IMB VISION STATEMENT

Creativity, motivation and intellectual freedom are the vital components of scientific discovery and technological process, and underpin the research philosophy of the Institute for Molecular Bioscience.

Our research mission is to understand the information contained in our genes and proteins – the very foundation of our existence and health.

By understanding how and why humans and animals develop the way they do, we will be better equipped to understand the basis of our differences and how and why things go wrong in disease states like cancer.

In time, our collaborative research will lead to improved therapies and diagnostics, enhancing our ability to combat common diseases and genetic disorders. It will also give rise to new ideas, technologies and knowledge-based industries to improve the health and quality of life of future generations.
2008 has been a year of progress and consolidation for the Institute for Molecular Bioscience in the vital areas of human capital, material infrastructure, national and international reputation, and returns to the community.

The freeing up of laboratory space previously rented by a government department gave the IMB an opportunity to expand its discovery workforce by adding four research groups. A successful recruitment campaign showed that three senior employees had the ability to step up as group leaders, and the appointments of Dr Brett Collins, Dr Nick Hamilton and Dr Dagmar Wilhelm reflect well on training and mentorship in the Institute.

The fourth new group leader is Professor Kirill Alexandrov, who came to us from the prestigious Max Planck Institute in Germany. Arriving in September, he quickly succeeded in the 2008 Australian Research Council (ARC) and National Health and Medical Research Council grant rounds, in much the same way as Brett Collins succeeded in the ARC grant round.

The recruitment focus will now turn to early career researchers, who will make significant immediate and short-term contributions and gain the expertise to augment the next generation of group leaders.

Throughout 2008 the IMB continued to justify the significant investments in cutting-edge equipment made in previous years by The Atlantic Philanthropies, the Queensland and Federal Governments, the University, and industry partners such as Applied Biosystems.

The latter company has supplied new generation SOLiDTM sequencers which have enabled IMB experts to pioneer globally significant territory in genomics and transcriptomics – specialisations that will influence the worldwide direction of healthcare. It speaks volumes for the reputation of IMB researchers that the institute was only the third venue, and the first outside of the United States of America, to host these sequencers through an early-access program to develop applications for the technology.

In late 2007 IMB received two of these machines and in 2008 Associate Professor Sean Grimmond and his team developed a new method for sequencing an entire biological sample in a single experiment, published in the high-impact journal Nature Methods. Such progress is typical of an institute that is resolutely focused on high-quality research which has strong potential to translate into tangible human benefits, particularly in relation to health.

I congratulate IMB Director Professor Brandon Wainwright, Deputy Directors Dr Ian Taylor and Professor Jenny Stow, all IMB staff and students, and the team at IMBcom, on achievements made throughout 2008.

I thank board directors for their contributions to the IMB’s success, and for the advice and support they have provided me since I became chair on January 1. Their experience and sagacity will prove invaluable as the interlocked circles of research and business face up to deepening challenges linked to the global economic slowdown.

Professor Paul Greenfield, AO
The University of Queensland
Vice-Chancellor
2008 has been another busy year for the Institute with some changes at the senior management level, the appointment of four new Group Leaders to the IMB, success in national competitive grant funding schemes and the graduation of 18 PhD students. In our report to the Queensland State Government in November of 2008 we continued to exceed all of our Key Performance Indicators for the State Government – a testament to the ability and hard work of our academic and support staff and our commercialisation company, IMBiC.com.

In April of 2008 Professor Jenny Stow was appointed as the new Deputy Director (Research) for the IMB, following the departure of Professor John Hancock to the USA on leave of absence. Since this appointment was made Jenny has instigated reviews of a number of our policies and procedures, including the introduction of a publication incentive bonus scheme, has been closely involved in the appointment of new Group Leaders, and has provided valuable advice and mentoring to a number of our Junior Group Leaders and senior postdocs. Jenny and Associate Professor Alpha Yap also led the successful bid to Australian Cancer Research Foundation (ACRF) for the establishment of the ACRF Cancer Biology Imaging Facility at IMB, a facility that will come on line early in 2009 and will provide sophisticated imaging equipment and technologies to cancer researchers across Queensland.

