on experience in large-scale single-cell and multi-omics data analysis, foundation model development, high-performance computing, and biological discovery, while helping create new tools for studying gene regulation at unprecedented scale.

### **For more information about this project contact:**

Prof Jose Polo

Email: [jose.polo@adelaide.edu.au](mailto:jose.polo@adelaide.edu.au)

Dr Ning Liu

Email: [ning.liu@adelaide.edu.au](mailto:ning.liu@adelaide.edu.au)

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<https://researchers.adelaide.edu.au/profile/ning.liu>

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**Project Title:** Understanding cellular identity using partial reprogramming  
**Project Supervisor(s):** [Prof Jose Polo](#), [Dr Clara Blotas](#)  
**Suitable for:** M Res, M Phil, PhD  
**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### **Project outline**

Stem cells possess the unique ability to self-renew and differentiate into diverse cell types, making them powerful tools for regenerative medicine, disease modelling and drug discovery. The discovery that mature cells can be reprogrammed into induced pluripotent stem cells (iPSCs) through expression of the Yamanaka factors (OCT4, SOX2, KLF4 and c-MYC; OKSM) revolutionised stem cell biology yet the mechanisms governing cell fate transitions remain poorly understood.

This project will investigate how cellular identity is remodelled during reprogramming, focussing on the “point of no return” where cells become committed to a new fate, and their ability to revert to their original state. Using transient and partial reprogramming approaches, with sequencing and epigenetic techniques like ATAC and ChIP-seq, the project will map cell state trajectories and identify molecular changes associated with commitment and reversibility.

This research will provide fundamental insights into cellular plasticity and advance strategies for regenerative medicine and disease modelling.

### **For more information about this project contact:**

Prof Jose Polo

Email: [jose.polo@adelaide.edu.au](mailto:jose.polo@adelaide.edu.au)

Dr Clara Blotas

Email: [clara.blotas@adelaide.edu.au](mailto:clara.blotas@adelaide.edu.au)

Ms Suzanne Maiolo

Email: [suzanne.maiolo@adelaide.edu.au](mailto:suzanne.maiolo@adelaide.edu.au)

### **Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/jose.polo>

<https://researchers.adelaide.edu.au/profile/clara.blotas>

# Projects in Cancer Epigenetics

## Molecular Epigenetics Research Group



Dr Luke Isbel  
Group Leader

We seek to understand how epigenetic processes drive cellular identity, particularly in stem cells and disease states like cancer.

Transcription factors are the proteins that 'read out' DNA sequence to drive complex gene expression patterns that arise during development, or go awry in diseases like cancer. Of course, our genomes are not naked, instead, they are wrapped up by histone proteins to form chromatin. We are particularly fascinated by interactions between transcription factors and chromatin, as targeting this interface may enable a novel means of modifying transcription factor activity to treat cancer.

### Projects Available in the Molecular Epigenetics Research Group

We are an inclusive and inquisitive functional genomics group, including 7 researchers, staff and students across all stages. Our primary drive is to utilise a variety of *in vitro* and *in vivo* systems to move beyond correlation and establish causation, an elusive but highly satisfying goal. At the end of the day, the information behind any disease is buried in our genome and it is our job to discover the 'how' of it all.

The Molecular Epigenetics Research Group has projects available suitable for passionate graduate research candidates and coursework placement students. Please enquire directly with Dr Luke Isbel for further information.

#### **For more information about this project contact:**

Dr Luke Isbel

Email: [luke.isbel@adelaide.edu.au](mailto:luke.isbel@adelaide.edu.au)

#### **Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/luke.isbel>

# Projects in Cancer Epigenetics

## Development & Epigenetics Research Group



Dr Adrienne Sullivan  
Group Leader



Dr Kate Dredge  
Research Fellow



Dr Ashleigh Geiger  
Research Fellow

The identity of a cell is primarily determined by the specific complement of gene products it expresses. This expression program is highly dependent on the accessibility and activity of enhancers, which are non-coding regions of the genome that are bound by transcription factor proteins to regulate gene expression. But what happens when a cell changes identity? How does it remodel its repertoire of enhancers to 'forget' the previous type and establish a new one? And how are these processes impaired or co-opted in cancers?

The Development & Epigenetics Research Group seeks to understand how epigenetic remodelling of gene regulatory regions drives changes in cell identity and behaviour in development, as well as how misregulation of these processes can cause a cell to become cancerous or develop drug resistance. We use molecular biology techniques and multi-omics together with genetic engineering, 2D and 3D cell culture models of development, and live fluorescent readouts to study these fundamental processes.

Dr Adrienne Sullivan is a Group Leader with the Adelaide Centre for Epigenetics (ACE) and the Cancer Epigenetics Program at SAIGENCI.

### Projects Available in the Development & Epigenetics Research Group

|                               |                                                                           |
|-------------------------------|---------------------------------------------------------------------------|
| <b>Project Title:</b>         | Modulation of hormone receptor activity by mutant GATA3 in breast cancer  |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Adrienne Sullivan</a> & <a href="#">Dr Ashleigh Geiger</a> |
| <b>Suitable for:</b>          | Summer Placement, Hons/M Res, M Phil, PhD                                 |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide      |



## Project outline

Around 70-80% of breast cancers express estrogen receptor (ER) and hence utilise estrogen signalling pathways to drive their growth. Conversely, recent studies have shown that androgen receptor (AR) signalling is growth-refractory in these cancers – indeed, treatment with selective androgen receptor modulators (SARMs) is currently being explored as a therapeutic strategy in the field. The transcription factor GATA3 is a key cofactor of both ER/AR which directs where they bind on the genome and hence which target genes are regulated. However, GATA3 is mutated in 10-15% of breast cancers. Previous studies have shown that some GATA3 mutant proteins alter where ER binds DNA, but effects on AR activity are unknown. By defining how mutations in GATA3 affect ER/AR activity at the molecular level, and hence impact responsiveness of cancer cells to hormone-based therapeutics, this work will inform treatment strategies for breast cancer patients.

The candidate will develop skills in cell biology (including culture of cancer cell lines), and molecular biology (including ChIP, ATAC and plasmid cloning). M Phil and PhD candidates will also develop bioinformatics skills for working with large genomics datasets.

The ideal candidate will have a strong academic record and relevant experience and interest in cancer cell biology, gene regulation, epigenetics, and molecular biology.

## For more information about this project contact:

Dr Adrienne Sullivan

Email: [adrienne.sullivan@adelaide.edu.au](mailto:adrienne.sullivan@adelaide.edu.au)

Ph: +61 8 8313 3006

## Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/adrienne.sullivan>

<https://researchers.adelaide.edu.au/profile/ashleigh.geiger>

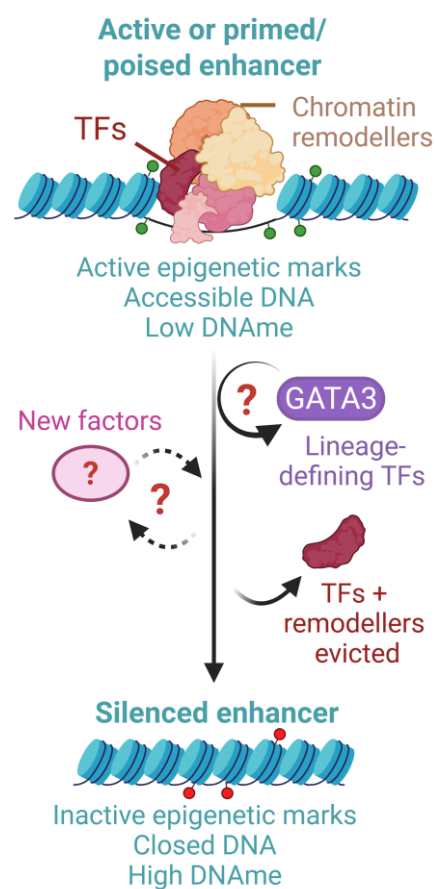
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|                               |                                                                                                               |
|-------------------------------|---------------------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | An epigenetic roadmap to silencing: the molecular events of enhancer remodelling in stem cell differentiation |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Adrienne Sullivan</a> , <a href="#">Dr Ning Liu</a> , <a href="#">Dr Kate Dredge</a>           |
| <b>Suitable for:</b>          | Hons/M Res, M Phil, PhD                                                                                       |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                                          |

## Project outline

Cells change type constantly in our bodies as we grow, repair, and maintain tissues. When this change occurs – for example, an immature stem cell becoming a specialised mature cell – cells need to activate expression of genes associated with their new type and switch off expression of genes associated with their old type. This occurs through epigenetic regulation of key regulatory regions of genomic DNA known as enhancers. Enhancer remodelling is important for proper development but is also frequently hijacked by cancerous cells to become more aggressive and resistant – it is therefore critical to understand these molecular processes.

To define the epigenetic changes that occur as enhancers remodel, the Sullivan Lab has recently generated matched ChIP-Seq samples for different histone marks and transcription factors, ATAC-Seq, and RNA-Seq datasets capturing the state of differentiating stem cells across 7 timepoints. There are opportunities for both wet-lab/dry-lab projects in the lab to investigate the molecular events of enhancer decommissioning using this dataset.



When a cell changes type, some regulatory regions become silenced and inaccessible through epigenetic remodelling. What molecular events underly this silencing? This project will characterise when and where different epigenetic changes occur as enhancers are decommissioned in differentiating cells.

**Bioinformatics Project:** This project will analyse these datasets to characterise the molecular events of enhancer decommissioning. Under the supervision of senior bioinformatician Dr Liu (Polo Lab), the candidate will develop skills in sequencing data analysis and performing integration of various multi-omics datasets, such as ChIP-Seq, ATAC-Seq, RNA-Seq and DNA methylation. HDR candidates will have the opportunity to work together with wet-lab scientists in the Development & Epigenetics Research Group for follow-up experiments.

The ideal candidate will have a strong academic record with experience in programming/data science and/or machine/deep learning and interest in gene regulation and epigenetics.

**Experimental Project:** This project will perform targeted perturbations of epigenetic marks in differentiating stem cell cultures to determine the epigenetic events that are critical for enhancer shut-down, with the ultimate goal being to understand how misregulation of these events contributes to cancer development.

The ideal candidate will have a strong academic record and relevant experience and interest in cell biology, gene regulation, epigenetics, and molecular biology.

**For more information about these projects contact:**

Dr Adrienne Sullivan

Email: [adrienne.sullivan@adelaide.edu.au](mailto:adrienne.sullivan@adelaide.edu.au)

Ph: +61 8 83133006

**Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/adrienne.sullivan>

<https://researchers.adelaide.edu.au/profile/kate.dredge>

<https://researchers.adelaide.edu.au/profile/ashleigh.geiger>

<https://researchers.adelaide.edu.au/profile/ning.liu>

# Projects in Cancer Epigenetics

## Epigenetics and Gene Regulation Laboratory



Dr Qi Zhang  
EMBL-Australia  
Group Leader

Despite all cells within a multicellular organism sharing the same DNA sequences, their individual cellular identity is determined by epigenetic processes. Dysregulation of these processes is highly relevant in pathologies such as cancer, developmental growth disorders and other human diseases.

We are interested in understanding the basic mechanisms of epigenetic regulation, with the ultimate goal of translating fundamental lab-based discoveries into novel therapeutic strategies. The current focus of the lab is to investigate the role of chromatin-modifying complexes in gene regulation and cancer. To achieve this, we employ a diverse range of methods, including biochemistry, structural biology, cell biology, genomics, and bioinformatics.

