2024/2025

SAGC | SOUTH AUSTRALIAN GENOMICS CENTRE

Annual Report

Celebrating Five Years of Growth and Impact

Table of Contents

Acknowledgement of Traditional Owners

We would like to acknowledge the Kaurna people as the Traditional Custodians of the Land on which the SAGC is located. We pay our respects to Kaurna Elders, past, present and future, and recognise their continuing connection and contribution to this land.

The SAGC staff, Scientific Advisory Committee and Steering Committee are committed to ensuring that Indigenous Genomics is conducted in a culturally appropriate manner with Indigenous governance and oversight.

The SAGC has adopted the FAIR and CARE principles (Findable, Accessible, Interoperable, Reusable, and for the Collective Benefit, with Authority to Control, Responsibly, and Ethically) and will implement Guiding Principles recommended by the Aboriginal and Torres Strait Islander Advisory Group on Health Genomics.

BIOINFORMATICS

HEAPS GOOD GENOMICS

ECONOMICS

Disclaimer

Our Vision

The vision of the SAGC is to enable innovative genomics research by providing state-of-the-art, collaborative end-to-end genomics and bioinformatics services, know-how, and cutting edge infrastructure.

Our Mission

The SAGC aims to provide comprehensive, cost-effective and readily accessible genomics and bioinformatics services, and infrastructure of the highest possible standard to support research excellence in human, agricultural, environmental and microbial genomics.

About Us

The South Australian Genomics Centre (SAGC) was established in July 2020 as a state-wide genomics facility to support genomics research in South Australia, as well as nationally and internationally. The SAGC is South Australia's only NCRIS-supported genomics facility, with funding support from BioPlatforms Australia (BPA), the SA State Government, the James and Diana Ramsay foundation (JDRF) and our partner institutes - South Australian Health and Medical Research Institute (SAHMRI), The University of South Australia, Flinders University and The University of Adelaide. Our affiliate partners include the Australian Genome Research Facility (AGRF) and the Australian Wine Research Institute (AWRI).

The SAGC provides a broad range of services, including single cell genomics and spatial transcriptomics, bulk RNA sequencing, small RNA sequencing, exome and genome sequencing, epigenomics, metagenomics and a range of other custom methods. These services are supported by a dedicated bioinformatics team that supports users of the facility by developing advanced and customised approaches for data analysis, integration and visualisation. The SAGC is pleased to support researchers and clinicians from our partner institutes, as well as industry and other external clients. All areas of genomics including animal, plant, environmental, microbial, and human genomics are supported. The SAGC also offers a range of educational activities, including seminars, bioinformatics workshops, while also fostering valuable connections with industry.

SAGC Central Hub
South Australian Health and Medical Research Institute (SAHMRI)

Adelaide SA 5000 Australia

Flinders Node
Health and Medical Research Building at Flinders Village (HMRB)

Bedford Park SA 5042 Australia

Expanding Horizons at our Flinders node

This year, the SAGC was delighted to welcome Dr. Ayla Orang as our new Sr. Genomics Research Coordinator for our Flinders Node at the new Health and Medical Research Building (HMRB) on the Bedford Park campus. Ayla has a strong background in molecular biology, functional genomics, and cancer research, underpinned by a PhD in Molecular Biology and several years of postdoctoral research. Her expertise extends across RNA biology, automation workflows, and collaborative high-throughput sequencing projects, which will help to expand the SAGC's capacity to deliver large-scale, high-quality genomics research support.

This last year marked an important period of transition for our Flinders Node. After successfully moving into HMRB, we have laid the groundwork for an exciting new phase of growth at HMRB.

With new capabilities, expanded lab space, and the new team getting established, the SAGC is poised for a dynamic year ahead.

"It's exciting to see the SAGC Flinders node relocate to the stunning new HMRB, joining other core facilities to provide high-quality, integrated and comprehensive support for our users."
Dr Sen Wang SAGC Manager

Flinders University

Scientific Director's Message

The SAGC is an exemplar of cooperation between the major institutes in South Australia and shows what can be achieved if we work together and collaborate rather than compete.

I am pleased to present this year's Annual Report, marking another year of strong progress for the South Australian Genomics Centre (SAGC) as we celebrate five years since the facility was established. Prior to SAGC, South Australia lacked an NCRIS-supported genomics facility, and genomics and bioinformatics services were fragmented across small, uncoordinated units. These facilities lacked the critical mass, expertise, and scale required to support large research projects, leading many researchers to seek services interstate or overseas.

Since opening in 2020, the SAGC has expanded rapidly, with 334% growth in service revenue as an indicator of activity in the Centre. Over this period, the Centre has also obtained NATA accreditation, strengthened outreach and education programs, delivered market-competitive turnaround times, and provided researchers with access to advanced genomics technologies and specialist expertise.

Key investments have driven this growth, including the establishment of multiple spatial transcriptomics capabilities and the acquisition of the MGI T7. The T7 has enabled nationally and internationally competitive high-throughput sequencing, offering SAGC a point of differentiation within the Australian genomics landscape. Demand has exceeded expectations, with 116 T7 runs completed in 2024/25 —nearly 80% above forecast.

The SAGC has grown over the last 5 years to a nationally recognised facility with a team of 13 staff. To date, the Centre has supported more than 650 projects and over 1,200 researchers locally, nationally, and internationally. Interstate users have risen from under 3% in 2020/21 to 19% in 2024/25. Supporting researchers remains central to our mission: since inception, SAGC has contributed to more than 300 grant applications, providing consultation and experimental design guidance, budgeting guidance and letters of support. Researchers supported by the Centre secured $13.45 million in competitive funding this year, bringing total awarded funding over five years to ~$85 million. Since establishment the SAGC has contributed to more than 200 publications and delivered >20 seminars and 12 bioinformatics workshops to over 1,000 participants.

I extend my sincere gratitude to the Steering Committee (SC) for their continued guidance. In particular, I acknowledge Yvette van Eenennaam, Independent Chair, whose leadership during establishment and throughout the past five years has been instrumental in shaping our strategic direction and strengthening alignment across partners. I also extend special thanks to our Scientific Advisory Committee, chaired by Professor Robert Edwards and comprising 13 distinguished genomics researchers from across South Australia. Their expertise has been instrumental in ensuring the SAGC remains at the forefront of scientific innovation, underpinning both our current operations and future growth.

Finally, I want to acknowledge our highly skilled SAGC team. As the Centre has expanded rapidly, the adaptability, professionalism, and commitment of our staff have been fundamental to our success. I would particularly like to recognise our Centre Manager, Sen Wang, for his exceptional leadership. Sen has played a pivotal role in guiding day-to-day operations, supporting strategic planning, and ensuring the seamless integration of new capabilities as the SAGC has grown.

Looking ahead to 2025/26, demand for genomics will continue to accelerate, with the global market projected to reach USD $60 billion by 2027. The SAGC will continue to build engagement with industry and expand collaborations across spatial omics, lipidomics, proteomics, metabolomics, machine learning and artificial intelligence, continuing to support world-class multidisciplinary research locally, nationally and internationally.

Prof David Lynn, SAGC Scientific Director

Manager's Message

The SAGC has continued its remarkable growth, achieving a 50% increase in revenue compared to 2023/24, and an impressive 334% growth since the facility's establishment five years ago.

This success is mirrored across all key metrics for 24/25: data output has nearly doubled (95%), researchers supported increased by 44%, and interstate users grew by 20%. Notably, 46% of projects now include bioinformatics support, up from 13% in 2023/24.

A key highlight this year has been the adoption of spatial and single-cell technologies that the SAGC has invested in over the past 5 years. Data generation from single-cell projects increased by 106% and from spatial projects by 171%. A standout achievement was the application of Stereo-seq™ single-cell spatial transcriptomics to wheat spikelets—the first use of this advanced technology in South Australia. The insights gained extend beyond traditional bulk transcriptomics, providing a foundation for precision breeding to enhance yield, resilience, and quality in wheat, one of the world's most important crops.

The facility supported 65 grant applications this year, with $13.45 million in funding awarded to SAGC-supported projects—reflecting the high calibre of research within our community. In partnership with Bioplatforms Australia (BPA), the SAGC also launched the South Australian Multiomics Framework Initiative, funding five successful projects through a $500,000 internal scheme. Each project is progressing well, and we look forward to sharing their outcomes in the coming year.

SAGC continues to support a diverse research portfolio spanning environmental, biomedical, agrifood, and livestock research at local, national, and international levels. This year, 46 publications acknowledged SAGC or listed our staff as co-authors, underscoring our growing research impact.

Public engagement remains a core focus. The facility hosted nine seminars featuring local and international experts and three bioinformatics workshops. In partnership with Indigenous Genomics research groups, the SAGC contributed to the PROPHECY Project—the largest longitudinal diabetes study in Aboriginal Australians—processing over 2,600 Indigenous samples. Workforce development also remained a priority, highlighted by the completion of the first 12-week paid Indigenous Genomics Internship, during which the interns sequenced the genome of the South Australian white-backed magpie, gaining hands-on laboratory and bioinformatics training. Given its educational impact and overwhelmingly positive feedback, the facility will continue the Indigenous Genomics Internship this year.

The achievements of 2024/25—and the past five years—reflect the collective effort of the SAGC team. We extend our sincere thanks to the Steering Committee chaired by Yvette Van Eenennaam, Scientific Director (Prof. David Lynn), and the Scientific Advisory Committee chaired by Prof. Rob Edwards, for their strategic guidance and leadership. I also want to congratulate Dr John Salamon on his appointment as the newest JDRF Bioinformatics Fellow, recognising his leadership and significant contribution towards the facility's bioinformatic development. I especially acknowledge the genomics, bioinformatics, business development and quality assurance teams, whose dedication, adaptability, and sustained commitment have been instrumental in driving the SAGC's continued success and growth.

We look forward to continuing to empower our research, clinical, and industry communities in the years ahead.