### Projects Available in the Epigenetics & Gene Regulation Research Group

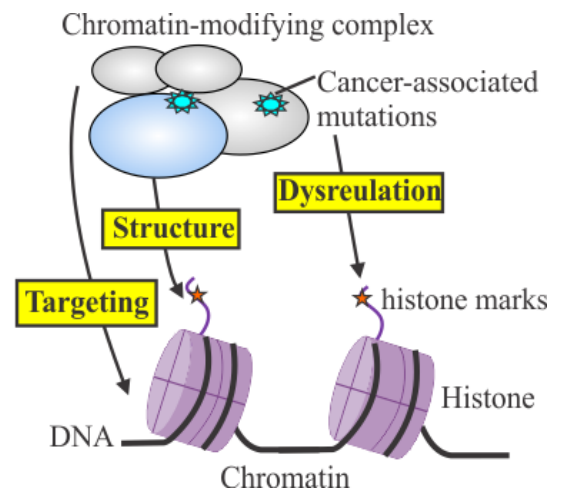
|                               |                                                                      |
|-------------------------------|----------------------------------------------------------------------|
| <b>Project Title:</b>         | Chromatin-modifying enzymes and cancer                               |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Qi Zhang</a>                                          |
| <b>Suitable for:</b>          | Summer Placement, Hons/M Res, M Phil, PhD                            |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide |

#### **Project outline**

Our DNA is wrapped around histones to form chromatin. Chromatin-modifying enzymes, which add or reverse post-translational modifications to chromatin, play a crucial role in the dynamic regulation of gene expression. These enzymes often form multi-subunit protein complexes to ensure precise targeting to chromatin and regulation of their enzymatic activities. Dysregulation of these complexes is associated with various diseases, including cancer and developmental disorders.

This project aims to address the following three questions through multidisciplinary approaches:

1. How are multi-subunit chromatin-modifying enzymes assembled, and how do they bind and modify chromatin substrates?
2. How are these enzymes recruited to their target genes?
3. How do the cancer-associated mutations dysregulate these enzymes?



Potential students can choose to focus on one or several questions, depending on their interests, and will have opportunities to gain hands-on experience in at least ONE of the following methodologies:

- **Biochemistry and Biophysics:** including but not limited to expression and purification of multi-subunit protein complexes, and biophysical characterisation.
- **Structural Biology:** including but not limited to Cryo-EM and various proteomic-based methods.
- **Molecular and Cell Biology:** including but not limited to cancer and stem cell lines and genome editing.
- **Genomics and Bioinformatics:** including but not limited to ChIP, CUT&RUN, ATAC etc and data analysis with bioinformatic tools.

Ideal candidates should be highly motivated and have a background in life sciences, chemistry and/or computer science, with a strong INTEREST (experience not required) in gene regulation and epigenetics.

#### For more information about this project contact:

Dr Qi Zhang

Email: [qi.zhang@adelaide.edu.au](mailto:qi.zhang@adelaide.edu.au)

Ph: +61 8 8313 3755

#### Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/qi.zhang>

## Projects in Computational Systems Oncology

### Integrated Network Modelling Laboratory



Back L-R: Dr Sungyoung Shin, Zikang Xu, Taha Osman. Front L-R: Dr Anthony Hart, Professor Lan Nguyen, Dr Chui Yan (Shanice) Mah.

#### Lab Head - Professor Lan Nguyen

Cancer cells operate through complex networks of interlinked molecular pathways that control their growth, survival, and response to treatment. The Nguyen Laboratory investigates how cancer cells make decisions through these complex communication networks. By a combination of predictive mathematical modelling, bioinformatics and AI, as well as wet-lab experiment, the team deciphers how these networks rewire under treatment pressure and identifies new ways to overcome resistance.

This unique integration of computational and experimental science provides exciting opportunities for students to engage in truly interdisciplinary cancer research.

Professor Lan Nguyen also leads the Computational Systems Oncology Program at the South Australian immunoGENomics Cancer Institute (SAiGENCI), bringing extensive expertise in integrating advanced computational modelling with cutting-edge biological approaches to understand and combat cancer.

### Projects Available in the Integrated Network Modelling Laboratory

Our current work focuses on better understanding how cells communicate through complex molecular networks and how these communications go awry in cancer. We build predictive, data-driven models to uncover the logic of adaptive drug resistance and to design smarter, combination and time-optimised therapies.

By integrating mechanistic modelling, AI-driven data analysis, and experimental validation, our lab bridges computational prediction with biological discovery in an iterative, interdisciplinary setting. Students gain hands-on experience in techniques spanning computational modelling (e.g. ODEs, network analysis, machine learning, data visualisation) and experimental methods (e.g. cell signalling assays, omics, molecular perturbations, drug response studies).

This mixed-skill environment provides an ideal training ground for future systems biologists. Students with backgrounds in mathematical/computational disciplines (mathematics, computer science, engineering) and/or experimental sciences



(biomedical sciences, pharmacology, biochemistry) are encouraged to contact Professor Lan Nguyen to discuss potential research projects in areas of mutual interest.

**Project Title:** Cracking cancer's code: Modelling how cells outsmart drugs

**Project Supervisor(s):** [Prof Lan Nguyen](#) & [Dr Sungyoung Shin](#)

**Suitable for:** Hons/M Res, M Phil, PhD

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### Project outline

Resistance to targeted therapies remains a major challenge in cancer treatment. This project combines computational systems modelling with experimental data to understand how cancer cells adapt to targeted drugs and to design drug combinations that can overcome resistance.

Students will build and simulate mechanistic models of key signalling networks (e.g. PI3K-AKT, MAPK-ERK, FGFR) to predict synergistic and time-dependent effects. A variety of projects are available, each tailored to specific critical pathways and cancer contexts - such as breast, prostate, and lung cancer - depending on the dominant molecular drivers and feedback mechanisms unique to each disease type.

By integrating computational predictions with biological experiments, students will gain hands-on experience in model building, data analysis, and experimental interpretation. The goal is to identify optimal combination and scheduling strategies that maximise tumour response while minimising toxicity, providing valuable translational insights for precision oncology.

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**Project Title:** Designing smarter drug combinations against cancer

**Project Supervisor(s):** [Prof Lan Nguyen](#), [Dr Sungyoung Shin](#) & Dr Anthony Hart

**Suitable for:** Hons/M Res, M Phil, PhD

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### Project outline

While single-agent (monotherapy) treatments almost inevitably lead to resistance, combination therapies are rapidly becoming the mainstream of cancer treatment. Yet, despite their promise, we still lack systematic knowledge for selecting the right drugs to combine – and how to combine them most effectively. This project aims to address this gap by developing predictive computational models to optimise both treatment timing (through sequential scheduling) and dosage (through multi-low-dose strategies) to enhance efficacy while minimising toxicity and resistance emergence.



Students will employ ordinary differential equation (ODE)-based modelling to simulate how drug combinations interact dynamically within signalling networks. Models will be developed using in-house experimental data, and key predictions will be tested in the laboratory, closing the loop between computation and experiment. This interdisciplinary project provides hands-on training in predictive modelling, systems oncology, and the rational design of next-generation combination therapies.

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**Project Title:** AI meets biology: Network-guided machine learning for cancer biomarkers

**Project Supervisor(s):** [Prof Lan Nguyen](#) & [Dr Sungyoung Shin](#)

**Suitable for:** Hons/M Res, M Phil, PhD

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

#### Project outline

Predicting which patients will respond to specific treatments remains a key challenge in oncology. This project applies artificial intelligence (AI) and network-based machine learning to identify biomarkers of drug sensitivity and resistance. Students will integrate multi-omics and pharmacogenomic datasets to build predictive models that leverage biological network information for improved accuracy and interpretability.

An additional theme of this project is exploring the exciting interface between AI/ML and mechanistic modelling - combining the interpretability of mechanistic models with the scalability and pattern-recognition power of AI. By developing such hybrid models, the project aims to create predictive frameworks that are both more transparent and more powerful than either approach alone.

Training will include data integration, feature engineering, and model validation using Python or R, alongside exposure to deep learning methods. This project suits students interested in AI-driven systems oncology and precision medicine.

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**Project Title:** Discovering synthetic lethal interactions for cancer therapy

**Project Supervisor(s):** [Prof Lan Nguyen](#)

**Suitable for:** Hons/M Res, M Phil, PhD

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

#### Project outline

A major challenge in cancer treatment is selectively killing tumour cells while sparing normal tissue. This project aims to uncover synthetic lethal gene interactions - where inhibition of one gene becomes lethal only when another is mutated - revealing cancer-specific vulnerabilities. Using large-scale genomic, transcriptomic, and drug-response

datasets, students will apply bioinformatics and network-based data science approaches to identify novel synthetic lethal pairs in breast and prostate cancers. The project offers the opportunity to work with real-world biomedical data and gain experience in data processing, integration, and analysis using Python or R. Findings from this work will provide valuable leads for developing more effective and selective targeted therapies.

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**Project Title:** Decoding cellular decision-making: Building multi-pathway models

**Project Supervisor(s):** [Prof Lan Nguyen](#)

**Suitable for:** Hons/M Res, M Phil, PhD

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### Project outline

Cells constantly receive and process information from their environment through intricate networks of signalling pathways that determine whether they grow, divide, or die. Understanding this complexity is central to modern cancer biology. This project aims to uncover the information-processing capabilities of key signalling networks, including for example the PI3K-mTOR, MAPK-ERK, Hippo-YAP, NF-B and other pathways, using mathematical modelling closely integrated with experimental data generation and validation.

Students will employ ordinary differential equation (ODE)-based modelling and network analysis to quantify how these pathways interact and influence one another. A major focus is expanding beyond single-pathway models to build larger, multi-pathway frameworks that reveal how crosstalk shapes cellular decision-making at a truly systems level. This work forms part of Professor Nguyen's new ARC Future Fellowship, and leveraging his role as Chief Investigator in the ARC Centre of Excellence MACSYS, whose mission is to build predictive whole-cell models. The project provides a unique opportunity to contribute to next-generation, cutting-edge computational systems biology.

### For more information about projects contact:

Prof Lan Nguyen

Email: [lan.nguyen@adelaide.edu.au](mailto:lan.nguyen@adelaide.edu.au)

Ph: +61 0437 609 766

### Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/lan.nguyen>

# Projects in Computational Systems Oncology

## Data Sciences Unit



Dr Simran Kaur  
Group Leader

The Data Sciences Unit, led by Dr. Simran Kaur, is responsible for data stewardship and provides core biostatistical support, as well as enabling the design, analysis, and interpretation of complex biomedical data with a strong focus on integrative and translational research. The Unit has expertise in the management and analysis of multi-omics datasets, including genomics, proteomics, lipidomic, and metabolomics, and works closely with researchers to ensure robust study design, reproducibility, and statistical inference.

Dr Kaur's current research centres on how inherited variation in the immune system shapes cancer susceptibility.

**Core research goals of Dr. Kaur's group include:**

- Mapping HLA-disease association landscapes across cancers and IMDs
- Characterizing pleiotropic HLA alleles with concordant/discordant directionality
- Developing and integrating machine learning methods into HLA/genomics workflows
- Building multi-ethnic, HLA-integrated polygenic risk scores for prostate cancer

**Key domain areas:** HLA pleiotropy, polygenic risk scores (PRS), PRS portability across ancestries.

## Projects Available in the Data Sciences Unit

|                               |                                                                                                        |
|-------------------------------|--------------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Identifying prostate cancer susceptibility through HLA haplotypes                                      |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Simran Kaur</a> , <a href="#">Prof Christopher Sweeney</a> & <a href="#">Dr Fuyi Li</a> |
| <b>Suitable for:</b>          | PhD                                                                                                    |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                                   |

### Project outline

The human leukocyte antigen (HLA) region is the most polymorphic locus in the human genome and the single strongest genetic determinant of immune-mediated disease

risk, yet its contribution to cancer risk remains comparatively underexplored and poorly integrated into risk prediction. This project leverages large-scale biobank and prostate cancer clinical datasets and employs HLA imputation and fine-mapping, colocalization analyses, machine learning, and polygenic risk score (PRS) development to generate risk prediction models that perform equitably across diverse ancestries.

This bioinformatics and statistical genetics PhD project will leverage large-scale biobanks and prostate cancer clinical datasets to develop and evaluate multi-ethnic polygenic risk scores (PRS) for prostate cancer risk prediction. The project will provide training in genotype data quality control, HLA imputation, genome-wide association analyses, fine-mapping, PRS development and validation, machine learning, and the integration of genomic and clinical data to improve risk prediction across diverse ancestral populations.

We are seeking a candidate with a background in bioinformatics, computational biology, statistics, computer science, or a related discipline, with proficiency in at least one programming language (R or Python) and experience or willingness to work in a high-performance computing (HPC) environment. Prior experience in statistical genetics, immunology, GWAS summary statistics, linkage disequilibrium, genotype quality control is advantageous.

**For more information about projects contact:**

Dr Simran Kaur

Email: [simran.kaur@adelaide.edu.au](mailto:simran.kaur@adelaide.edu.au)

**Supervisor Researcher Profile**

<https://researchers.adelaide.edu.au/profile/simran.kaur>

<https://researchers.adelaide.edu.au/profile/christopher.sweeney>

<https://researchers.adelaide.edu.au/profile/fuyi.li>

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**Project Title:** Dissecting HLA-mediated genetic pleiotropy across immune-mediated diseases and cancer

**Project Supervisor(s):** [Dr Simran Kaur](#), & [Dr Kristen Feher](#)

**Suitable for:** M Res

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

**Project outline**

Classical HLA alleles are associated with an extraordinary range of human diseases, from type 1 diabetes and coeliac disease to Hodgkin lymphoma and cervical cancer. Because HLA molecules govern which peptides are presented to T cells, the same allele can influence both the risk of losing tolerance to self (autoimmunity) and the efficiency with which transformed cells are recognised and eliminated (immune surveillance). This makes the HLA region unusually pleiotropic in addition to being the most polymorphic loci in the human genome.

This bioinformatics and statistical genetics project suitable for a Master of Research or MPhil will leverage large-scale genotype and phenotype data from publicly available biobank and consortium resources for a defined set of cancers and IMDs. Students will apply bioinformatics and network-based approaches to identify pleiotropic HLA alleles, specifically concordant alleles that may point to shared mechanisms such as impaired antigen presentation, chronic antigenic stimulation, or persistent viral infection across various cancers and IMDs. The project offers the opportunity to gain experience in data harmonization, HLA imputation pipelines, colocalization and conditional analysis.

We are seeking a candidate with bioinformatics, computational biology background with competence in at least one computational language (R or Python), comfort working in a high-performance computing (HPC) environment. Prior experience in statistical genetics, immunology, GWAS summary statistics, linkage disequilibrium, genotype quality control is advantageous.

**For more information about projects contact:**

Dr Simran Kaur

Email: [simran.kaur@adelaide.edu.au](mailto:simran.kaur@adelaide.edu.au)

**Supervisor Researcher Profile**

<https://researchers.adelaide.edu.au/profile/simran.kaur>

<https://researchers.adelaide.edu.au/profile/kristen.feher>

## Projects in Computational Systems Oncology

### Artificial Intelligence for Biological Innovation Research Group



Dr Fuyi Li  
Group Leader

Our group specialise in the intersection of Artificial Intelligence (AI) and Big Data in Bioinformatics. Our research revolves around harnessing the power of AI and leveraging Big Data analytics to address various bioinformatics challenges in cancer studies.

By developing AI-driven bioinformatics tools, platforms, software, pipelines, and resources, our research aims to unravel the complexities of cancer and contribute to advancements in the field.

One key aspect of our research involves exploring gene regulation mechanisms in cancer. We aim to uncover the intricate interplay between genetic factors and their impact on cancer development and progression by utilising AI algorithms and analysing large-scale genomic and epigenomic data. Understanding these mechanisms can provide crucial insights into identifying biomarkers, potential therapeutic targets, and novel treatment strategies.

Additionally, our research focuses on developing innovative approaches for multi-omics data processing in cancer research. With the integration of diverse omics datasets, such as genomics, transcriptomics, proteomics, and metabolomics, we aim to unravel the complex molecular networks underlying cancer.

By developing advanced machine learning approaches, our research aims to extract meaningful patterns and correlations from multi-omics data, enabling a comprehensive understanding of cancer biology. Through our research endeavours, we strive to contribute to the field of Bioinformatics by providing novel insights and tools that facilitate precision medicine, personalised therapies, and improved patient outcomes in cancer research and treatment.

We are excited to invite you to delve into the captivating realm of AI-driven Bioinformatics in cancer research. If you are passionate about leveraging cutting-edge technologies, such as Artificial Intelligence and Big Data analytics, to unravel the mysteries of cancer, we would be thrilled to explore potential research projects with you.

By joining our research team, you will have the opportunity to work on developing state-of-the-art bioinformatics tools and platforms, unravel gene regulation mechanisms, and



delve into the analysis of complex multi-omics data in the context of cancer. If you are motivated to make a meaningful impact in the field of cancer research, we encourage you to reach out to us. Let's embark on a collaborative journey where we can contribute to advancements in AI in bioinformatics, cancer biology, and precision medicine. We look forward to discussing your research interests and the potential for us to work together.

## Projects Available in the Artificial Intelligence for Biological Innovation Research Group

**Project Title:** Robust multimodal learning for cancer prognosis analysis  
**Project Supervisor(s):** [Dr Fuyi Li](#)  
**Suitable for:** Hons M Res, M Phil, PhD  
**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### **Project outline**

Accurately predicting the prognosis of cancer patients is crucial for aiding clinicians in planning appropriate treatment, reducing cancer-related medical expenses, and significantly enhancing patients' quality of life. Multimodal prediction of cancer patient prognosis offers a more comprehensive and precise approach.

This project will focus on the development of advanced multimodal learning techniques that can seamlessly fuse information from different data modalities to enhance the accuracy and reliability of cancer prognosis models. By integrating diverse molecular and clinical features, the proposed approach aims to capture the complex interplay between genetic alterations, molecular signatures, and clinical characteristics that influence cancer progression and patient outcomes.

The student will gain expertise in developing and implementing multimodal learning algorithms to integrate diverse data modalities for cancer prognosis analysis. The ideal candidate will have proficient programming skills in languages such as Python and R, and experience in machine learning and deep learning techniques.

### **For more information about this project contact:**

Dr Fuyi Li  
Email: [fuyi.li@adelaide.edu.au](mailto:fuyi.li@adelaide.edu.au)  
Ph: +61 8 8313 3424

### **Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/fuyi.li>



**Project Title:** AI-driven drug-target interaction prediction  
**Project Supervisor(s):** [Dr Fuyi Li](#)  
**Suitable for:** Hons/M Res, M Phil, PhD  
**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### **Project outline**

Accurate prediction of drug-target interactions is fundamental in drug discovery and development processes, facilitating the identification of potential drug candidates and reducing the time and cost associated with experimental validation.

This project focuses on leveraging AI-driven approaches to enhance the prediction of drug-target interactions through the integration of diverse data modalities. By combining molecular, structural, and pharmacological data, advanced multimodal learning techniques will be developed to provide a comprehensive understanding of the complex interactions between drugs and their targets. The project aims to develop robust predictive models that capture the intricate relationships between chemical structures, biological activities, and target properties, ultimately improving the efficiency and success rate of drug discovery pipelines.

The student involved in this project will gain hands-on experience in developing and implementing AI-driven algorithms for drug-target interaction prediction. Proficiency in programming languages such as Python and R, along with a strong background in machine learning and deep learning techniques, will be essential for effectively integrating and analysing diverse data sources. The ideal candidate will have a keen interest in computational biology and drug discovery, coupled with a proactive attitude towards exploring innovative solutions to address challenges in predicting drug-target interactions.

### **For more information about this project contact:**

Dr Fuyi Li

Email: [fuyi.li@adelaide.edu.au](mailto:fuyi.li@adelaide.edu.au)

Ph: +61 8 8313 3424

### **Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/fuyi.li>

### Computational Cancer Immunogenomics Laboratory



Dr Stefano Mangiola  
Group Leader

The Computational Cancer Immunogenomics group, led by Dr Mangiola, is interested in applying cutting-edge computational methods for the study of the immune system's role in cancer progression and treatment response. Dr Mangiola's hybrid laboratory is at the edge of artificial intelligence and multi-omic data production.

By profiling a patient's immune system through modern spatial and single-cell technologies, we model the propensity to enter metastatic progression and be resilient to metastatic spread (e.g., in breast cancer). Similarly, we intend to identify systemic immune features that explain local immunity (within the tumour microenvironment) and predict resistance to neoadjuvant therapy in breast and other cancer types.

The immune system is diverse across the human population. We have pioneered population-scale immune system modelling using large-scale single-cell data (Human Cell Atlas) and quantified its heterogeneity across tissues. This heterogeneity includes tissue-specific ageing programs, sexual dimorphism, and ethnic diversity in immunotherapy targets. Now, we aim to use artificial intelligence (AI) models (i.e. large language models) to extend our immune map to cancer. Specifically, we are interested in building foundation models that can identify stable immunotherapy targets across ethnic groups.

Our work includes the construction of scalable infrastructure and interfaces that allow multi-atlas-level analyses and annotation. This includes tidyomics, CuratedAtlasQuery and HPCell.

We are particularly interested in the following areas:

- Integration of spatial and single-cell transcriptomics and proteomics.
- Machine learning and classification.
- Large-language AI models applied to cellular biology.
- Cancer immunodiagnosis.
- R tidy programming applied to multi-omics.
- Large-scale inference from single-cell multi-atlases.

## Projects Available in the Computational Cancer Immunogenomics Laboratory

|                               |                                                                         |
|-------------------------------|-------------------------------------------------------------------------|
| <b>Project Title:</b>         | Large-language AI models to study the immune system                     |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Stefano Mangiola</a>                                     |
| <b>Suitable for:</b>          | PhD                                                                     |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace,<br>Adelaide |

### **Project outline**

Demographic factors like age and sex critically influence disease outcomes and treatment responses, including cancer treatments targeting the immune system (immunotherapy).

Australia has an ethnically diverse and ageing population. Despite its importance, a unified resource to test the population-level diversity of therapy and diagnosis targets is missing. The current paradigm of population-level investigation of complex cancer traits still relies on homogenised tissue data, such as the 15-year-old Cancer Genome Atlas (TCGA) database.

With a recent breakthrough, we pioneered the population-level immune system investigation from massive-scale single-cell resources. Across 12,981 healthy individuals and 30 organs, we mapped profound immunological changes across ages, sex and ethnicity, uncovering diversity in key pathways used in immunotherapy (e.g. LAG3, SLAMF7 and CD83).

As the lead researcher on this project, you will translate cutting-edge technology. You will adapt and implement our existing infrastructure to generative single-cell large-language models, akin to ChatGPT, but specifically tailored to identify novel immune targets conserved in ageing and across sexes. Your role will involve pushing the boundaries of AI in cell biology, pivoting this technology to analyse our extensive clinically annotated cancer cell compendium. This will allow for the identification of critical therapeutic targets in cancer, which is a step towards more personalised and effective treatments. You will contribute to the next generation of AI models by extending beyond the current static-cell paradigm, working towards a dynamic representation of cells. This will involve creating models that capture cellular behaviour's complexity and variability in different biological contexts.

Skills you will learn:

- **Single-cell Analysis:** Master state-of-the-art techniques in single-cell RNA sequencing, understanding cellular heterogeneity at an unprecedented resolution.
- **Artificial Intelligence and Machine Learning:** Gain expertise in developing and applying generative models and large-language models to biological data, equipping you with skills that are at the forefront of AI-driven research.
- **Bioinformatics:** Develop strong bioinformatics skills, including data processing, integration, and analysis of large-scale, clinically annotated datasets.

- **Computational Modelling:** Learn how to build and refine dynamic cell models, moving beyond static representations to capture the temporal and spatial variability of cellular behaviour.
- **Translational Research:** Engage in translational research by applying computational findings to clinically relevant questions, bridging the gap between basic science and potential therapeutic applications.

The ideal candidate for this PhD project will have a strong background in computational biology, bioinformatics, or a related field, with experience in handling large-scale datasets. Proficiency in programming languages such as Python or R is essential, as well as familiarity with machine learning techniques and AI applications. Prior experience with single-cell RNA sequencing or other omics data would be highly advantageous. The candidate should be highly motivated, with a keen interest in translational research and a desire to apply computational methods to solve clinically relevant problems. Excellent problem-solving skills, attention to detail, and the ability to work independently as well as part of a multidisciplinary team are also crucial.