Dr Sen Wang, SAGC Manager

FY 2024/2025 Operational Report

422 users**

1220 Researchers supported

+44%

Researchers supported* across >70 organisations

+20%

Out of state users*

9 Scientific Seminars

4 Bioinformatics Workshops

46 Publications

65 Grants Supported

>$13M Successful Supported Grants Announced

Biomedical

Cancer
Allergy
Microbiome
Immunology
Indigenous Genomics
Neurobiology
Vaccines

Industry

Biotech
Clinical trials
Livestock
Vaccines
Partnerships

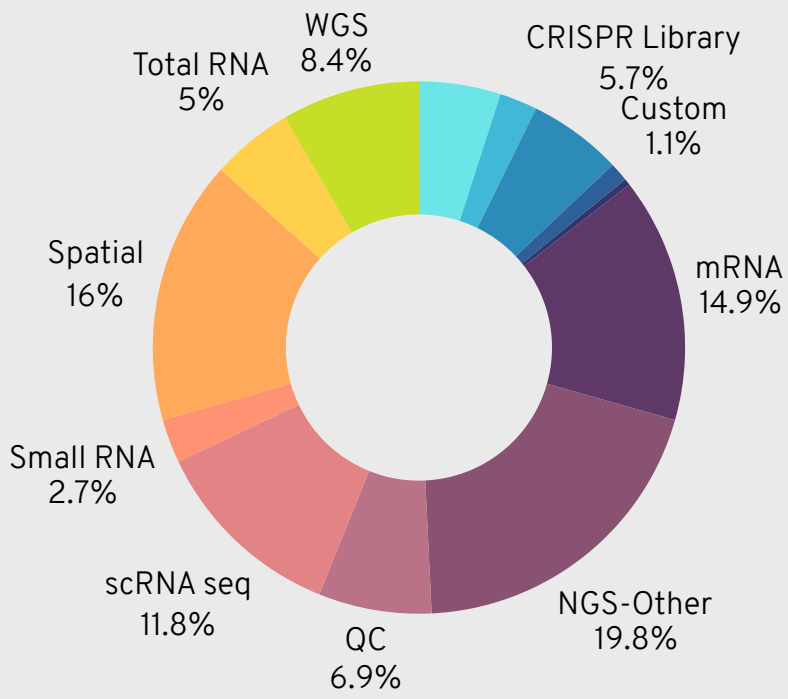
Environment

Metagenomics
Marine ecosystems
Biodiversity
Conservation

Agrifood

Livestock
Crops
Breeding

Genomics Projects 24/25



Areas of growth Y/Y

Spatial RNA
9% ➡ 16%

CRISPR Library
1% ➡ 6%

Projects with Bioinformatics
13% ➡ 46%

+31%

Next Generation Sequencing **runs***

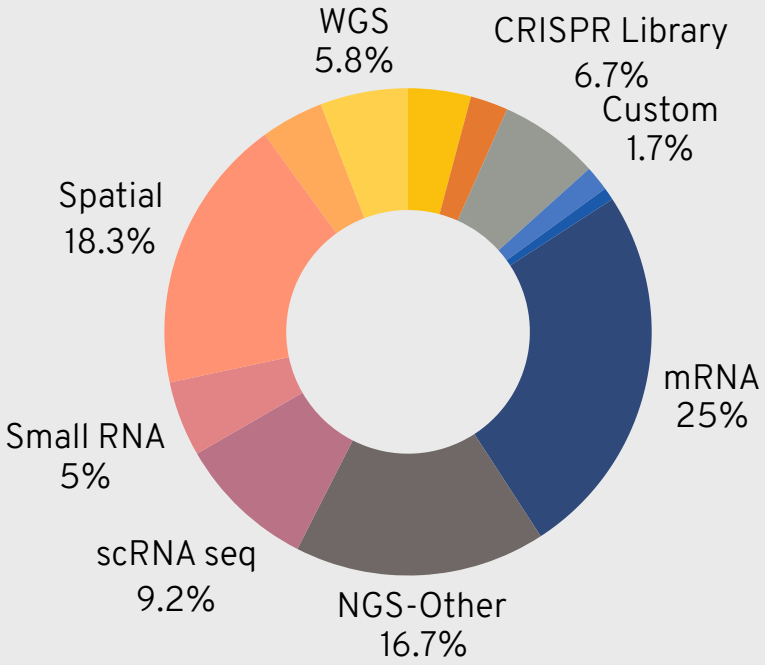
+95%

Total Data generated*

+171%

Data generated from **spatial projects***

Bioinformatics Projects 24/25



* Compared to 2023-24 FY

**Clients who have accessed genomics or bioinformatics services

STOmics in Cereal Crops: Advancing Insights into Plant Development and Yield

Dr. Scott Boden, ARC Future Fellow at the University of Adelaide, leads research into the genetic regulation of wheat's flowering structures, flowering time, and grain quality. His goal is to understand the developmental and genetic processes that set yield potential and resilience in cereal crops.

In earlier work, Dr. Boden's team used bulk transcriptomics to identify and characterise key genes controlling flowering time and spike architecture. This approach revealed how these genes influence the timing of flowering, spikelet initiation, and final spike structure, and uncovered how environmental cues like day length and temperature interact with genetic pathways. The team also mapped regulatory hierarchies between genes, linked genetic variation to agronomic traits, and validated gene functions using mutant and transgenic lines.

While these studies provided valuable insight into which genes are important, they could not reveal where in the developing spike these genes were active or which cell types drove these processes. Identifying this gap led Dr. Boden to become interested in spatial transcriptomics. Among the spatial technologies available, Stereo-seq™ (STOmics) has the highest-resolution, species-agnostic platform for unbiased RNA detection in plant tissues.

By applying this technology at the SAGC and collaboratively work with Dr Boden's team to optimise STOmics workflow on wheat spikelets at early and late developmental stages.

This enabled the generation of high-resolution spatial maps of gene expression, linking specific genes to distinct cellular functional groups. The ability to pinpoint where, and in which cells, genes are switched on provides an unprecedented view of wheat inflorescence development. This is particularly powerful in wheat, with its complex hexaploid genome, where different sub-genomes may contribute unequally to development. The project brought together expertise from Genomics, Histology, and Microscopy teams, along with Dr Boden's lab to successfully implement the STOmics workflow on these wheat samples.

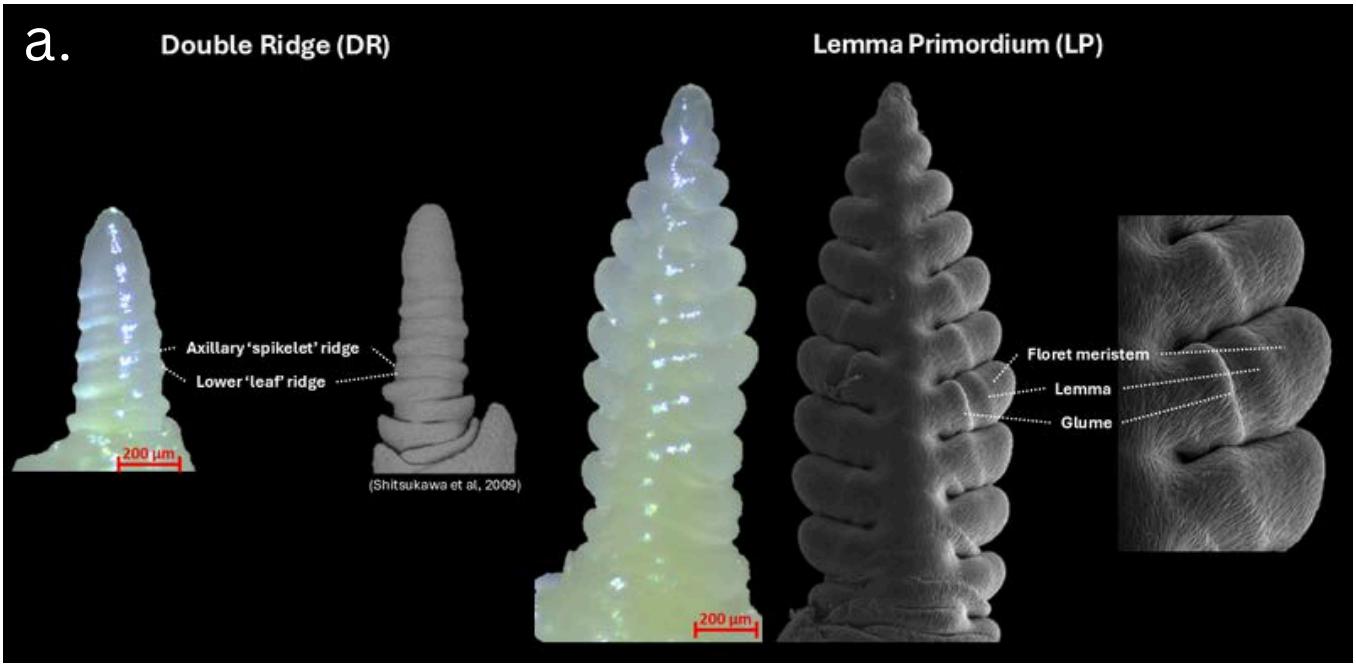
"The hexaploid wheat genome made processing these samples quite a challenge, being nearly 5x larger than the human genome, as well as causing read alignment issues due to homologs within the sub-genomes. Fortunately, we did manage to process all samples through the SAW pipeline after tweaking parameters to optimise memory usage and better handle multi-mapping reads."

This important work has the potential to inform breeding strategies aimed at optimising inflorescence architecture, improving grain quality, and enhancing resilience to stresses such as heat and drought—critical steps towards the next generation of high-performance cereal crops.

Spatial transcriptomics identifies distinct domains regulating yield-related traits of the wheat ear

Yue Qu, Cong Tan, Liujing Yang, Marianna Pasquariello, Abdul Kader Alabdullah, Shiyu Sun, Munir Iqbal, John Salamon, Scott Boden

doi: https://doi.org/10.1101/2025.08.12.670006



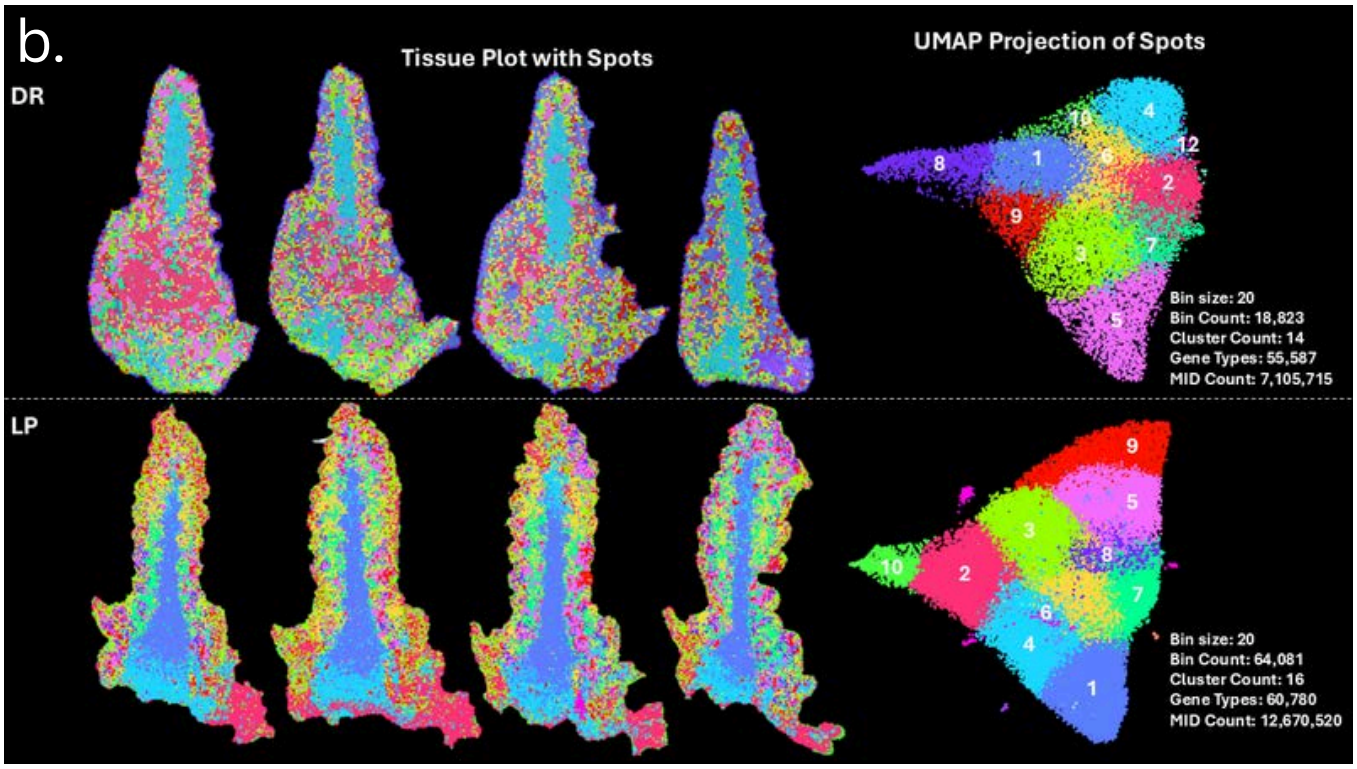
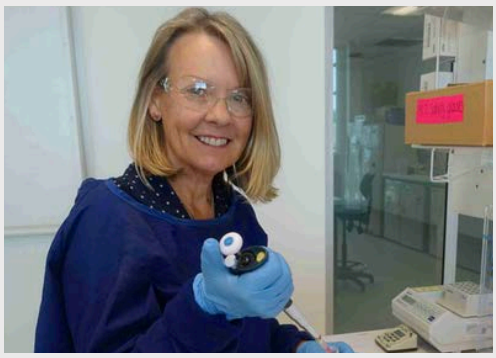


Figure 1 - Spatial transcriptomics workflow and identification of transcriptional 118 domains in early wheat inflorescence development. a, Study Design: 2 Stages of Wheat shoot apex development were selected b, Gene cluster analysis from SAW pipeline, 14 distinct clusters were identified by gene expression profile in early stage and 16 in late stage. Distinct patterns emerged which were consistent across the tissues. Total gene count was about 60K, 7M

Full article

Grant Highlights

The SAGC provided letters of support for 65 grant applications in 2024/2025. We are pleased to highlight 7 of the 14 success stories announced this year, totalling ~$13.45 M funding.



Assoc. Prof. Theresa Hickey

The University of Adelaide

Grant Title: Rebalancing sex hormone signalling in the breast ecosystem to reduce cancer risk

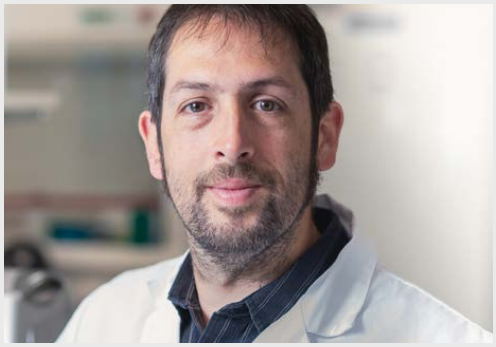
Amount Awarded:
$1,414,094
NHMRC 2024 Ideas Grant

Assoc. Prof. Philip Gregory

University of South Australia

Grant Title: Uncovering the functions of splice variants driving breast cancer progression

Amount Awarded:
$1,166,928
NHMRC 2024 Ideas Grant



Prof. Simon Conn

Flinders University

Grant Title: Targeting the Alternative RNA Splicing Dichotomy of Brain Cancer as a Novel Anticancer Strategy

Amount Awarded:
$2,954,575
Investigator/Leadership 2

Prof. Paul Thomas

The University of Adelaide/SAHMRI

Grant Title: Leveraging mouse t-haplotype transmission bias for mammalian pest control

Amount Awarded:
$803,784
ARC Discovery

Dr. David Sharkey

The University of Adelaide

Grant Title: Sperm - a novel role in human reproduction beyond fertilisation

Amount Awarded:
$1,781,257
NHMRC 2024 Ideas Grant

Prof. Robert Edwards

Flinders University

ARC Laureate Fellowship: New horizons for synthetic phages
$3,890,346 awarded

ARC Discovery Grant: Discovering new ways to generate targeted mutations
$685,781 awarded

Dr. Martha Menberu

Flinders University

Grant Title: Developing a Microbiome-Driven tool for Personalized Screening and Risk Stratification in Young-Onset Bowel Cancer

Amount Awarded:
$49,920
Dr Sarah Barlow Bowel Cancer Foundation Research Grant

SAGC Supported Grant Applications in 2024-25FY

65

SAGC Supported Successful Applications funding announced 2024-25FY

$13.45M

South Australian Multiomics Framework Initiative

Supported by Bioplatforms Australia

In FY23 - 24, SAGC launched the Multiomics Framework Initiative, a **$500,000 program** designed to promote collaboration across South Australia's Bioplatforms Australia-supported NCRIS facilities. Partners include Metabolomics SA and UniSA Proteomics. The initiative is supporting five multi-institutional collaborative projects, requiring participation from at least two BPA facilities. The five awarded projects were selected following a competitive review of 26 strong applications.

The selected projects span solid tumour, leukaemia, agriculture, and supportive oncology, all proposing advances through integration of multi-omic approaches.

In November 2024 the SAGC hosted a special seminar to hear from the 5 awarded research teams. The event gave the selected research teams the opportunity to showcase their innovative use-cases for 'omics' technologies and highlight the important problems their research aims to address.

Aims:

- *Support the innovative application of multi-omics technologies to tackle important new research questions.*
- *Build capability and expertise in multi-omics data integration and analysis.*
- *Foster collaborations between SAGC partner institutes and across BPA platforms in SA.*

Between July 2024 and June 2025, all five funded Multiomics Framework Initiative projects have progressed on track, with optimisation and pilot phases largely completed and data generation underway.

University of South Australia · AWRI · METABOLOMICS AUSTRALIA · BIOPLATFORMS AUSTRALIA

Prostate Cancer

Identifying novel metabolic drivers of lethal prostate cancer

Team: Dr Michael Cilento (SAHMRI & CALHN), A/Prof Luciano Martelotto (The University of Adelaide, ACE) and team

Progress: Successfully validated long-stored patient specimens and completed first spatial transcriptomics runs, scaling up the study to uncover new metabolic drivers.

Genomics Metabolomics Proteomics

University of South Australia · Health Central Adelaide Local Health Network · SAHMRI · THE UNIVERSITY of ADELAIDE

Biomanufacturing Therapeutics

A multiomics driven approach to deliver scalable biomanufacturing of the anti-cancer therapeutic, parthenolide

Team: A/Prof Jenny Mortimer (The University of Adelaide), Dr. Agnieszka Kumorkiewicz-Jamro (The University of Adelaide, SAiGENCI) and team

Progress: Demonstrated parthenolide production in feverfew under different growth conditions; multi-omics analyses now underway to support scalable cancer therapy manufacturing.

Genomics Metabolomics Proteomics

Crop Stress & Growth

Identifying the molecular mechanisms of chickpea respiration and growth during stress using integrated multiomic analysis

Team: Dr Crystal Sweetman (Flinders University), Dr Julie Hayes (The University of Adelaide) and team

Progress: Collected and analysed 600 chickpea samples, identifying variation in stress responses and advancing to deep metabolomics and transcriptomics profiling.

Genomics Metabolomics Proteomics

Acute Myeloid Leukaemia

Dissecting molecular mechanisms underpinning a new cytokine signalling axis governing leukaemia stemness

Team: Dr Winnie Kan (UniSA, CCB), Dr Adrienne Sullivan (The University of Adelaide, SAiGENCI) and team

Progress: Established optimised protocols and launched pilot sequencing, while analysing patient samples to inform single-cell and metabolic studies of IL-3 signalling.

Genomics Metabolomics

Gut–Brain–Immune Interactions

Leveraging multi-omics to combat chemotherapy-induced cognitive impairment

Team: Dr Feargal Ryan (SAHMRI, Flinders University), Dr. Hannah Wardill (SAHMRI, The University of Adelaide) and team

Progress: Pilot study confirmed sample quality and detection of key microbiome-linked metabolites; advancing toward integrated multi-omics analysis and publications.

Genomics Metabolomics Proteomics

Ongoing Partnership with JDRF

The SAGC is delighted that the **James and Diana Ramsay Foundation (JDRF)** has renewed its funding commitment to support Bioinformatics at the SAGC for a further three years. The foundation has significantly supported the SAGC since its inception - providing seed funding to establish the facility in 2020. The SAGC builds on the already solid reputation of South Australian researchers in genomics and bioinformatics and has further increased partnerships in the field, including non-traditional collaborations that bring together researchers working in the plant and agriculture research fields with those working in biomedical research.

The early investment by JDRF in SAHMRI's bioinformatic capability has helped establish connections with more than 140 researchers, who have used SAGC services for more than 270 projects and contributed to 30 peer-reviewed publications. Included in this diverse list of research projects have been Prof Cedric Bardy's vital work to understand drivers in Parkinson's disease, A/Prof Erin Symonds' work to develop non-invasive diagnostics for colon cancer and a collaboration with SA Water and SA Pathology to conduct waste-water surveillance around South Australia to detect COVID variants.

The JDRF-funded Bioinformatics Fellowship exemplifies the exciting opportunities made possible through SAGC's partnership with the JDRF. In addition to developing innovative analysis pipelines, the Fellowship strengthens multiple facets of the SAGC Bioinformatics team, including the delivery of Bioinformatics workshops aimed at building bioinformatics capacity across South Australia (See pg. 23 for more information). Dr John Salamon has recently been appointed as the newest JDRF Bioinformatics Fellow. This recognition reflects John's outstanding leadership, technical expertise and significant contributions to strengthening SAGC's bioinformatics capability. Since joining the Centre, John has led key initiatives to enhance infrastructure, cybersecurity and data-management systems, in addition to supporting a wide range of research projects and delivering training to build capacity across the sector.

To further this goal, JDRF is partnered with the SAGC to subsidise costs for students attending the 2025 ABACBS Conference. This joint investment provided students with valuable opportunities for networking and exploring career pathways within the bioinformatics field.

JDRF Bioinformatics Fellow Dr. John Salamon with JDRF Board member Tim Edwards at the 2025 ABACBS Conference

JAMES & DIANA RAMSAY FOUNDATION

BPA All Hands Meeting

In the idyllic setting of the Yarra Valley representatives from all Bioplatforms Australia (BPA) nodes across the country came together for a two-day meeting. A delegation from the SAGC attended this event, including the Scientific Director, the Centre Manager, the Business Development Manager and the Project Officer. The event provided an excellent opportunity for networking, collaboration, and the sharing of innovative research. Professor David Lynn, SAGC Scientific Director was invited to participate as a panel member in a discussion focused on "Big Picture: Future Directions," contributing valuable insights into the evolving genomics landscape. Each node presented an exciting collaborative project, showcasing the strength and diversity of the BPA network which spans facilities focused on genomics, proteomics, metabolomics, synthetic biology, and bioinformatics

Joel Bathe, Business Development Manager, presented cutting-edge research led by Dr. Scott Boden and his team at the University of Adelaide (see pg 12), highlighting the use of Spatial Transcriptomics in studying wheat inflorescence development — an impressive example of the technology's application in plant genomics.

Building connections across the 'omics network— genomics, proteomics, metabolomics, synthetic biology, and bioinformatics — will be instrumental to unlocking a deeper understanding of complex biological systems. The emphasis on multi-omics and collaboration was highlighted by the SAGC Multi-Omics Framework, which is supporting five multi-institutional omics projects in SA. Through funding and capability support, the Framework aims to facilitate the innovative application of multi-omics technologies to address significant new research questions and foster collaborations across BPA platforms in South Australia.

Seminar Series

In FY 2024-2025, the SAGC hosted 9 seminars promoting local and national excellence in genomics research. The seminars series covered a broad range of topics including, microbiome, spatial transcriptomics, single cell sequencing, high performance computing, artificial intelligence and population genomics.

Thank you to all of our amazing speakers for sharing their expertise.

Coral Reef Arks & the BioToy Universe

The SAGC and the Flinders Accelerator for Microbiome Exploration (FAME) hosted Professor Forest Rohwer from San Diego State University, a pioneering viral ecologist. Prof. Rohwer discussed how his lab uses metagenomics and thermodynamic modelling to explore the immense biodiversity of coral reefs—home to tens of millions of life forms, particularly bacteriophages. His talk highlighted the Coral Reef Arks initiative, a novel approach to understanding and reconstructing reef systems through a realistic, physics-based model. The event was kindly sponsored by Illumina.

July 2024

From the Human Cell Atlas to the Body Map of the Immune System

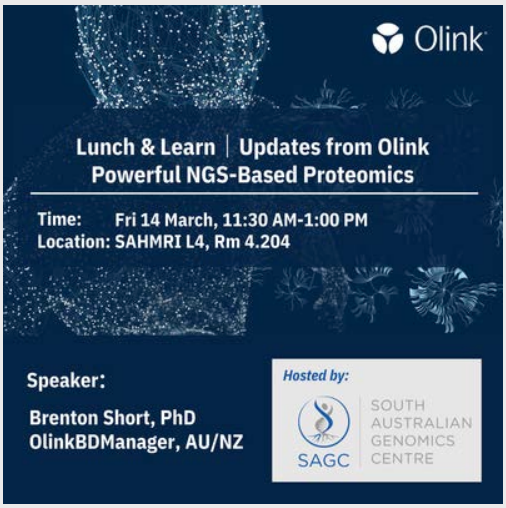
Dr Stefano Mangiola from SAiGENCI presented an outstanding seminar on mapping the human immune system using large-scale single-cell RNA sequencing. His team harmonised nearly 13,000 samples, curating 29 million cells from 45 anatomical sites to build a reference of immune cell composition and gene expression across tissues, age, sex, and ethnicity. Advanced modelling revealed tissue-specific immune ageing, sex-based differences, and immune checkpoint diversity—laying foundations for precision immunology and cancer research. The seminar was generously sponsored by Decode Science.

October 2024

Powerful NGS-Based Proteomics (Updates from Olink)

Researchers gathered at SAHMRI to hear the latest from Olink® Proteomics in a seminar led by Brenton Short, ANZ Business Manager. The session highlighted Olink's new NGS-based proteomics assay—focused on inflammation, immune response, and druggable targets to support high-throughput proteogenomics applications. Key use cases included identifying biomarkers, validating drug targets, and enabling population-level studies across disease areas such as cancer, autoimmune disorders, cardiovascular and neurological diseases.