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|                               |                                                                                                                                  |
|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Build large-scale and scalable computational infrastructure for analysis, deployment and exploration of the single-cell universe |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Stefano Mangiola</a>                                                                                              |
| <b>Suitable for:</b>          | PhD                                                                                                                              |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                                                             |

### Project outline

Single-cell and spatial omic technologies have fundamentally transformed biological research by generating vast quantities of data. This influx challenges existing bioinformatics pipelines and individual users' capacity to keep up with the rapidly evolving demands of impactful data-driven research.

As part of this project, you will collaborate with our industry partner to enhance the capabilities of CuratedAtlasQuery and HPCell, focusing on establishing a privately deployable intelligence hub for single-cell and spatial data. You will expand the existing CuratedAtlasQuery database, which has already facilitated extensive profiling of the immune system at the human population level, by integrating biological annotations and developing data summarisation techniques. This effort will help democratise access to large-scale single-cell analyses. Additionally, you will contribute to developing HPCell, an analytical language designed to execute massively parallel single-cell analysis workflows in a tidy R style and enable their deployment on high-performance computing platforms. This project allows you to work at the forefront of computational biology and translational research.

The key skills and techniques the PhD candidate will learn by working on this project include:

- **Single-cell and Spatial Data Analysis:** Gain expertise in analysing and managing large-scale single-cell and spatial datasets.
- **Bioinformatics Tool Development:** Develop skills in enhancing and expanding bioinformatics tools like CuratedAtlasQuery and HPCell, focusing on integrating biological annotations and data summarisation techniques.
- **High-performance Computing:** Learn to execute and optimise single-cell analysis workflows on high-performance computing platforms using the HPCell analytical language.
- **Data Integration and Summarisation:** Master techniques for integrating diverse biological datasets and creating summarised outputs that facilitate large-scale analyses.
- **Collaborative Industry Research:** Experience working directly with an industry partner, gaining insights into the application of bioinformatics in a commercial setting.
- **R Programming and Tidyverse:** Enhance your proficiency in R, particularly in the tidyverse style, for organising and analysing complex data.
- **Translational Research:** Engage in translational research by applying computational methods to address clinically relevant questions.

The ideal candidate for this project should have a strong background in bioinformatics, computational biology, or a related field, with experience in analysing single-cell and spatial data. Proficiency in R programming, particularly with tidyverse, and familiarity with high-performance computing environments are essential. Prior experience in developing bioinformatics tools or working with large-scale biological datasets would be highly beneficial. The candidate should also possess strong problem-solving skills, the ability to work collaboratively with industry partners, and a keen interest in translational research. Excellent communication skills and a demonstrated ability to manage and interpret complex data are also important for success in this role.

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**Project Title:** Developing the Tidyomics ecosystem

**Project Supervisor(s):** [Dr Stefano Mangiola](#)

**Suitable for:** PhD

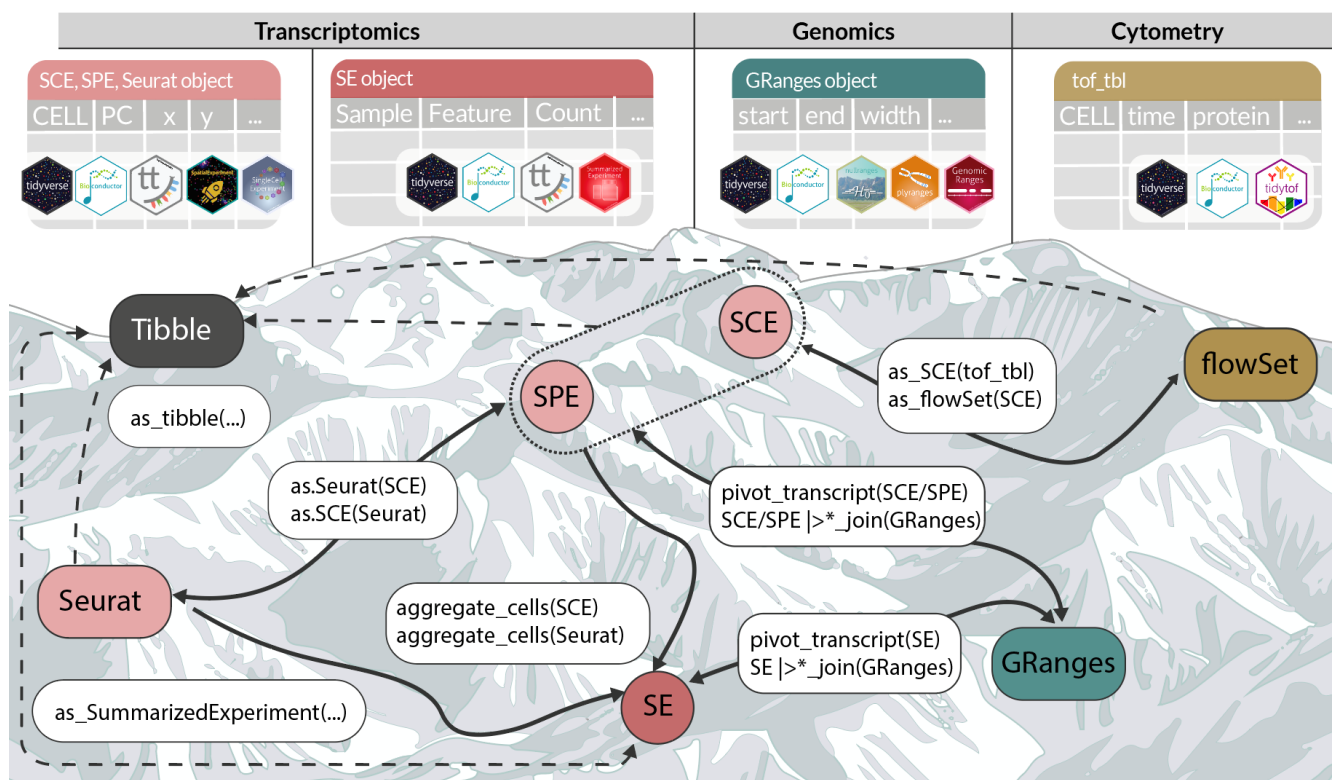
**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### Project outline

As part of this project, you will work on improving the Tidyomics R software ecosystem, which enhances the analysis and visualisation of high-dimensional omics data by applying the principles of tidy data analysis. Your primary responsibilities will include improving the documentation, robustness, and interoperability of the Tidyomics



ecosystem, ensuring it remains accessible and user-friendly for the growing community of computational biologists. You will also focus on extending Tidyomics to support spatial profiling technologies, enabling its application to cutting-edge research in tissue biology at the single-cell level. In addition, you will contribute to the development of a user-friendly grammar that facilitates the manipulation of popular data containers across various omics (genomics, transcriptomics, cytometry) and platforms (Bioconductor, Seurat). As part of your work, you will engage with the international Tidyomics community, collaborating with developers and users across five continents, and contribute to the ongoing roadmap for the ecosystem through our community GitHub Project space. This project offers you the opportunity to be at the forefront of computational biology, with a focus on interfacing with large-scale single-cell atlas collections like The Human Cell Atlas and Curated Cancer Atlas.



The key skills and techniques the PhD candidate will learn by working on this project include:

- **R Programming and Tidyverse:** Enhance your proficiency in R, focusing on tidy data principles and the tidyverse ecosystem for data manipulation and analysis.
- **Software Development:** Gain experience in improving and extending bioinformatics software, focusing on documentation, robustness, and interoperability of the Tidyomics ecosystem.
- **Spatial Profiling Technologies:** Learn to apply and integrate spatial profiling technologies within the Tidyomics ecosystem, enabling advanced analysis of tissue biology at the single-cell level.
- **Data Visualisation:** Develop skills in visualising high-dimensional omics data, making complex biological data more accessible and interpretable.

- **Community Collaboration:** Engage with a global community of developers and users, contributing to an international network that spans five continents.
- **GitHub Project Management:** Participate in collaborative software development using GitHub, contributing to the ongoing roadmap and development of the Tidyomics ecosystem.
- **Interfacing with Single-Cell Atlas Collections:** Work with large-scale single-cell data repositories like The Human Cell Atlas and Curated Cancer Atlas, enhancing your understanding of cutting-edge single-cell research.

The ideal candidate for this project should have a solid background in bioinformatics, computational biology, or a related field, with strong proficiency in R programming and a deep understanding of tidy data principles and the tidyverse ecosystem. Experience in software development, particularly in improving and documenting bioinformatics tools, would be highly advantageous. Familiarity with spatial profiling technologies and single-cell analysis is also beneficial, as is prior experience with large-scale omics data. The candidate should have excellent problem-solving skills, be comfortable working collaboratively within a global community of developers and users, and have a keen interest in contributing to advancing computational biology through open-source software development. Strong communication skills and a proactive approach to learning and innovation are essential for success in this project.

**For more information about these projects contact:**

Dr Stefano Mangiola

Email: [stefano.mangiola@adelaide.edu.au](mailto:stefano.mangiola@adelaide.edu.au)

Ph: +61 8 8313 4024

**Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/stefano.mangiola>



## Projects in Resistance Prevention

### Prostate Cancer Research Group



Prof Lisa Butler  
Group Leader



Dr Maggie Centenera  
Research Fellow

Prostate cancer is a major public health issue, killing approximately 3,300 men in Australia every year.

The Prostate Cancer Research Group (PCRG) is tackling localised and metastatic prostate cancer by developing more robust diagnostics tests, biomarkers for responsiveness to current treatments and new drugs for clinical development.

Professor Lisa Butler leads the PCRG which consists of some 18 researchers, support staff, PhD and honours students.

### Projects Available in the Prostate Cancer Research Group

Researchers in the Prostate Cancer Research Group use a wide range of techniques and skills to undertake their research. These include; cell and molecular biology techniques, cell culture, flow cytometry, metabolomics, lipidomic profiling, tissue imaging, drug candidate testing, animal models and bioinformatics.

The PCRG group is not actively recruiting students for 2027. However, if students with a background in biomedical sciences or pharmacology have a strong passion for prostate cancer research, please contact Professor Butler to discuss potential research project options.

#### **For more information about projects contact:**

Prof Lisa Butler

Email: [lisa.butler@adelaide.edu.au](mailto:lisa.butler@adelaide.edu.au)

#### **Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/lisa.butler>

<https://researchers.adelaide.edu.au/profile/margaret.centenera>

## Projects in Resistance Prevention

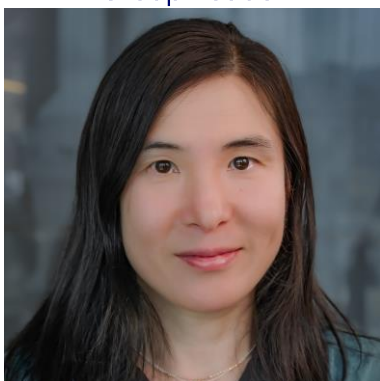
### 3D Chromatin Organisation Research Group



Dr Joanna Achinger-Kawecka  
Group Leader



Dr Daniel Thomson  
Research Fellow



Dr Fiona Zhou  
Research Fellow



Geraldine Laven-Law  
Research Manager

The 3D Chromatin Organisation Research Group (PI Dr Joanna Achinger-Kawecka) is an experimental biology and bioinformatics laboratory studying the principles of 3D genome folding in cancer.

The 3D genome architecture brings together genes and distant regulatory elements to orchestrate gene transcription, and has been implicated in many diseases, including cancer.

Our research focuses on understanding the role of 3D chromatin alterations in driving cancer development, progression and treatment resistance, with a focus on hormone-dependent cancers, such as breast and prostate cancers. We use cutting-edge methods (multi-omics, single-cell, genome editing as well as various pre-clinical model systems) to study the interplay of the 3D chromatin, epigenome and transcriptome in cancer to increase our understanding of cancer biology and accelerate the development of new therapies.

### Projects Available in the 3D Chromatin Organisation Research Group

**Project Title:** Establishing the regulatory function of transposable elements in cancer (Bioinformatics)

**Project Supervisor(s):** [Dr Joanna Achinger-Kawecka](#) and [Dr Daniel Thomson](#)

**Suitable for:** Hons/M Res, M Phil, PhD  
**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### Project outline

Transposable elements (TEs), also known as “jumping genes” are repetitive genomic elements that represent almost half of the human genome. While the majority of TEs in the human genome have lost the ability to transpose, their sequences hold a significant regulatory potential. TEs contain binding sites for transcription factors, enabling them to function as alternative promoters or enhancers regulating the gene expression.

TEs are frequently activated during tumorigenesis, promoting oncogenic gene expression. While some TEs have been previously documented to contribute to gene deregulation in cancer, a comprehensive view of the regulatory landscape of TEs in cancer remains incomplete.

This bioinformatics project, suitable for Honours, Masters, or PhD, will leverage large, publicly available pan-cancer transcriptome, chromatin, and 3D genome datasets to carry out a comprehensive systematic study of the contribution of TEs to the regulatory cancer genome.

We are seeking a candidate with prior research experience in next generation sequencing (NGS) data processing and analyses, working within a high-performance computing (HPC) environment, and knowledge of at least one computational language (e.g., Python, R). Datasets you will have access to include ATAC-seq (chromatin accessibility), RNA-seq (transcriptome) Hi-C (3D genome structure), ChIP-seq/CUT&RUN (transcription factor binding), ONT Nanopore DNA and RNA sequencing (long-read sequencing), and single-cell data. We have access to two HPCs, established bioinformatics pipelines (Nextflow nf-core), and strong in-house bioinformatics expertise to streamline any large data processing and machine learning applications, and grow your bioinformatics skillsets.

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**Project Title:** Dissecting transposable elements contribution to cancer  
**Project Supervisor(s):** [Dr Joanna Achinger-Kawecka](#), [Dr Daniel Thomson](#) and [Geraldine Laven-Law](#)  
**Suitable for:** Hons/M Res, M Phil, PhD  
**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

### Project outline

Transposable elements (TEs), also known as “jumping genes” are repetitive genomic elements that represent almost half of the human genome. While the majority of TEs in the human genome have lost the ability to transpose, their sequences hold a significant

regulatory potential. TEs contain binding sites for transcription factors (TFs), enabling them to function as alternative promoters or enhancers regulating the gene expression.

TEs are often hijacked in cancer to drive oncogenic gene expression. Yet, paradoxically, reactivation of these TEs in cancer cells can trigger an innate immune response known as viral mimicry and inhibit tumour growth. Therefore, TEs may pose as double-edged sword, with not only an underexplored role in promoting tumorigenesis (see project #1), but also representing a key vulnerability that could be exploited in targeted therapy. A deeper understanding of the role of TEs in oncogene expression and viral mimicry is crucial for developing novel TE-based cancer therapies and biomarkers.

This wet laboratory and bioinformatics project, suitable for Honours, Masters, or PhD, is focused on understanding the role of TEs in cancer, particularly their impact on transcription, viral mimicry and immune evasion. To do this, you will use various molecular (Hi-C, RNA-seq, ATAC-seq) and functional (CRISPR, DEGRON) methods to study selected TEs and establish their role in gene regulation and treatment response in cancer.

We are seeking a candidate with prior research experience and proficiency in cellular and molecular biology. Prior experience in interpreting next-generation sequencing data, and knowledge of at least one computational language (e.g., Python, R) would be an advantage. Wet laboratory techniques and datasets you will have access to include Hi-C (3D chromatin structure), CUT&RUN/ChIP-seq (transcription factor binding), ATAC-seq (chromatin accessibility), RNA-seq (transcriptome), ONT Nanopore DNA and RNA (long read) sequencing, and single-cell data. We have access to high performance computing (HPC) and established analytical pipelines to streamline any large data processing and machine learning applications. You will be supported by two senior bioinformaticians and an experienced wet laboratory researcher to further develop your molecular biology and computational skillsets

**For more information about any of these projects contact:**

Dr Joanna Achinger-Kawecka

Email: [joanna.achinger-kawecka@adelaide.edu.au](mailto:joanna.achinger-kawecka@adelaide.edu.au)

**Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/joanna.achinger-kawecka>

<https://researchers.adelaide.edu.au/profile/daniel.thomson>

<https://researchers.adelaide.edu.au/profile/fiona.zhou>

<https://researchers.adelaide.edu.au/profile/geraldine.laven-law>

## Projects in Resistance Prevention

### Precision Oncology Group



Dr Zeyad Nassar  
Group Leader

The Precision Oncology Group investigates molecular and metabolic vulnerabilities that drive prostate cancer progression, treatment resistance, and patient heterogeneity.

Our research integrates functional genomics, cancer metabolism, biomarker discovery, and patient-derived models to identify clinically actionable therapeutic targets and guide personalised treatment strategies. We use CRISPR screening, multi-omics, spatial technologies, ex vivo tumour models, and in vivo validation to uncover synthetic lethal interactions and metabolic dependencies.

A major focus is translating laboratory discoveries into biomarkers and therapeutic approaches that can stratify patients and improve treatment selection.

### Projects Available in the Precision Oncology Group

|                               |                                                                                         |
|-------------------------------|-----------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Metabolic biomarkers for patient stratification and targeted therapy in prostate cancer |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Zeyad Nassar</a> & <a href="#">Prof Lisa Butler</a>                      |
| <b>Suitable for:</b>          | MPhil, PhD                                                                              |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                    |

#### Project outline

Prostate cancer has a distinctive metabolism that differs from many other solid cancers, including greater reliance on fat-processing pathways rather than the sugar-focused metabolism commonly seen in other tumour types. This creates an opportunity to develop new ways to identify and treat aggressive disease. However, previous clinical trials targeting cancer metabolism have often been unsuccessful because treatments were tested in broad patient groups, without selecting those most likely to benefit.

This PhD project will investigate whether fat-related molecules measured in blood can act as biomarkers to identify prostate cancers with specific metabolic vulnerabilities. The student will combine blood-based metabolic profiling with laboratory models and

patient-derived tumour samples to better understand how prostate cancer uses nutrients to grow, survive and resist treatment. The project will provide training in cancer biology, biomarker discovery, patient-derived models and translational oncology.

Our ideal candidate will have a first class Honours or Masters qualification in biomedical sciences, pharmacology or biochemistry.

**For more information about this project contact:**

Dr Zeyad Nassar

Email: [zeyad.nassar@adelaide.edu.au](mailto:zeyad.nassar@adelaide.edu.au)

**Supervisor Researcher Profile**

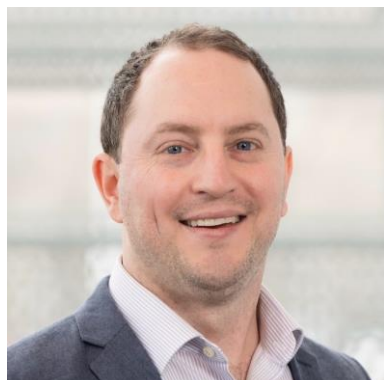
<https://researchers.adelaide.edu.au/profile/zeyad.nassar>

<https://researchers.adelaide.edu.au/profile/lisa.butler>



## Projects in Resistance Prevention

### Molecular and Proximity Discovery Laboratory



Dr Michael Roy  
Group Leader



Dr Sunita KC Basnet  
Research Fellow



Dr Mihaela Ficu  
Research Fellow



Dr Jackson Henneveld  
Research Fellow

The Molecular and Proximity Discovery (MPD) Laboratory (PI Dr Michael Roy) works at the intersection of medicinal chemistry, chemical biology, structural biology and cancer drug discovery.

We study protein function and develop tools to rewire protein-protein interactions (PPIs) in faulty cancer cell signalling pathways—paving the way for safer, more effective cancer therapies.

Our key research toolbox includes:

- Synthetic/Medicinal Chemistry
- Structural Biology & Biophysics
- Cellular Biology
- Computational & AI-driven Discovery

We are specialists in small molecule and Chemically Induced Proximity (CIP) drug discovery, in particular modalities such as Targeted Protein Degradation (TPD) using PROTACs and molecular glues, to hijack the cell's recycling system and eliminate disease-causing proteins.

Our research dives deep into protein structure and function — including ubiquitin E3 ligases, kinases/pseudokinases, and epigenetic regulators — to understand biology, uncover targetable cancer vulnerabilities and design innovative molecules that can reprogram cellular signalling.

## Projects Available in the Molecular & Proximity Discovery Laboratory

Researchers in the Molecular & Proximity Discovery Laboratory use a broad range of techniques and skills to undertake their research. These include synthetic organic and medicinal chemistry, protein biochemistry and structural biology (e.g. recombinant protein production, X-ray crystallography), biophysics, cell culture, flow cytometry and proteomics, and incorporation of computational approaches (e.g. machine learning, *de novo* design) for design and analysis of proteins and small molecules.

We have current projects focussed on approaches to study and drug target cancer-associated ubiquitin E3 ligases, modulate transcription factor function, use *de novo* AI-based methods to discover PPI modulators, and develop novel biological tools and computational approaches for chemically induced proximity.

Students with a background in biomedical sciences, chemistry, biochemistry, pharmacology or computational biology are encouraged to contact Dr Michael Roy to discuss potential research projects in areas of mutual interest.

### **For more information about projects contact:**

Dr Michael Roy

Email: [michael.roy@adelaide.edu.au](mailto:michael.roy@adelaide.edu.au)

Ph: +61 8 8313 5382

### **Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/michael.roy>

<https://researchers.adelaide.edu.au/profile/sunita.kcbasnet>

<https://researchers.adelaide.edu.au/profile/mihaela.ficu>

## Projects in Resistance Prevention

### Sweeney OncoTherapeutics and Biology Laboratory



Prof Christopher Sweeney  
Group Leader



Dr Katherine Morel  
Research Fellow



Dr Mark Bunting  
Research Fellow



Dr Kimberley Clark  
Research Fellow



Dr Kristen Feher  
Research Fellow

The Sweeney OncoTherapeutics and Biology Laboratory has a translational research focus and works to better understand the underlying biology of prostate cancer and improve therapies for patients.

Prostate cancer is a complex disease that affects millions of men globally. Development of prostate cancer involves corruption of the normal prostate transcriptional network, following deregulated expression or mutation of key transcription factors. The group is interested in understanding how many of these transcription factors affect prostate cancer development, from localised disease to castration-resistant metastatic prostate cancer, and subsequently finding viable therapeutic approaches to benefit patients.

The research team is led by Professor Christopher Sweeney, who has devoted his clinical and academic career to developing strategies to improve the care of patients with genitourinary malignancies with a major focus on prostate cancer and testicular cancer.