March 2025



Spatial Transcriptomics in Cereal Crops

Dr. Scott Boden, ARC Future Fellow at the University of Adelaide, delivered a seminar at Waite Campus, on the application of spatial transcriptomics in cereal crop research. Dr. Boden shared his team's experience using Stereo-seq™ single-cell resolution spatial transcriptomics to investigate spikelet development in wheat. The seminar highlighted how understanding the genetic control of inflorescence architecture, flowering time, and grain quality can directly impact breeding strategies and improve crop yield and resilience. His talk underscored the power of spatial technologies to map gene expression in situ, offering valuable insights into plant development and environmental responsiveness—critical tools for enhancing global food security through advanced cereal breeding programs.

March 2025

Beyond Detection – The Future of eDNA Research

The SAGC and FAME hosted Beyond Detection: The Future of eDNA Research at Flinders' City Campus, uniting experts to discuss eDNA's expanding role in ecological monitoring and conservation. Keynote Dr Elise Furlan (University of Canberra) showcased eDNA's evolution from species detection to applications in population genetics, eRNA, and biomass estimation. Talks by Dr Vilma Pérez, Dr Jamie Wood, and Dr Michael Doane highlighted its use from ancient DNA to microbial monitoring. The seminar, sponsored by Illumina, underscored eDNA's transformative potential for environmental management.

March 2025

Illumina Multiomics Innovation Roadmap

The SAGC hosted Illumina to showcase the company's latest advancements in multiomics technologies, including new product launches in proteomics, single cell and spatial transcriptomics planned for 2026. Dr Ivonne Petermann presented the expanded portfolio and data analysis solutions to support the integration of multiomics data sets.

March 2025

Transforming Drug Development with Single Cell and Spatial Multiomics

The SAGC hosted 10x Genomics for a seminar about the increasing utilisation of advanced genomics tools (*e.g.*, single cell and spatial transcriptomics) across stages of the drug development pipeline—from identifying new targets and profiling mechanisms of action, to evaluating safety, uncovering biomarkers, and improving translational research outcomes. Real-world examples illustrated how high-resolution, multi-dimensional tissue profiling can reduce clinical trial risks and accelerate therapeutic innovation.

May 2025

Unlock Your Blocks – Overcoming Challenges with FFPE Samples

The SAGC hosted a hybrid event with QIAGEN, focused on tackling the challenges of working with formalin-fixed, paraffin-embedded (FFPE) samples to gain expert insights into best practices for FFPE sample collection, storage, extraction, and sequencing. The session covered practical strategies to improve nucleic acid quality, enhance reproducibility, and minimise variability in FFPE-based workflows. The event offered valuable, actionable guidance for improving outcomes when working with challenging clinical sample types.

June 2025

Bioinformatics Workshops

In FY 2024-2025, the SAGC hosted 4 Bioinformatics workshops, which were attended by ~180 researchers and students contributing to building bioinformatics capacity in SA and nationally.

Intro to Nextflow & Snakemake

This hands-on workshop offered a practical introduction to Nextflow and Snakemake, two essential workflow management tools in bioinformatics. Aimed at both beginners and experienced users looking to broaden their toolkit. The sessions covered building basic pipelines, comparing features, and running external workflows using the BioCommons Seqera Platform. Expert instruction was provided by Dr Michael Roach (Snakemake), Dr John Salamon (Nextflow), and Dr Ziad Al Bkhetan (Seqera Platform), who shared real-world insights into workflow configuration and tool selection.

August 2024

RNAseq Bioinformatics Workshop

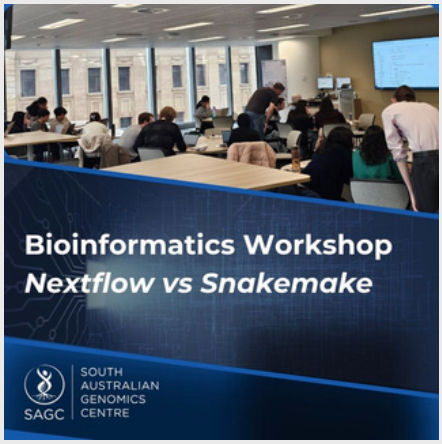
Dr. Daniel Thomson from the SAGC led a full-day RNAseq analysis workshop at Flinders University's new City Campus, providing hands-on training in using nf-core pipelines with Nextflow, offering participants a practical and reproducible approach to RNA sequencing analysis. The workshop highlighted how tools like nf-core are making advanced genomics workflows more accessible, efficient, and reproducible. Attendees gained valuable skills in setting up and running RNAseq pipelines.

October 2024

Australian Society for Immunology (ASI) Spatial Workshop 2024

Dr John Salamon and Cathal King presented at this satellite workshop to the ASI's annual conference. The meeting took place in Sydney and 30 attendees took part in a whole day spatial transcriptomics workshop learning about the analysis of Visium, Stereo-seq and Xenium data.

November 2024



Nextflow vs Snakemake Take Two

Back by popular demand, the SAGC's Dr John Salamon (Nextflow), and Flinders FHRMI's Dr Michael Roach (Snakemake), led a follow-on workshop on how to build and run basic bioinformatics pipelines. Attendees compared the tools in terms of usability, flexibility, and performance, gaining valuable insights into how to enhance reproducibility, scalability, and collaboration in computational research.

June 2025

Enhancing Target Discovery and Translational Success With Advanced Genomics

Last year, the SAGC delivered several programs centered on the growing adoption of single-cell and spatial transcriptomics technologies across the drug development pipeline. These initiatives highlighted how advanced genomics tools are driving efficiency and enabling researchers to refine target selection, prioritise lead candidates, elucidate mechanisms of action, assess safety and toxicity, identify biomarkers of response and resistance, with the ultimate goal of reducing the risk of clinical trial failure.

It is exciting to see technologies such as spatial transcriptomics now being integrated into clinical research. Early adoption has been most prominent in solid tumor studies, including hepatocellular carcinoma, lung cancer, melanoma, and other cancer types, where spatially resolved insights are helping to link molecular heterogeneity with clinical outcomes.

"It's exciting to think of the potential for how high-resolution, multi-profiling of tissues/cells will lead to actionable insights for drug discovery and development." Joel Bathe, SAGC Business Development Manager

Key themes included:

- Single cell **insights for target** selection and MOA studies
- Spatial transcriptomics for **understanding tissue architecture and microenvironments**
- Scalable applications for **biomarker discovery** and early-stage R&D
- **Opportunities for start-ups** to leverage these technologies early in development

Technology Highlights

10X Chromium OCM Kit

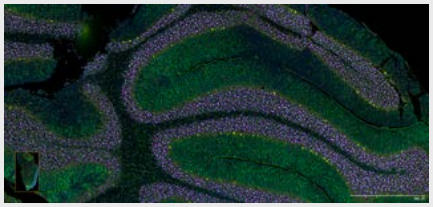
OCM ("On Chip Multiplexing") *allows users to split reactions into 2 or 4 samples (10k or 5k cells), significantly reducing the price per sample.*

Xenium Protein

The **27-plex protein panels** enable RNA and protein detection on the same tissue section. The initial off-the-shelf panels focus on well-characterised proteins involved in cell growth, signalling, and immune response. The focus on cancer and immunology is designed for studies exploring spatial heterogeneity of tumour micro-environments and immune checkpoint dynamics.

10X Chromium GEM-X 5' Immune Profiling

Enables simultaneous measurement of gene expression and immune receptor diversity (BCR and TCR) from the same cell. The new chemistry doubled the throughput, and improved sensitivity. This assay allows researchers in clinical and translational settings to deeply characterize immune responses—such as those occurring in cancer immunotherapy, infectious disease, and vaccine trials.



Expanding the Spatial Biology Community with Xenium In Situ Analyser

In recognition of our Team's technical capabilities and quality standards, we became only the 2nd certified Xenium Service Provider for 10x Genomics in Australia. This certification reinforces our place as a trusted provider of spatial multiomics.

Innovative Pilot Program to Reduce Barriers to Adoption

Recognising cost remains a key barrier to adoption of spatial technologies, and with 10X Genomics launching their "off-the-shelf" 5k Prime gene panel, we saw an opportunity to play matchmaker and pair projects together. Working with our partners at Millennium Science and 10X Genomics, we came up with the concept for the 5K Prime Pilot Program.

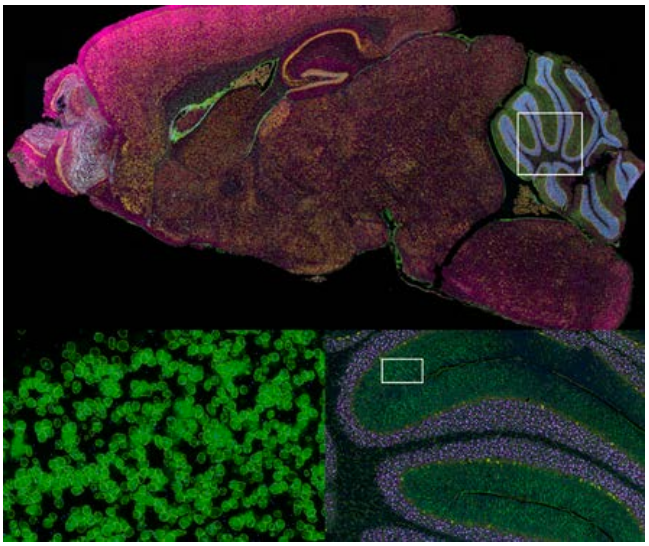
With custom gene panels this type of program was previously not feasible. With 5K prime we could match "like with like" and generate one slide worth of data for research groups to help support proof-of-concept studies and generate meaningful data sets to support grant applications. The Pilot program attracted strong interest, and four outstanding applicants were selected.

These pilot studies were completed successfully and generated promising early data and experience helping to showcase the immense amounts of quality data possible from even a single run.

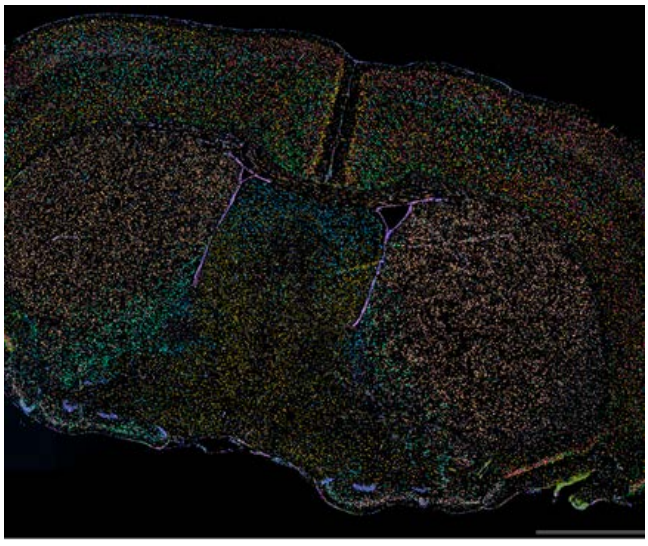
Building a Community of Spatial Users

Engagement and education were also a key focus. SAGC hosted a highly successful Xenium Roadshow, bringing together researchers, clinicians, and technology specialists for live demonstrations and expert discussions. The roadshow helped illustrate important use cases for spatial transcriptomics in diverse areas such as cancer, neuroscience, and infectious disease.

Complementing these efforts, we ran a series of bioinformatics workshops aimed at building user confidence in spatial data analysis. We also organised our first Xenium User Group Meeting, bringing together early adopters to share learnings, explore challenges, and provide meaningful input to the SAGC and 10X Genomics. The engagement and interactive discussions underscored the growing momentum behind the Xenium platform.



Mouse brain sagittal section run with Xenium 5K Prime gene panel. Provided courtesy of Courtney Cross.



Mouse CNS run with 5K Prime Gene Panel. Provided Courtesy of Megan Monaghan.