## Projects Available in the Sweeney OncoTherapeutics and Biology Laboratory

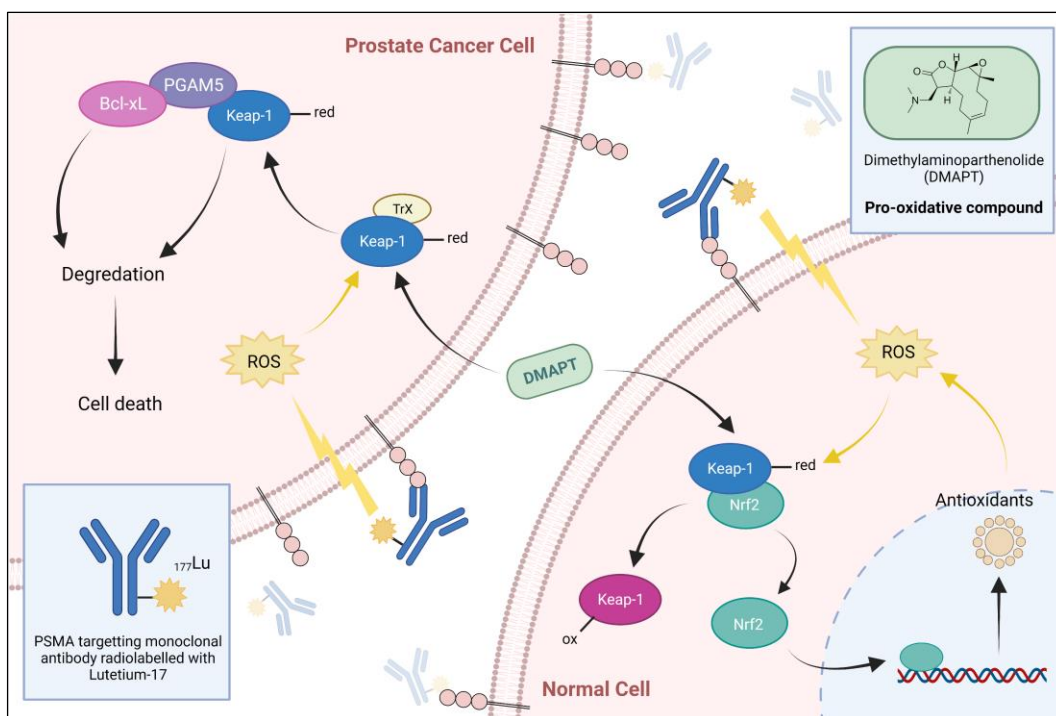
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|-------------------------------|------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Modulating oxidative stress responses to augment radiation therapy efficacy in prostate cancer |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Katherine Morel</a> & <a href="#">Prof Christopher Sweeney</a>                  |
| <b>Suitable for:</b>          | PhD                                                                                            |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                           |

### **Project outline**

Radioligand therapy (RLT), which targets the prostate specific membrane antigen (PSMA), is a recent development in the treatment of metastatic castration resistant prostate cancer. The limiting factor in RLT is to keep the absorbed dose to normal tissue low while delivering high absorbed doses to cancer cells. Strategies to reduce damage to normal tissues are key to more effective PSMA-targeted RLT. Elevated oxidative stress is observed more frequently in cancer cells than in normal cells. It is therefore expected that additional exposure to a low level of reactive oxygen species will push cancer cells toward death, whereas normal cells might maintain redox homeostasis through adaptive antioxidant responses. This would allow for lower radiation doses to be used, reducing toxicity in normal tissues. We aim to investigate the ability of pro-oxidative compounds to increase efficacy of RLT in prostate cancer and understand the underlying mechanisms of this effect.

This project will involve a range of techniques which may include molecular biology and cloning (qPCR, primer design, PCR sequencing, bacterial work, cell line modification), protein analysis (western blotting, ELISA), histology (IHC and IF analysis of tissues) and microscopy. This project will utilise multiple models of prostate cancer, including animal models, 3D organoids and 2D cell lines.

Candidates are required to have a first-class Honours or Master's qualification, ideally with experience working in a molecular wet-laboratory research environment. Candidates working on this project may be required to register as a radiation worker.



**Proposed mechanism of action for modulation of radioligand therapy (RLT) by DMAPT:** Pro-oxidant compound, DMAPT, sensitises cancer cells to RLT, in part, by maintaining Keap1 in a reduced state and enhancing its interaction with PGAM5 and Bcl-xL, resulting in degradation of Bcl-xL in mitochondria. In contrast, DMAPT protects normal cells against radiation via oxidation of Keap1 and release of the Nrf2 transcription factor for activation of mitochondrial antioxidant enzymes.

#### For more information about this project contact:

Dr Katherine Morel

Email: [katherine.morel@adelaide.edu.au](mailto:katherine.morel@adelaide.edu.au)

Ph: +61 8 8313 7336

#### Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/katherine.morel>

<https://researchers.adelaide.edu.au/profile/christopher.sweeney>

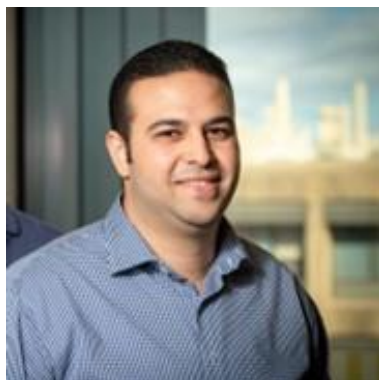


## Projects in Tumour Inflammation & Immunotherapy

### Cancer and Immune Signalling Laboratory



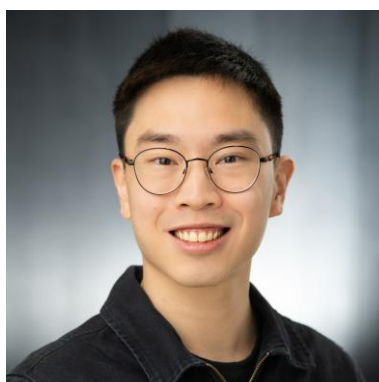
Prof Brendan Jenkins  
Group Leader



Dr Mohamed Saad  
Research Fellow



Dr Ruby Dawson  
Research Fellow



Dr Joshua Chey  
Research Fellow

The projects undertaken in our group combine molecular biological and genetic approaches in pre-clinical disease models, together with human translational studies, to identify the mechanisms by which key regulators of the innate immune system promote the pathogenesis of inflammation-associated cancers of the stomach, lung and pancreas.

Key molecular targets of innate immunity include:

- pattern recognition receptors (e.g. toll-like receptors, cytosolic DNA sensors)
- inflammasomes
- ADAM and iRhom family proteases
- cytokine signalling pathways (e.g. interleukin (IL)-6 cytokine family, JAK-STAT axis)

The research team is led by Professor Brendan Jenkins, who is a leading international authority on innate immunity and cancer, impacting on multiple fields (oncology, immunology, gastroenterology, respiratory medicine).

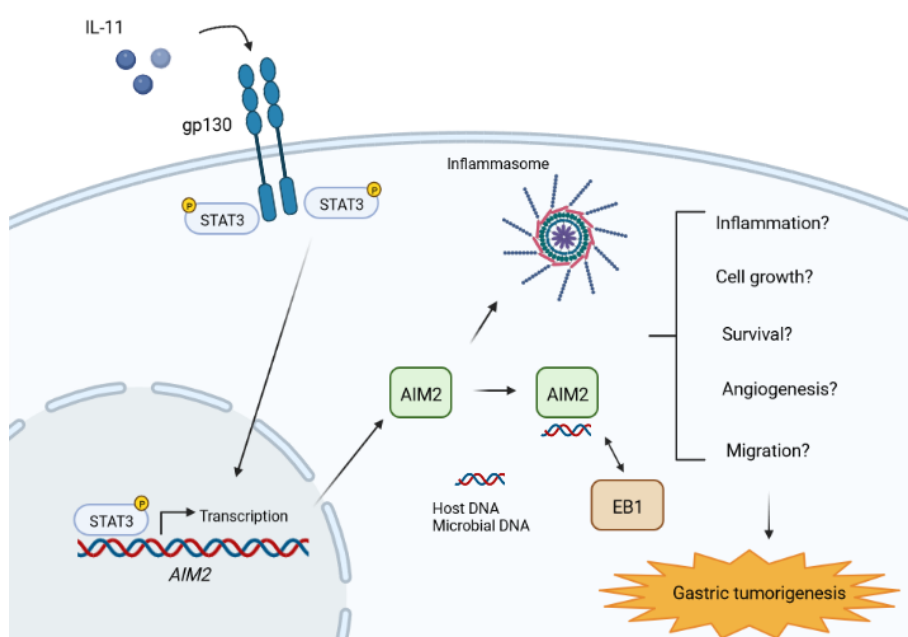


## Projects Available in the Cancer and Immune Signalling Laboratory

|                               |                                                                       |
|-------------------------------|-----------------------------------------------------------------------|
| <b>Project Title:</b>         | Identification of novel immune regulators in stomach (gastric) cancer |
| <b>Project Supervisor(s):</b> | <a href="#">Prof Brendan Jenkins</a> & <a href="#">Dr Ruby Dawson</a> |
| <b>Suitable for:</b>          | Hons/M Res, M Phil, PhD                                               |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide  |

### Project outline

Stomach (gastric) cancer is among the most common cancers worldwide, and is strongly linked with a deregulated immune response, leading to chronic inflammation. However, the identity of regulators of the innate arm of the immune system with oncogenic potential in the stomach remains largely unknown.



Schematic overview of the cross-talk between the IL-11/JAK-STAT3 cytokine signalling cascade and the AIM2 pattern recognition receptor in promoting gastric cancer.

Using preclinical genetically engineered and xenograft mouse models for gastric cancer, we aim to identify and understand how novel immune regulators (pattern recognition receptors, inflammasomes) in the stomach trigger chronic inflammatory and oncogenic responses that lead to gastric cancer.

This project encompasses a wide range of molecular and cell biological and genetic approaches (including CRISPR/Cas9).

Ideal candidates will have at the least a Bachelor's or first-class Honours degree in the broad biomedical science discipline, ideally with experience in a molecular wet-laboratory research environment. Candidates must also have a willingness to work with animal models.

**For more information about this project contact:**

Prof Brendan Jenkins

Email: [brendan.jenkins@adelaide.edu.au](mailto:brendan.jenkins@adelaide.edu.au)

**Supervisor Researcher Profiles**

<https://researchers.adelaide.edu.au/profile/brendan.jenkins>

<https://researchers.adelaide.edu.au/profile/ruby.dawson>

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|                               |                                                                                                         |
|-------------------------------|---------------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | The role of innate immune regulators in pancreatitis and pancreatic cancer                              |
| <b>Project Supervisor(s):</b> | <a href="#">Prof Brendan Jenkins</a> , <a href="#">Dr Mohamed Saad</a> & <a href="#">Dr Joshua Chey</a> |
| <b>Suitable for:</b>          | Hons/M Res, M Phil, PhD                                                                                 |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                                    |

**Project outline**

Pattern recognition receptors (PRRs) are key molecules of the innate immune system that recognise microbial- and/or host-derived products to trigger the inflammatory response.