For more info on spatial capabilities at the SAGC visit our website

Stereo-seq OMNI Allows Simultaneous Spatial Profiling of Host and Pathogen RNAs on FFPE

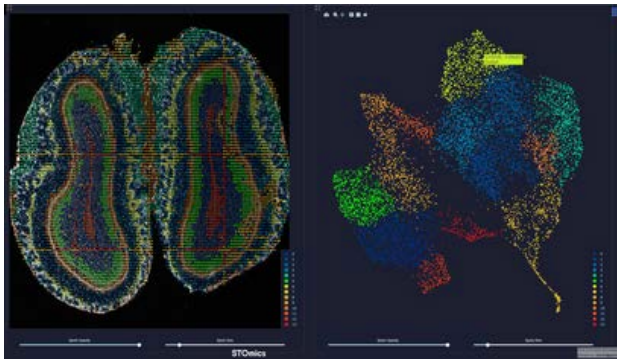
In early 2025, MGI released Stereo-seq v2 (OMNI), the first spatial omics platform to enable the mapping of total RNA from FFPE tissue at single-cell resolution. Stereo-seq OMNI enables simultaneous analysis of mRNA, long non-coding RNA, and host–microorganism interactions within the spatial context of archival tissues.

Formalin-fixed paraffin-embedded (FFPE) tissue is the gold standard and largest reservoir of clinically annotated specimens. Unlike other FFPE compatible technologies that rely on targeted probes, Stereo-seq OMNI uses a random-priming capture strategy that pulls in total RNA—not just poly(A) ends. **That change matters:** it increases gene body coverage, reduces 3′ bias, and opens the door to RNAs that conventional poly-T chemistries often miss, like from microorganisms.

The SAGC has completed numerous projects across a variety of species and tissues. The DNBSEQ-T7 platform is required to meet OMNI's massive sequencing demands (~1.5–2B reads per chip). The introduction of OMNI gives researchers a powerful new tool to investigate complex mechanisms of infection, immunity, and cancer.

The SAGC's early experience with OMNI

"*Working with FFPE makes sectioning and handling more straightforward, and access to archival blocks is a huge advantage*," said Dr. Munir Iqbal. "*We have had to make a few adjustments since the early runs - initially, even with 2B reads per sample, we weren't reaching saturation. We added a ribodepletion step and this has made a big difference*," added Munir.



Mouse brain -STOmics

Pathogen Detection *In Situ* - Our Favourite Bit!

Since OMNI captures total RNA, it can pick up bacterial, viral, and fungal transcripts alongside host RNA in the same section. This is a leap-forward and has important applications across areas like infectious disease and microbiome-tumor studies.

Examples of OMNI applications:

- Co-localise pathogen and host transcriptomes in tissue
- Map infection gradients, immune infiltration, and damage/repair programs spatially
- Generate hypotheses about host–pathogen interactions that would be invisible without spatial context

What makes OMNI different?

- Random priming capture: Instead of relying on poly-T, OMNI uses random primers to capture total RNA, which:
  - Enables even coverage across the gene
  - Reduces 3′ read bias
  - Enables detection of non-poly(A) transcripts and microorganism RNAs
- Species-agnostic: Total RNA capture plus unbiased priming makes cross-species and multi-organism samples feasible.

Specs at-a-glance

- Chip area: 10 mm × 10 mm
- Sub-cellular resolution: 500 nm
- Capture chemistry: random priming (total RNA, including microbes)
- Tissue quality: compatible with DV200 > 30%

Empowering Discovery with Parse Evercode™

Global Spotlight on SAGC's Leadership in High-Throughput Single-Cell Sequencing

The South Australian Genomics Centre (SAGC) continued to establish itself as a national and international leader in single-cell genomics by becoming the first Certified Service Provider (CSP) for Parse Biosciences in the Asia–Pacific region. As an early adopter of Parse's Evercode™ technology, SAGC has contributed to advancing high-throughput single-cell sequencing in Australia.

This collaboration significantly boosts local capabilities by offering flexible, scalable, and cost-effective single-cell sequencing—enabling breakthroughs across diverse biological and medical research areas.

Full SAHMRI Article

Empowering Research Through Bioinformatics & Training

SAGC's bioinformatician Cathal King was globally recognised by U.S.-based Parse Biosciences in their feature article "Unlocking the Power of Multi-Omics Biology through Data Science." The article celebrated SAGC's leadership in adopting Evercode technology and its commitment to capacity building through training workshops and webinars focused on single-cell bioinformatics.

The success of these early efforts led to SAGC's selection as the first Certified in the APAC region. In collaboration with Parse and Decode Science, the SAGC hosted Dr. Zac Moore (WEHI) as part of the Adelaide Cancer Series, where he presented groundbreaking research in glioblastoma (GBM). At the event, Dr. Tessa Gargett (title/group to be confirmed) was awarded a Parse grant (~$50K) to support CAR-T cell therapy investigations.

Scaling Single-Cell Capability with New Technologies

SAGC's implementation of Parse Evercode™ technology has been strongly complemented by its access to high-throughput, cost-effective sequencing on the MGI DNBSEQ-T7 platform. The recent release of MEGA and PENTA kits has expanded single-cell profiling capacity to an unprecedented 1–5 million cells per workflow, marking a major leap in data generation and analytical requirements.
These advances were recently featured in Cosmos Magazine, where Munir Iqbal and Joel Bathe of SAGC were interviewed about the centre's contribution to scaling national capability in single-cell RNA sequencing.

Full Cosmos Article

For more info on single cell capabilities at the SAGC visit our website

Indigenous Genomics

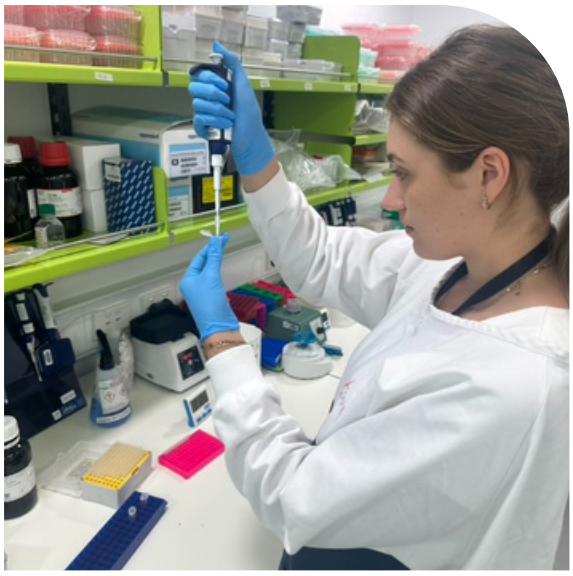
In 2025, the SAGC continued to advance and support Indigenous genomics initiatives through close collaboration with Wardliparingga (SAHMRI), The Kids Research Institute, and the Australian Alliance for Indigenous Genomics (ALIGN).

A highlight of the year was the annual ALIGN Symposium in September, which provided an important opportunity to reconnect with colleagues across the country and to gather insights guiding the development of the National Indigenous Genomics Capacity and Capability Building Roadmap, scheduled for completion in late 2025. Building on last year's identification of fourteen key strategies to strengthen Aboriginal and Torres Strait Islander participation in genomics and enhance the cultural capability of non-Indigenous genomics professionals, this year's focus shifted toward implementation. We convened a panel discussion with representatives from government, research, health services, and Aboriginal community-controlled organisations. The panel, alongside the wider ALIGN network, underscored the critical importance of sustainable funding, targeted upskilling of the Aboriginal health workforce, and innovative community-level communication strategies to inspire interest in genomics pathways.

This year's symposium also incorporated contributions from CONNECT – the Consortium for National Indigenous Genomics Capacity – broadening opportunities to share expertise and experiences across national jurisdictions. We contributed South Australian perspectives to discussions on national priority projects, including Indigenous data sovereignty, precision medicine, genome biology, pharmacogenomics, immunogenomics, and rare diseases.

Another major achievement in 2025 was the completion of transcriptomic sequencing for the Prophecy project, which investigates Type 2 diabetes in South Australian Aboriginal communities. In partnership with The Kids Research Institute, we sequenced the RNA of 1,255 blood samples, generating a rich dataset that has now been returned to collaborators for analysis. This successful collaboration demonstrated the value of strong institutional partnerships and established a foundation for future Indigenous genomics projects supported by SAGC.

Workforce development remained a central priority this year, with the successful completion of our first 12-week paid Indigenous Genomics Internship. Our inaugural interns sequenced the genome of the South Australian white-backed magpie, gaining hands-on laboratory and bioinformatics training throughout the process.



'As interns at the SAGC, this experience has been inspiring and deeply rewarding. The hands-on training and mentorship from both Indigenous and non-Indigenous experts have fuelled our passion for genetic research and its potential to create meaningful change in healthcare, especially within Indigenous communities and potential conservation initiatives. We have gained invaluable skills and insights that would typically be beyond our reach at this stage of our studies. Most importantly, being part of a project that prioritises cultural safety has reinforced how research can not only acknowledge but actively celebrate and integrate Indigenous perspectives.'

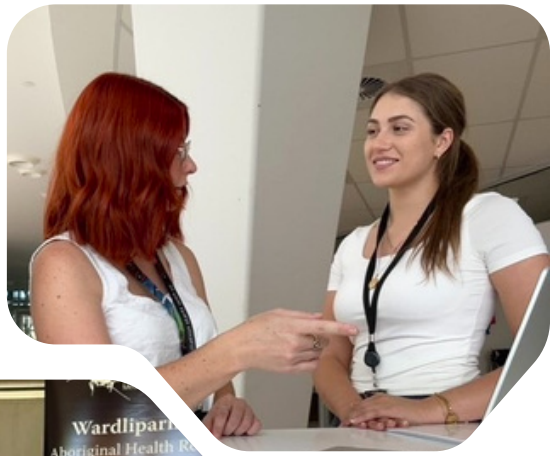
Savannah Stawiarski, Indigenous Genomics Intern

Guided by SAGC staff and supported by our collaborators, the interns extracted DNA from museum specimens, prepared sequencing libraries, and used the MGI G400 platform to generate data. They then assembled the genome using a black-backed magpie scaffold and engaged in comparative analyses. Feedback from the interns has been instrumental in refining the program for future cohorts. Encouragingly, interest in the program continues to grow, with seven applications received this year (up from four in 2024). Two new Aboriginal interns will join us at the end of 2025, undertaking a soil microbiome sequencing project that integrates wet-lab training with advanced metagenomic analyses.

Community outreach and engagement also remained a strong focus. SAGC contributed to activities identified as critical by the ALIGN network, particularly the need to engage young people and communities in conversations about the value of genomics. Marlie represented SAGC and ALIGN at key events, including the 2024 Aboriginal STEM Learners Congress hosted by the Department of Education and facilitated by the Young Aboriginal STEM Thinkers of South Australia. For the second consecutive year, we delivered a 90-minute workshop that combined education about Indigenous health genomics with a practical DNA extraction activity using quandongs. The workshop, attended by Aboriginal and Torres Strait Islander students in years 5–10, offered participants the chance to experience genomics in action and generated strong enthusiasm among students.

This year's program was expanded to include insights from the Prophecy study, particularly the impact of Type 2 diabetes on eye health, further linking genomics education to health outcomes relevant to Aboriginal communities.

Looking ahead to 2026, SAGC will continue its active role in national ALIGN initiatives and will support the release and implementation of the National Indigenous Genomics Capacity and Capability Building Roadmap. We remain committed to fostering Indigenous leadership in genomics, strengthening cultural capability across the field, and engaging the next generation of Aboriginal and Torres Strait Islander scientists.



Decoding the Harmful Algal Bloom

The SAGC is playing a key role in the whole genome assembly of Karenia mikimotoi, which will be a crucial tool for research into bloom dynamics, toxicity, and mitigation in South Australian waters

Researchers at Flinders University, led by Dr Michael Doane and Professor Elizabeth Dinsdale from the Flinders Accelerator for Microbiome Exploration (FAME), in collaboration with the SAGC, launched an initiative to sequence the whole genome of *Karenia mikimotoi*, the suspected microscopic algae linked to the harmful algal bloom devastating South Australia's coast. The project aims to deliver the first high-quality reference genome for this disruptive species and the important work is being supported by **Bioplatforms Australia**.

"Globally, *K. mikimotoi* blooms have caused severe economic losses across Europe and Asia. Despite this, we lack critical knowledge about its toxicity, bloom drivers, and ecological impacts," said **Dr Michael Doane**. "Genomic research can help fill this knowledge gap, directly informing monitoring, mitigation, and ecosystem management strategies for South Australia and beyond."

SAGC Business Manager **Joel Bathe** said a high-quality reference genome will be a foundational resource for researchers. "This genome is **~16 times larger** than the human genome and will require a substantial amount of sequencing – underscoring the importance of having strong local capacity to deliver this work," he said.

These efforts can contribute to providing critical insights into:

- **Toxin production** – identifying the genes and proteins linked to the harmful compounds that damage marine life.
- **Bloom dynamics** – describing the genetic traits that enable micro-algae, like K. mikimotoi to affect the ecosystem dynamics, persist in changing conditions, and outcompete other plankton.
- **Evolutionary history** – revealing how this species has evolved unique genomic structures, including unusual repeat regions and extra-nuclear DNA, that may explain its ecological success.
- **Future management** – identify vulnerability in the micro-algae genome that could help identify areas to be targeted for mitigation strategies.

"*The SA Algal bloom highlights how little we know about the genomic seascape in Australia*" said Professor Elizabeth Dinsdale.

Bioplatforms Australia (part of NCRIS) is supporting this work as part of its mission to build foundational molecular datasets to address environmental and biodiversity challenges.

Flinders University

Flinders Accelerator for Microbiome Exploration

BIOPLATFORMS AUSTRALIA

The dFLASH Breakthrough: Like A 'Highlighter' for Gene Regulation

Transcription factors (TFs) are like molecular "conductors" that coordinate gene expression and play vital roles in everything from development and disease to how cells respond to their environment. Yet capturing their activity in real time and with high precision has been a major challenge. The ability to observe TFs in living cells—accurately, in real time, and at scale—can accelerate drug discovery, revealing compounds that fine-tune gene expression for therapies in cancer, regenerative medicine, and beyond, while offering deeper insight into fundamental cell biology.

Dr David C. Bersten is a Researcher at the University of Adelaide, specialising in how TFs sense physiological and environmental signals to control gene expression, particularly in the brain. Combining molecular, cellular, and animal models with genomic and proteomic tools, he investigates targets such as Hypoxia Inducible Factor (HIF), NPAS proteins, and hypothalamic regulators of appetite and energy balance. This year, Dr Bersten and colleagues unveiled **dFLASH (dual FLuorescent transcription factor Activity Sensor for Histone-integrated live-cell reporting)**, a modular, genome-integrated sensor that enables scientists to watch TFs in action—live, in real time, and with striking clarity. The system produces two distinct nuclear fluorescent signals: a TF-dependent "reporter" and an internal "control," allowing highly accurate, normalized measurements of TF activity.

Developing dFLASH required a fusion of cutting-edge methods. CRISPR-Cas9 genome editing (including CRISPRoff) and whole-genome CRISPR knockout screening were used to test and validate TF regulation.

Lentiviral-mediated genomic integration ensured robust, enhancer-driven reporting across stable cell lines. High-content imaging and flow cytometry allowed dynamic monitoring of TF activity and precise single-cell analysis, while custom plasmid construction provided the modular framework for adapting the system to different transcription factors.

The SAGC has contributed to this important work by sequencing the CRISPR libraries.

Application in Drug Screening and Beyond

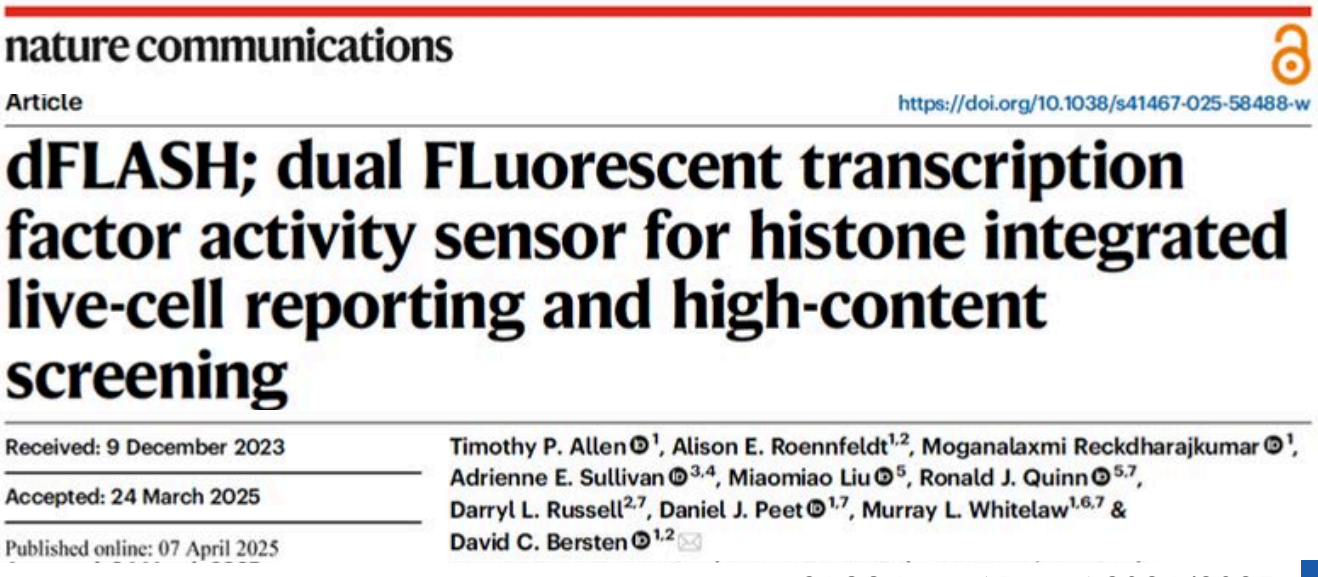
Dr. Bersten and his colleagues were able to demonstrate the utility of dFLASH in drug discovery, by screening a 1,600-compound natural product library which led to the identification of new HIF pathway modulators, including both inhibitors and stabilisers of HIF-1α—findings with clear potential in cancer and other hypoxia-related diseases.

Reach out to Dr Bersten for reagents or to collaborate: david.bersten@adelaide.edu.au

Find out more about this research

Full Article

Plasmid Info



nature communications

Article

https://doi.org/10.1038/s41467-025-58488-w

dFLASH; dual FLuorescent transcription factor activity sensor for histone integrated live-cell reporting and high-content screening

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Timothy P. Allen[1], Alison E. Roennfeldt[1,2], Moganalaxmi Reckdharajkumar[1], Adrienne E. Sullivan[3,4], Miaomiao Liu[5], Ronald J. Quinn[5,7], Darryl L. Russell[2,7], Daniel J. Peet[1,7], Murray L. Whitelaw[1,6,7] & David C. Bersten[1,2]

Tracking immune changes in children treated with CAR-T therapy

Diffuse midline glioma (DMG) is a rare, aggressive type of brain tumour that mainly affects children but can also occur in adults. Surgical removal is extremely difficult or impossible without damaging critical functions - it is incurable and uniformly fatal.

Dr. Tessa Gargett and her colleagues at the Centre for Cancer Biology (an alliance between SA Pathology and UniSA) are focusing on treating DMGs using a type of immunotherapy called **'CAR-T' (Chimeric Antigen Receptor T-Cell)**. CAR T-cell therapy for DMG is one of the most active areas of research right now, because conventional treatments haven't changed survival outcomes much in decades.

CAR-T therapy is a personalised cell therapy that involves genetically modifying T-cells collected from a patient's blood to express antigen receptors that can specifically recognise tumour cells. Selecting targets is very challenging as they need to be highly expressed on tumour cells, minimally present on healthy cells and accessible in the CNS.

There is tremendous excitement about the potential for CAR-T in DMG as it has been the first treatment to show any meaningful tumour control for these children. There are many challenges to overcome, including safety concerns (due to cytokine release syndrome and neurotoxicity), delivery challenges (e.g. blood-brain barrier access is required for CAR-T injected IV, and intraventricular delivery may improve delivery), and the many inherent challenges with manufacturing CAR-T therapies safely and affordably.

CAR T stands for **chimeric antigen receptor T-cell** therapy. In this approach:

- T-cells are collected from the patient's blood.
- They are genetically engineered in a lab to express a synthetic receptor (**CAR**) that specifically recognises a tumour-associated antigen.
- These modified T-cells are expanded and then infused back into the patient.
- Once inside the body, they seek out and destroy tumour cells with that antigen.
- Their action may be limited by the endogenous immune response, but this is poorly understood

Tessa and her colleagues are participating in a phase 1 trial of this therapy that is the first of its kind in Australia, or indeed anywhere in the world outside the US. The role of their lab is CAR-T preparation and biomarker analysis. They bank PBMCs (peripheral blood mononuclear cells) covering the time course in patients receiving CAR-T therapy. By performing single cell RNA sequencing on these samples, the aim is to track changes in CAR-T cells after infusion as they expand in the blood and detect any changes in potentially detrimental immune-suppressive cell populations.

Dr. Tessa Gargett was the successful recipient of the **Parse CSP Grant Award**, which entitled her lab to a Whole Transcriptome Evercode™ kit for 100,000 cells. Single cell sequencing was provided free of charge by the SAGC on the DNBSEQ-T7.

"The Parse Evercode technology was an excellent fit for this application as it allowed these precious samples to all be fixed as they became available at different time points and run together in a single round of library preparation helping to minimise batch effects."

Centre for Cancer Biology

University of South Australia

Find out more about this research

Rethinking Antibiotic Selection in the ICU: The Importance of Preserving the Gut Microbiome

Infection is one of the most pressing threats to patients in intensive care, often driving the need for rapid, broad-spectrum antibiotic use. However, new research from SAHMRI's Microbiome and Host Health Program has revealed that some antibiotics—specifically those targeting anaerobic bacteria—may disrupt the gut microbiome more profoundly than previously understood.

The MOCI Study Group Investigators led a multi-centre, longitudinal study, involving 110 critically ill adults, to explore how antibiotic type and exposure shapes the balance of gut microbes during intensive care. The findings suggest that the selection of antibiotics with anaerobic coverage may unintentionally deplete beneficial gut bacteria that play a crucial role in immune regulation and infection resistance.

Measuring and analysing the bacterial populations in these patients involved collecting faecal samples from critically ill adults at 48 hr intervals. The microbiome (16S rRNA amplicon) sequencing performed by the SAGC identified a total of 386 taxa, which were then categorised into four distinct functional groups for analysis: Butyrogenic anaerobes, anaerobes without known butyrogenic function, other non-anaerobic commensals, and pathobionts. To interpret the measured bacterial populations, the study modeled the relative abundance, temporal changes, exposure time to different types of antibiotics, and various clinical and demographic factors, as well as use of other medications.

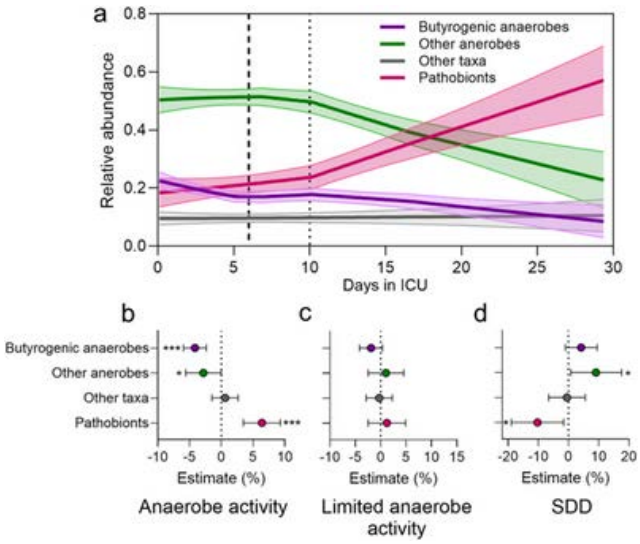


Figure 2: Looking at the time from ICU admission, there was a pronounced decline in relative abundance of "beneficial" anaerobes up to day 6, and an increase in "harmful" pathobionts from day 10. They were able to show this association was only evident with the use of antibiotics with anaerobic activity, and not with antibiotics that had limited anaerobe coverage.

Importantly, given the scope of this study and the relatively rare event of bacteraemia in hospitalised patients, the study was not able to show an association with events. Despite this limitation, the study still points to the potential benefits of limiting use of anti-anaerobic antibiotics to preserve "beneficial" gut microbes.

Taylor, S.L., Rogers, G.B., Papanicolas, L.E. et al. Intensive Care Med 51, 1940–1943 (2025).