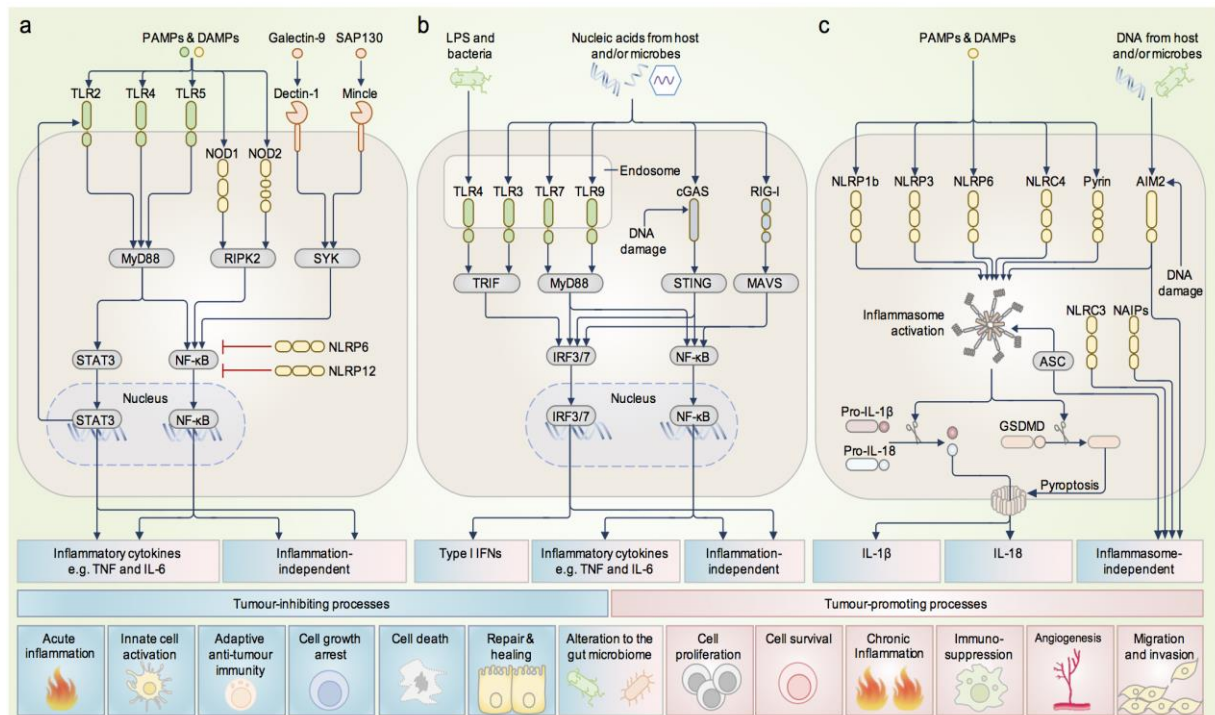


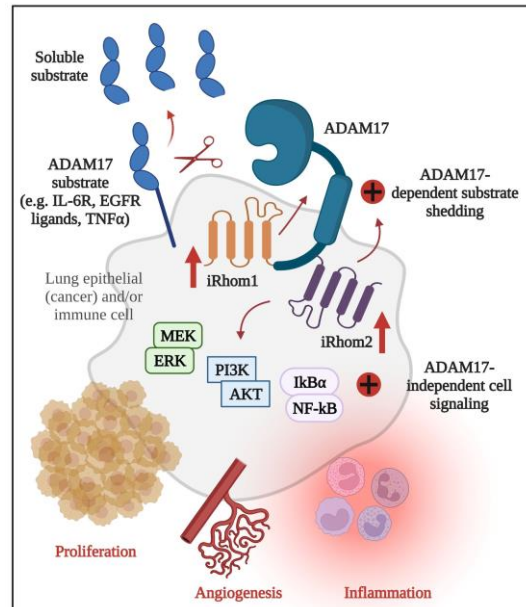
Figure 1

Pattern recognition receptors orchestrate diverse cellular processes relevant to cancer development and progression. a | Membrane-bound Toll-like receptors (TLRs) sense numerous pathogen-associated molecular patterns (PAMPs) and damage-associated molecular patterns (DAMPs) released by dying or tumour cells. The cytoplasmic nucleotide-binding oligomerization domain-like receptors (NLRs) NOD1 and NOD2 can sense peptidoglycan of bacteria. The C-type lectin receptors Dectin-1 and Mincle can sense PAMPs but also tumour-associated molecular patterns. These pattern recognition receptors signal via their respective adaptor proteins MyD88, RIPK2 and SYK, and activate the transcription factors NF-κB and STAT3, coordinating the production of inflammatory cytokines (for example, TNF and IL-6) and type I interferons that stimulate inflammatory or non-inflammatory processes. Some NLRs, such as NLRP6 and NLRP12, inhibit NF-κB signalling and suppress inflammation. b | Endosomal TLRs, the DNA sensor cGAS and the RNA sensor RIG-I activate their respective adaptors TRIF, MyD88, STING or MAVS, and via the transcription factors interferon regulatory factor 3 (IRF3), IRF7 or NF-κB trigger inflammatory or non-inflammatory processes. c | The cytosolic NLRs pyrin and absent in melanoma 2 (AIM2), via the adaptor protein ASC, form inflammasome complexes to induce proteolytic cleavage of pro-IL-1β, pro-IL-18 and gasdermin D (GSDMD). AIM2, NLRC3, members of the NLR family, apoptosis inhibitory proteins (NAIPs) and ASC also have inflammasome-independent functions in cancer.

This project aims to understand the molecular basis by which specific PRRs promote pancreatic cancer, one of the most lethal and aggressive cancers in the world that is strongly linked with a dysregulated immune response.

The project will also investigate the mechanisms by which the iRhom (rhomboid-like pseudoprotease) family of proteases, recently implicated in inflammatory conditions, contributes to pancreatitis and pancreatic cancer.

This research employs preclinical genetically engineered and xenograft (including patient-derived) mouse models, as well as translational studies using our large collection of biobanked pancreatic cancer patient samples. Such research will ultimately assist identifying genes for potential use as biomarkers for targeted therapy.



Schematic diagram of ADAM17 biological activity and its regulation by the iRhom pseudoproteases. Also shown are downstream signalling pathways activated and the pro-tumourigenic cellular processes.

Ideal candidates will have at the least a Bachelor's or first-class Honours degree in the broad biomedical science discipline, ideally with experience in a molecular wet-laboratory research environment. Candidates must also have a willingness to work with animal models.

#### For more information about this project contact:

Prof Brendan Jenkins

Email: [brendan.jenkins@adelaide.edu.au](mailto:brendan.jenkins@adelaide.edu.au)

#### Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/brendan.jenkins>

<https://researchers.adelaide.edu.au/profile/mohamed.saad>

<https://researchers.adelaide.edu.au/profile/yuchinnjoshua.chey>

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|                               |                                                                                  |
|-------------------------------|----------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Identification of immune system regulators as therapeutic targets in lung cancer |
| <b>Project Supervisor(s):</b> | <a href="#">Prof Brendan Jenkins</a> & <a href="#">Dr Mohamed Saad</a>           |
| <b>Suitable for:</b>          | Hons/M Res, M Phil, PhD                                                          |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide             |

## Project outline

iRhoms and ADAMs are key protease families whose role in the immune system and inflammation-associated cancers remain poorly defined.

This project studies the role of the ADAM and iRhom families of proteases as key upstream oncogenic regulators in the lung. This will fully elucidate the mechanistic basis by which ADAM and iRhom family proteases can influence lung carcinogenesis, and in doing so also identify how they potentially impact on innate immune responses triggered by pattern recognition receptors.

This project employs a combination of *in vivo* lung cancer mouse models (genetically engineered, xenograft - including patient-derived), CRISPR gene editing and clinical biopsies to foster translation, as well as a vast range of molecular and cellular biological techniques.

Ideal candidates will have at the least a Bachelor's or first-class Honours degree in the broad biomedical science discipline, ideally with experience in a molecular wet-laboratory research environment. Candidates must also have a willingness to work with animal models.

### For more information about this project contact:

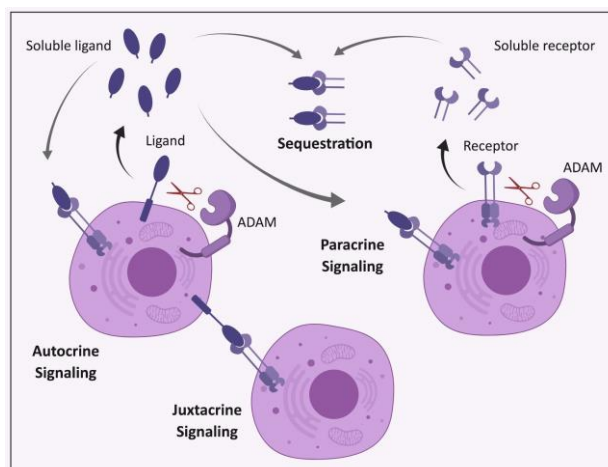
Prof Brendan Jenkins

Email: [brendan.jenkins@adelaide.edu.au](mailto:brendan.jenkins@adelaide.edu.au)

### Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/brendan.jenkins>

<https://researchers.adelaide.edu.au/profile/mohamed.saad>



Modes of action of ectodomain proteins. Schematic representation of the various autocrine, paracrine and/or juxtacrine modes of action by which biologically active processed ADAM17 substrates (i.e., ectodomains) act on cells.



## Projects in Tumour Inflammation & Immunotherapy

### Biomaterials and Immune Engineering Laboratory (BIEL)



Dr Yannan Yang  
Group Leader



Dr Moustafa Mabrouk  
Postdoctoral Researcher



Dr Than Loc Nguyen  
Postdoctoral Researcher

BIEL aims to leverage state-of-the-art biomaterials and nanotechnology-based approaches to modulate immune systems and create translational immunotherapy strategies with improved therapeutic efficacy and minimised adverse effects.

Our laboratory is specifically interested in designing and fabricating biocompatible nanoparticles, hydrogels, scaffolds and cell/bacteria derived biomimetic materials with immunomodulatory activities and controlled drug release profiles for engineering immunity. We stand at the materials-bio interface and investigate how biomaterials at different scales (nano, micro and bulk) can interact with bio-systems and tumour microenvironments, and how these interactions can be further controlled to benefit the outcome of immunotherapy that aims to prevent and treat cancer.

### Projects Available in the Biomaterials and Immune Engineering Laboratory

|                               |                                                                                                           |
|-------------------------------|-----------------------------------------------------------------------------------------------------------|
| <b>Project Title:</b>         | Nanotechnology-based in situ vaccines for cancer immunotherapy                                            |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Yannan Yang</a> , <a href="#">Dr Moustafa Mabrouk</a> & <a href="#">Dr Than Loc Nguyen</a> |
| <b>Suitable for:</b>          | Hons/M Res, M Phil, PhD                                                                                   |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide                                      |

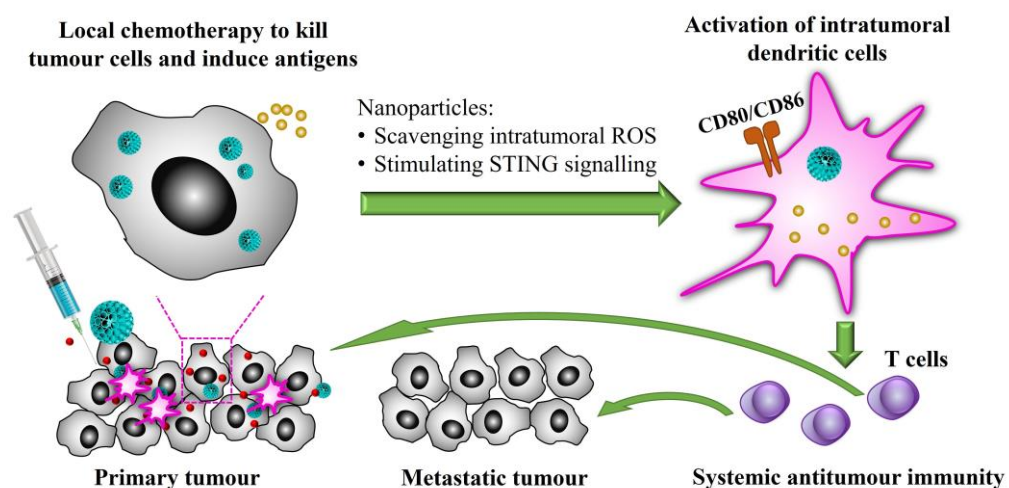
#### Project outline

In situ cancer vaccines are a new type of vaccination strategy. It reshapes the tumour microenvironment and converts the tumour burden into tumour antigens to evoke adaptive immune response against tumours. As in situ vaccines harness a patients'



own tumours as the source of antigens, the tumour heterogeneity can be largely overcome. In situ cancer vaccines can be utilised as a neo-adjuvant therapy in clinical settings to eradicate metastatic tumours and reduce the recurrence rate after primary treatments such as surgery. In addition, as in situ vaccines are a local treatment which mostly uses an intra-tumoural administration route, the toxicity in normal tissues and other adverse effects can be largely mitigated. However, the limited immune response generated by in situ vaccinations remains a major bottleneck that hinders their clinical translation.

This project aims to develop nanotechnology based in situ vaccines by fabricating novel nanoparticles with a range of activities, including activation of stimulator of interferon genes (STING), reshaping immunosuppressive tumour microenvironment for tumour immunotherapy. We will further investigate and maximise the synergy between nanomaterials and drugs to evoke robust anti-tumour immunity. It is envisioned that the outcomes from this research program will provide a new solution to address the bottleneck that accounts for the numerous clinical failures of in situ vaccines, with the potential to attract industry interest for translation of the vaccine nanotechnology.



Schematic illustration of the working mechanism of the nanotechnology-based in situ vaccine: a local chemotherapy strategy for inducing systemic antitumor immunity.

The skills/techniques you will learn by doing this project include:

- Nanomaterials fabrication and characterisation
- Bioanalysis (Flow cytometry, Confocal imaging, Western-blot, etc.) on nanomaterials-cell interactions
- Establishing in vivo tumour models
- Performance and biosafety evaluation of vaccines in animal models

Candidates with skills, experience, or educational backgrounds in biomaterial fabrication, nanobiotechnology, immunology/immunotherapy, pharmaceuticals or cancer biology are preferred to undertake this project.