About Steven

Dr. Steven Taylor leads the Respiratory Health Group within the Microbiome and Host Health Program at SAHMRI. His research employs tailored techniques that allow the lung environment to be characterised to a high level of accuracy, including detailed measurements of airway microbiology (microbiome), mucus composition, and inflammation.

SAHMRI South Australian Health & Medical Research Institute

Flinders University

Read the full article here

Publication Highlights

Bifidobacteria support optimal infant vaccine responses

Prof David Lynn (Flinders University and SAHMRI) and team
F. J. Ryan et al. *Nature* | 2025

SAGC Genomics Service: RNA sequencing

BACKGROUND: Accumulating evidence indicates that antibiotic exposure may lead to impaired vaccine responses; however, the mechanisms underlying this association remain poorly understood. Here Prof. Lynn and collaborators at the Women's and Children's Hospital prospectively followed 191 healthy, vaginally born, term infants from birth to 15 months, using a systems vaccinology approach to assess the effects of antibiotic exposure on immune responses to vaccination.

OUTCOME: Exposure to direct neonatal but not intrapartum antibiotics was associated with significantly lower antibody titres against various polysaccharides in the 13-valent pneumococcal conjugate vaccine and the Haemophilus influenzae type b polyribosylribitol phosphate and diphtheria toxoid antigens in the combined 6-in-1 Infanrix Hexa vaccine at 7 months of age. Blood from infants exposed to neonatal antibiotics had an inflammatory transcriptional profile before vaccination; in addition, faecal metagenomics showed reduced abundance of Bifidobacterium species in these infants at the time of vaccination, which was correlated with reduced vaccine antibody titres 6 months later. In preclinical models, responses to the 13-valent pneumococcal conjugate vaccine were strongly dependent on an intact microbiota but could be restored in germ-free mice by administering a consortium of Bifidobacterium species or a probiotic already widelyused in neonatal units.

IMPACT: This study suggests that microbiota-targeted interventions could mitigate the detrimental effects of early-life antibiotics on vaccine immunogenicity.

The influence of season, habitat and diet on the faecal microbiome of the yellow-footed rock-wallaby (Petrogale xanthopus xanthopus)

Dr David Taggart (The University of Adelaide) and team
L. E. Werner et. al. Aust J Zool | 2025

SAGC Genomics Service: Illumina MiSeq (v2) sequencing

BACKGROUND: Knowledge of an animal's microbiome is becoming increasingly recognised as an important consideration in the conservation of threatened species, particularly in the face of wide-spread changes to climate and rainfall patterns. The yellow-footed rock-wallaby (YFRW; Petrogale xanthopus xanthopus) is endemic to the semiarid regions of South Australia and New South Wales. This study aimed to characterise the faecal microbial diversity and its relationship to diet and season/rainfall in two geographically separated South Australian YFRW populations with differing habitat characteristics.

OUTCOME: Sequencing targeting the 16S rRNA gene revealed that location was the greatest driver of faecal microbial differences ($P < 0.01$), with season ($P < 0.01$) and the interaction of location × season also statistically significant ($P < 0.01$). The main phyla identified throughout were Firmicutes and Bacteroidota. Diet varied between individuals with Acacia species commonly detected at each study site, which appeared to be linked with an increase in the proportion of Firmicutes present, although further sampling is required to confirm this.

IMPACT: Further research and continued long term monitoring is required to understand microbial functions, how the role of these microbes may affect an individual's health, and how faecal microbiome can be manipulated to increase a species' resilience to dry times and drought.

Novel GABA$_A$R antagonists target networked gene hubs at the leading edge in high-grade gliomas

Assoc Prof Guillermo Gomez, Dr Chloe Shard and Dr Emily Fletcher (UniSA) and team
C. Shard, *Neuro-Oncology* | 2025

SAGC Genomics Service: Spatial Transcriptomics

BACKGROUND: Ion channel activity underlying biological processes that drive high-grade gliomas (HGG) is largely unknown. We aimed to determine the networking of ion channel genes and validate their expression within HGG patient tumors, to identify ion channel-targeting drugs that would inhibit tumor-promoting processes.

METHODS: We used weighted gene co-expression network analysis (WGCNA) of RNAseq data to identify ion channel gene hubs in diffuse midline glioma (DMG) and glioblastoma. Using scRNA-seq, spatial transcriptomics, and immunohistochemistry, we characterized the expression of identified hubs within patient tumors, validating their role by testing the efficacy of ion channel inhibitors alone or in combination with radiation and temozolomide on the growth and invasion of patient-derived glioblastoma explant organoids (GBOs).

OUTCOME: Network analysis revealed a preserved HGG "neuronal regulation" module, containing the greatest number of ion channels, with its corresponding genes concentrated at the tumor's leading edge. Hubs within this module included γ-Aminobutyric-acid type A receptor (GABA$_A$R) genes GABRA1 (α1) and GABRG2 (γ2), which immunohistochemically colocalized with GABAergic synaptic markers at the leading edge. GBOs failed to retain this synaptic architecture but expressed a glioblastoma hub GABRA5 (α5), a component of extrasynaptic GABA$_A$Rs. S44819, an α5-GABA$_A$R antagonist strongly inhibited GBO invasion, with GABA(A)-compound 1b, a partial antagonist of GABA$_A$Rs, robustly inhibiting GBO proliferation and invasion. Moreover, combined with standard-of-care (SOC) regimens, the anti-invasive properties of both compounds were enhanced in GBOs.

IMPACT: Co-expression network analysis identified key ion channels at the leading edge in HGGs, which can be targeted by GABA$_A$R-acting drugs to disrupt tumor progression.

mgikit: demultiplexing toolkit for MGI fastq files

Dr Sen Wang (SAGC) and Dr Ziad AlBkhetan (SAGC and Biocommons)
Z. Al Bkhetan et al., *Bioinformatics* | 2024

SAGC Genomic Service: Bioinformatics

BACKGROUND: MGI sequencing is an inexpensive solution to obtain genomics information. There is a growing need for software and tools to analyse MGI's outputs efficiently.

OUTCOME: mgikit is a tool collection to demultiplex MGI fastq data, reformat it effectively and produce visual quality reports. mgikit overcomes several limitations of the standard MGI demultiplexer.

IMPACT: It is highly customizable to suit different kinds of datasets and is designed to achieve high performance and optimal memory utilization.

SAGC Supported Publications in 2024-25FY

46

Genomics Services

- RNA Sequencing
- Microbiome and Metagenome
- Whole Genome Sequencing
- Whole Exome and Targeted Panels
- Epigenome
- Single Cell analysis
- Spatial Transcriptomics

Visit our services page for more information

Equipment

Single cell

- Parse Biosciences Evercode (Certified Service Provider)
- 10X Chromium X
- MGI C4 (library prep or NGS-only)

Spatial Transcriptomics

- 10X Xenium (CSP), Visium, Visium HD
- MGI STOmics: Stereo-seq v1.3 & v2 (OMNI, FFPE)
- Nanostring: CosMx

Sequencing Platforms

- MGI - DNBSEQ-T7, DNBSEQ-G400
- Illumina- NextSeq, MiSeq, MiSeqi100 plus
- via partners - Nanopore, PacBio, NovaSeq X

Collaborations

Our goal is to create a **comprehensive resource** that supports researchers across disciplines and provide a **single point of access** across platforms. To this end the SAGC has formed collaborative links with multiple facilities and can enable end to end solutions for **multiomics**:

- Proteomics
- Metabolomics
- Histology
- Epigenetics

Visit our website for info on Complex Biology Capabilities in SA

Bioinformatics

Standard Pipelines

We provide a suite of analysis pipelines and workflows developed externally and in-house, based on community best practices.

- Single Cell & Spatial Transcriptomics
- Microbiome and Metagenome
- Whole Genome & Exome Sequencing
- Epigenomics analysis approaches

The team is continually developing and refining new pipelines and services to keep pace with rapid technological progress and evolving research needs.

Bioinformatics

Custom and Strategic

- Bespoke Single Cell & Spatial Transcriptomics
- Genome Assembly
- Clinical Research Collaboration
- Researcher Training

At SAGC, we recognise the importance and complexity of data analysis in NGS experiments. Beyond providing a wide range of sequencing data, we are also committed to helping our customers to extract knowledge and insights from their sequencing data using advanced bioinformatics tools and analytical methods.

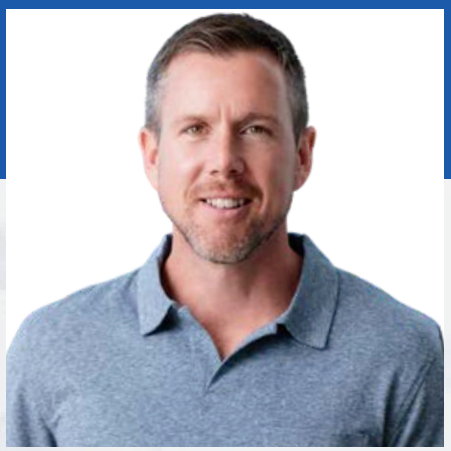
Our Team

The team brings together widespread and diverse experience in genomics and bioinformatics research and service provision, both in Australia and internationally. Collectively, the teams experience spans all a broad range of fields in research and industry, including the biomedical, agricultural, environmental and indigenous genomic domains.

SAGC Management

Prof. David Lynn
SAGC Scientific Director

Dr. Sen Wang
Centre Manager



Joel Bathe
Business Development

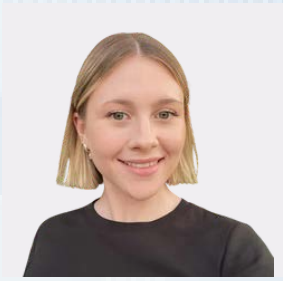
Genomics

Dr. Munir Iqbal
Genomics Staff Scientist
Single Cell and Spatial

Dr. Marlie Frank
Indigenous Genomics Co-ordinator

Dr. Renee Smith
Senior Genomics Scientist and Quality Manager

Dr. Phuong Doan
Next Generation Sequencing Specialist



Caitlin Leuders
Next Generation Sequencing Specialist

Dr. Ayla Orlang
Senior Genomics Research Coordinator
Flinders Node

Olivia Flynn
Next Generation Sequencing Specialist

Dr. Cara Fraser
Project Officer

Dr. John Salamon
Senior Bioinformatician

Dr. Simon Lee
Bioinformatician

Cathal King
Single and Spatial Cell Specialist

Sarah Shah
Bioinformatician

Bioinformatics

SAGC Steering Committee

The role of the Steering Committee is to help the SAGC set strategic direction for the centre, oversee the centre's management, stakeholder reporting, establishment and monitoring of compliance processes, performance reviews and managing any conflicts of interest. The Steering Committee is comprised of an independent Chair, and a representative from each partner organisation.

Independent Chair

Yvette van Eenennaam

Professor Michael Goodsite

Pro Vice-Chancellor (Res. Ops. & ComcIsn) The University of Adelaide

Professor Alan Boddy

Dean of Research and Institute Director Clinical & Health Science, UniSA

Professor Deborah White

Deputy Director and Theme Leader, Precision Cancer, SAHMRI

Assoc. Prof. Michael Michael

Head, Gene Expression Laboratory, Flinders University

Dr Markus Herderich

Group Manager, The Australian Wine Research Institute

Dr Cath Moore

Chief Scientific Officer AGRF

Committee Chair

Prof. Robert Edwards

Director of Bioinformatics and Human Microbiology, FAME, Flinders University

Dr. Luke Isbel
Group Leader Molecular Epigenetics Laboratory
SAIGENCI

Dr Anna Sheppard
Senior Lecturer in Bioinformatics and research group leader,
The University of Adelaide

Assoc. Prof. Bastien Llamas
Research Group Leader
University of Adelaide

Prof. Hamish Scott
Joint Director of the CCB
ACRF Cancer Genome Facility
SA Pathology

Assoc. Prof. Bettina Berger
Scientific Director, The Plant Accelerator - Australian Plant Phenomics Facility

Prof. Alex Brown
Professor of Indigenous Genomics
Australian National University and Telethon Kids Institute

Dr. Wai Yee Low
Senior Bioinformatician,
Livestock, Roseworthy campus,
The University of Adelaide

Prof. Luke Selth
Director of the Prostate Cancer Research Group
Flinders University

Dr. Anthony Borneman,
Principle Research Scientist,
The Australian Wine Research Institute

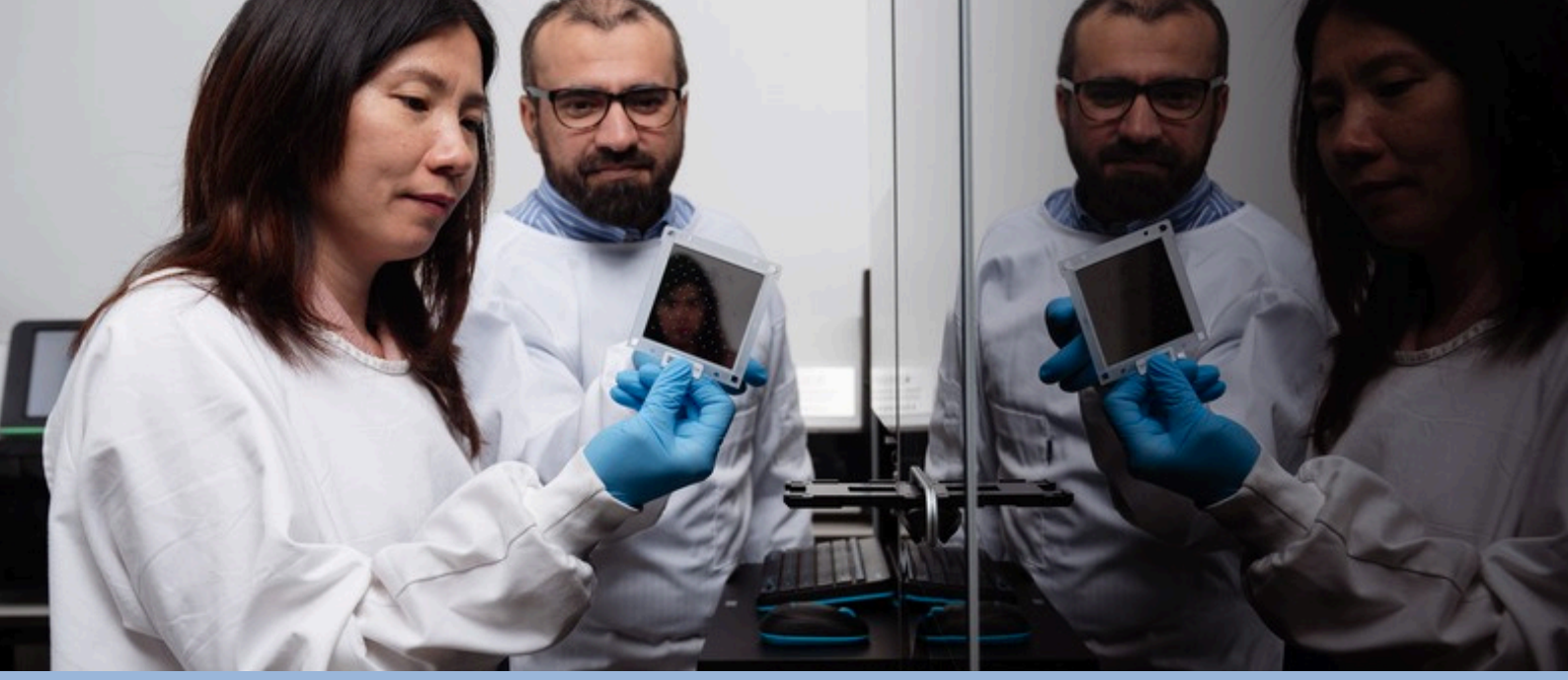
Assoc. Prof. Pascal Duijf
Group Leader Cancer Pharmacogenomics Laboratory,
University of South Australia

Dr. Jessica Marathe
Cardiologist
Royal Adelaide Hospital

Dr Yin Ying Wong
Molecular Immunology research group
The University of Adelaide

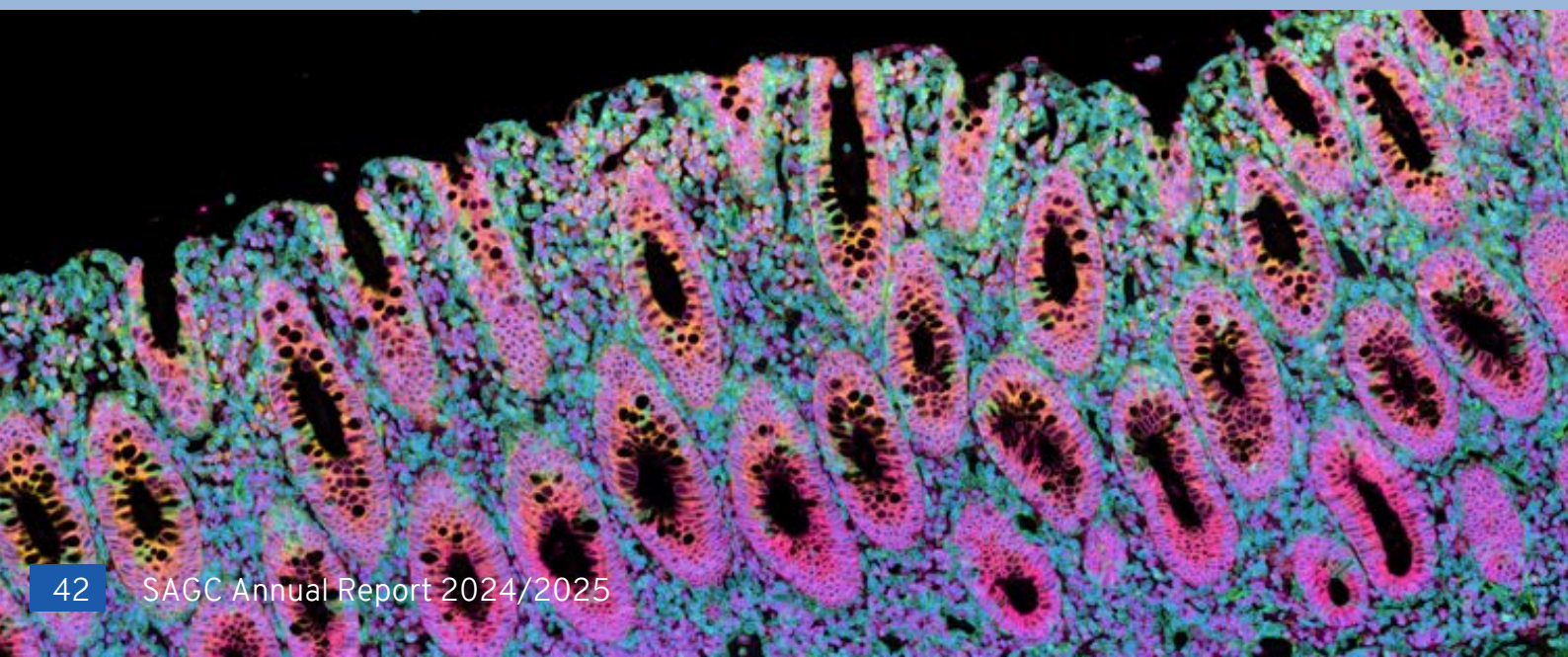
Scientific Advisory Committee

The SAC is comprised of local researchers, clinicians, consumers, and other important stakeholders. The role of the SAC is to advise and support the SAGC Steering Committee and provide input into the strategic direction of the SAGC.



Acknowledgements

The work that we do and the successes that we have achieved in 2024/2025 would not have been possible without the support from our partner organisations and funding bodies SAHMRI, UniSA, Flinders University, The University of Adelaide, BPA, NCRIS, the South Australian State Government and the James and Diana Ramsay Foundation. The SAGC would also like to sincerely acknowledge the SAGC staff members, the SAGC Steering Committee and the Scientific Advisory Committee, without whom none of the achievements listed in this document would have been possible.



Funding

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NCRIS National Research Infrastructure for Australia
An Australian Government Initiative

BIOPLATFORMS AUSTRALIA

Government of South Australia
Department of State Development

SAHMRI South Australian Health & Medical Research Institute

Flinders University

University of South Australia

THE UNIVERSITY of ADELAIDE

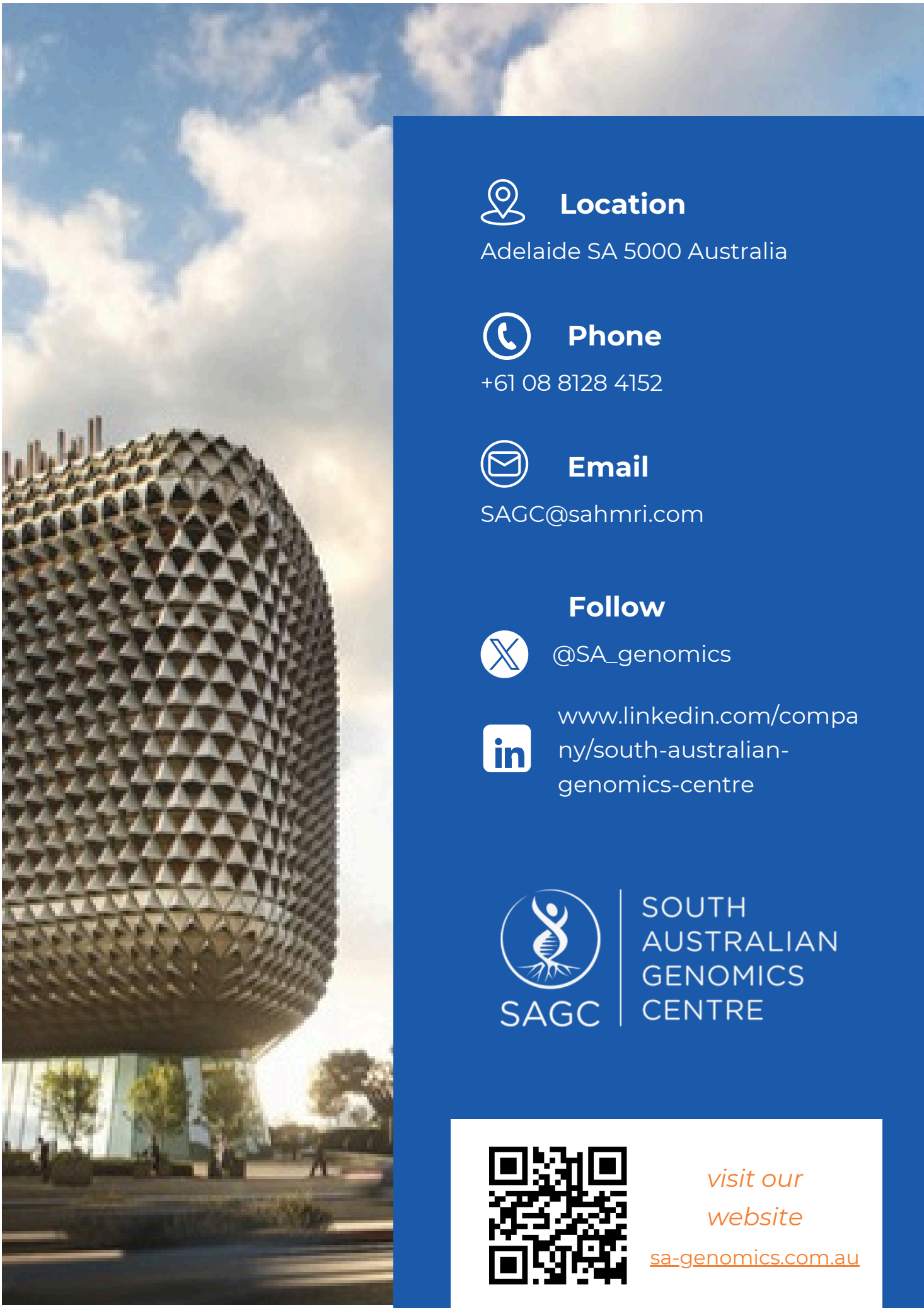
JAMES & DIANA RAMSAY FOUNDATION

AWRI Australian Wine Research Institute

agrf

NATA
WORLD RECOGNISED ACCREDITATION

The SAGC is proudly ISO/IEC 17025 accredited, a globally recognised standard for testing and calibration laboratories. Accreditation under NATA 17025 demonstrates the facility's technical competence and the reliability of its testing and calibration processes.



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visit our website

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