**For more information about this project contact:**

Dr Yannan Yang

Email: [yannan.yang@adelaide.edu.au](mailto:yannan.yang@adelaide.edu.au)

Ph: +61 8 8313 3776

**Supervisor Researcher Profile**

<https://researchers.adelaide.edu.au/profile/yannan.yang>

<https://researchers.adelaide.edu.au/profile/moustafa.mabrouk>

<https://researchers.adelaide.edu.au/profile/thanhloc.nguyen>

## Projects in Tumour Inflammation & Immunotherapy

### T Cell Immunotherapy Laboratory



Dr Mara Zeissig  
Group Leader



Dr Tamsin Lannagan  
Senior Research Fellow



Dr Charlotte Toomes  
Research Fellow

Immunotherapy has revolutionised the way we treat cancer. Immunotherapies such as CAR T cell therapy or immune checkpoint inhibitors all harness the ability of cytotoxic T cells to recognise and kill tumour cells. However, approximately 80% of solid cancer patients do not respond to immunotherapy.

The T Cell Immunotherapy Laboratory is focused on understanding how cancers evade the immune system to identify new ways to enhance response to immunotherapy. In particular, we work on cancers that are addicted to the oncogene KRAS such as lung, colorectal and pancreatic cancers. We utilise a range of tools including genetically engineered preclinical models of cancer, analysis of immune cell subsets and molecular biology techniques. We also harness large-scale genetic screening using CRISPR-Cas9 technology to find previously unknown targets and mechanisms that regulate response to immunotherapy.

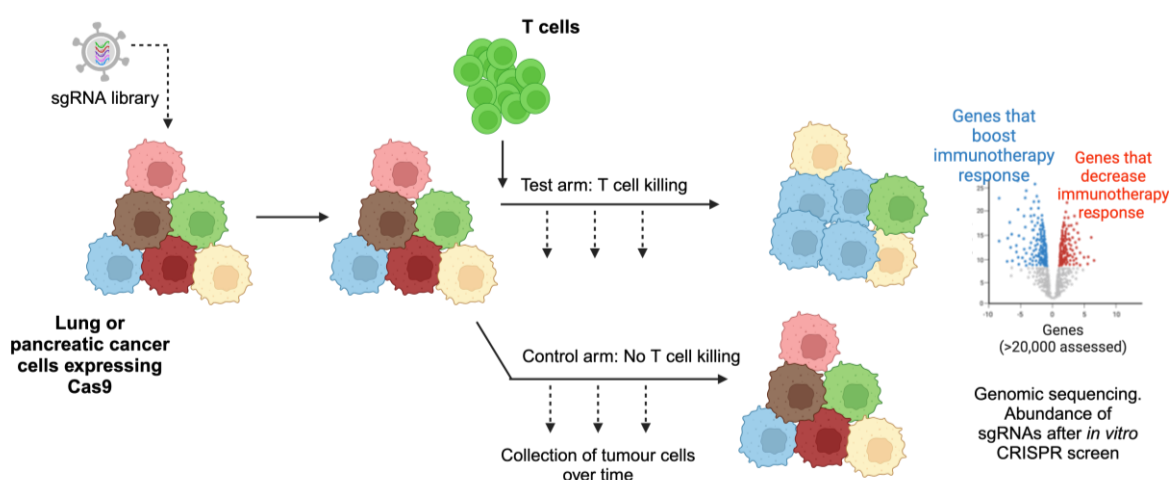
### Projects Available in the T Cell Immunotherapy Laboratory

|                               |                                                                       |
|-------------------------------|-----------------------------------------------------------------------|
| <b>Project Title:</b>         | Boosting response to immunotherapy in lung and pancreatic cancers     |
| <b>Project Supervisor(s):</b> | <a href="#">Dr Mara Zeissig</a> & <a href="#">Dr Charlotte Toomes</a> |
| <b>Suitable for:</b>          | M Res                                                                 |
| <b>Location of project:</b>   | Adelaide Health & Medical Sciences Building, North Terrace, Adelaide  |

## Project outline

Lung and pancreatic cancers are two of the most commonly diagnosed cancers and have very poor survival outcomes. They are characterised by immune-cold tumours, with poor infiltration of cytotoxic T cells and a lack of response to immunotherapy.

This project will use unbiased, whole-genome CRISPR-Cas9 genetic screening, in combination with T cell co-culture to identify new targets that could enhance the response of these tumours to immunotherapy. New drug targets identified in the screens will be characterised *in vitro* and *in vivo* to assess the effects on tumour growth, immune infiltration and response to immunotherapy. Potential new drug combination therapies will also be tested in mouse models of lung and pancreatic cancers.



New drug targets to increase response to immunotherapy will be identified by co-culturing lung or pancreatic cancer cell lines (expressing Cas9 and harbouring sgRNAs that target the whole genome) with tumour-killing T cells and conducting an unbiased whole-genome CRISPR-Cas9 screen.

The student will learn a range of techniques, including *in vivo* modelling, CRISPR-Cas9 gene editing, cell culture, flow cytometry, next-generation sequencing, immunohistochemistry and qPCR.

Candidates are expected to have a Bachelors degree in a field of biomedical science and ideally have wet-lab experience. Candidates should also be willing to work with animal models of cancer.

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**Project Title:** KRAS inhibitors for the treatment of pancreatic cancer  
**Project Supervisor(s):** [Dr Mara Zeissig](#) & [Dr Tamsin Lannagan](#)  
**Suitable for:** M Res

**Location of project:** Adelaide Health & Medical Sciences Building, North Terrace, Adelaide

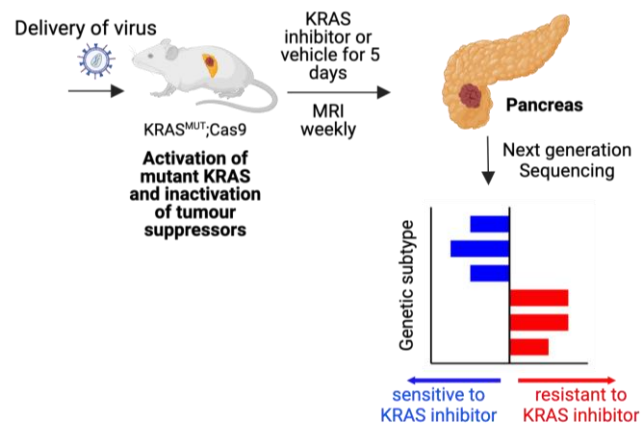
### Project outline

Pancreatic cancer is the 4th biggest cancer killer in Australia. Almost all (95%) pancreatic cancers are driven by mutations in the oncogene KRAS. In the past few years there has been the introduction of a new class of drugs that target KRAS. In clinical trials, KRAS inhibitors are only effective in a small number of patients but present a new therapeutic option that is targeted and has fewer side effects.

Our research has found that over 90% of pancreatic cancers have a high level of antioxidant production within the cancer cells. This gives the cancer cells the ability to be more resilient and survive cancer treatment. Importantly, we now have evidence that this causes resistance to KRAS inhibitors.

This project will study the effect of elevated antioxidant pathways on tumour biology and response to KRAS inhibitors.

The student will learn a variety of techniques, including in vivo modelling, CRISPR/Cas9 genetic editing, cell culture, in vitro drug assays, flow cytometry and immunohistochemistry.



**Figure 1. *In vivo* CRISPR-Cas9 screen to identify KRAS mutant subtypes resistant or sensitive to KRAS inhibitors**

Candidates will have a Bachelors degree in a field of biomedical science and ideally have wet-lab experience. Candidates should also be willing to work with animal models of cancer.

### For more information about these projects contact:

Dr Mara Zeissig

Email: [mara.zeissig@adelaide.edu.au](mailto:mara.zeissig@adelaide.edu.au)

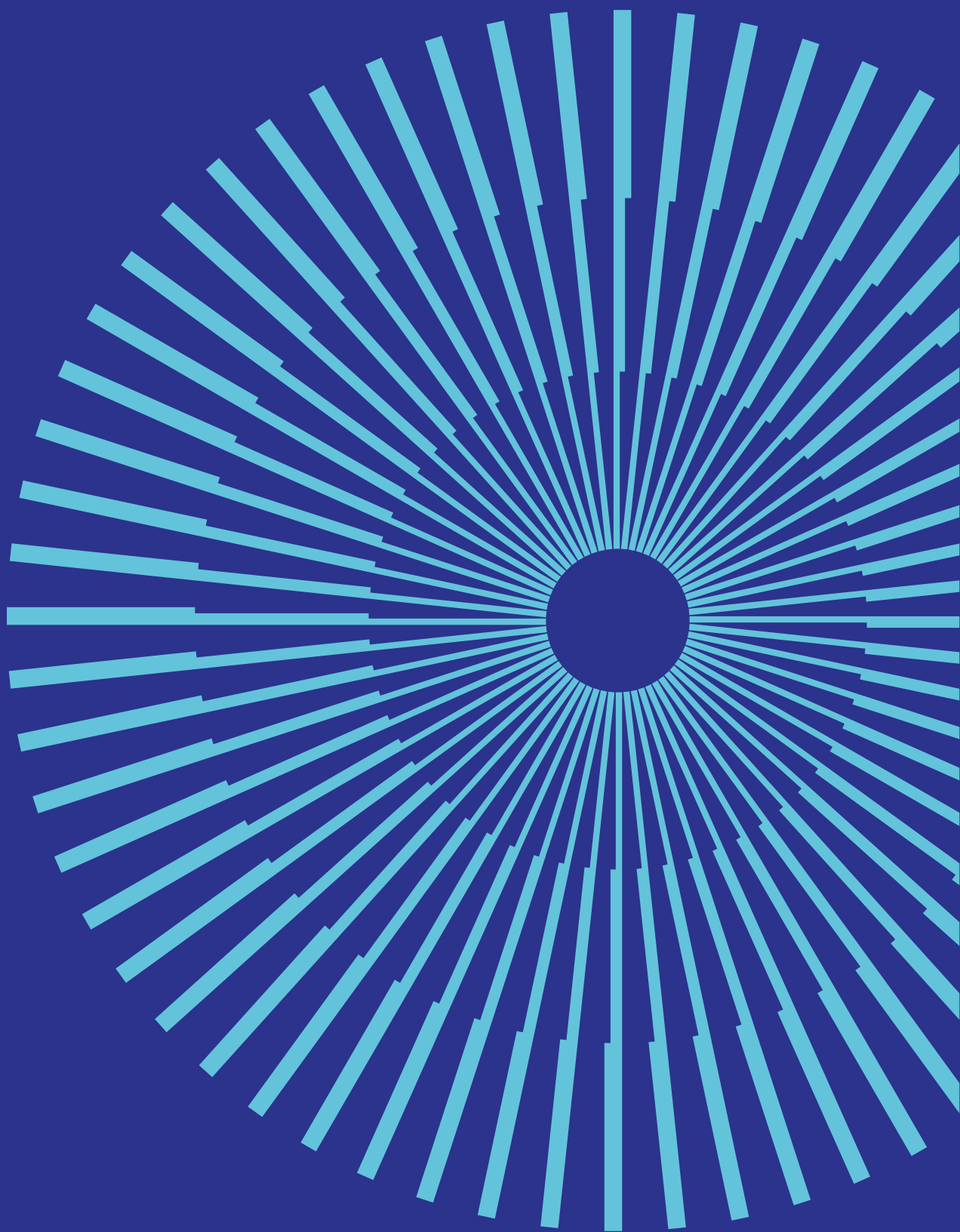
Ph: +61 8 8313 4474

### Supervisor Researcher Profiles

<https://researchers.adelaide.edu.au/profile/mara.zeissig>

<https://researchers.adelaide.edu.au/profile/tamsin.lannagan>

<https://researchers.adelaide.edu.au/profile/charlotte.toomes>



## Further enquiries

Adelaide University SA 5005 Australia  
enquiries [saigenci@adelaide.edu.au](mailto:saigenci@adelaide.edu.au)  
web [adelaide.edu.au/saigenci](http://adelaide.edu.au/saigenci)

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