The IMB was established in 2000 and many of the senior academic staff at the Institute have been with us since establishment and, indeed, came to the IMB from the QMIB and 3D Centre – the forerunners of the IMB. This year we set out to achieve some generational change and devoted considerable time and resources to the recruitment of new Group Leaders to the IMB, with an emphasis on scientists who would ‘value add’ to the current research strengths of the IMB or who would bring a new and complimentary specialisation to our existing research profile. We have already made four new appointments and expect to make at least two more appointments in 2009.

Dr Brett Collins joined IMB as a senior postdoctoral fellow 3 years ago and has consolidated his research profile since arriving. Brett’s research focuses on cell trafficking and his work utilises structural biology to answer important questions in cell biology. He holds an R. Douglas Wright Fellowship from the NHMRC as well as being the recipient of an Early Career Researcher Grant from The University of Queensland. His contributions have been excellent and this year was appointed to Group Leader.

At a more senior level, we appointed Professor Kirill Alexandrov to a Group Leader position held jointly between the IMB and AIBN. Kirill was previously a Group Head at the Max Planck Institute in Dortmund. He arrived to take up his position in early September 2008 and had success in both the recent ARC Discovery Grant and NHMRC Project Grant rounds. Kirill is a cross-Divisional appointee, with research interests that lie in structural biology, chemistry and cell biology. His major research interest is the control of the process of protein prenylation – a key regulatory step in many biochemical processes of medical relevance. He has developed novel chemistry to probe the “prenyloma” and, aligned with his expertise in structural biology/cell biology and his collaborative nature, we expect that he will have a significant impact on the research profile of the Institute.

Other internal recruits who have been achieving well in their respective areas for a number of years were appointed to Junior Group Leader roles in 2008. Dr Dagmar Wilhelm, a developmental biologist, has been working at the IMB since 2002 and has achieved success as a Chief Investigator in both the NH and the ARC schemes in the last two years. In the last year or so, Dagmar’s research interests have widened to encompass the role of non-coding RNA in embryonic development and her appointment as a Group Leader will give her the opportunity to explore these cross-Divisional collaborations more closely.

Dr Nick Hamilton has a PhD in Pure Mathematics from the University of Western Australia and works in bioinformatics. In 2004 he began collaborating with researchers in the ARC Centre of Excellence in Bioinformatics and he quickly established himself within the cell imaging community at the IMB, collaborating with Dr Rohan Teasdale, Professor Jenny Stow and Professor Mark Ragan in the building of mathematical models to assist with cell imaging work at the Institute. Nick has a growing publication record and has received a number of awards and prizes during his relatively short career. Appointment as a Group Leader gives him the opportunity to build on current collaborations and to work towards a self-funding research group through success in competitive grant schemes.

Congratulations and welcome to all of the new Group Leaders and I look forward to working towards a self-funding research group through success in competitive grant schemes.

A highlight for the Institute is when staff members receive peer recognition for their achievements at the highest level and this year I am pleased to report that Professors Peter Koopman and John Mattick were elected Fellows of the Australian Academy of Science in May of 2008. My congratulations to them both and, indeed, to all the staff at the IMB whose hard work and dedication every year ensures that we continue to be ranked as a leading national and international bioscience research institute.

Professor Brandon Wainwright
IMB Director
IMB researchers are supported by staff in a number of areas, including laboratory and infrastructure management, student co-ordination, administration, reception, HR, information technology, finance, central sterilisation, mail, stores, technical services, building maintenance, animal house, grant administration, and marketing and communications. These staff do an excellent job of providing the essential services that allow the institute to function.

There was some movement of senior staff over the year. The opening of new laboratory space on Level 6 necessitated the appointment of a Floor Manager for that level; Jana Weber, previously a Research Assistant with the Sweet group, was successful. Another change in floor managers occurred when Level 2 Floor Manager Dr Michelle Newman returned to live in the USA. She was replaced by Mikiko Miyagi, Barb Dyda, IMB’s HR Consultant, moved on to new challenges after 12 years in IMB, and our support staff, not only sustain the future. The dedication and serious talent of all those who work at IMB, our researchers and our support staff, not only sustain the Institute but also add something special to the way of all good things scientific — it will be hard to produce and I look forward to my role in making sure we have much to offer in this regard.

Professor Jenny Stow
IMB Deputy Director

Dr Ian Taylor
IMB Deputy Director

The Queensland Bioscience Precinct, which houses the IMB, is still considered to be a leading example in laboratory design, even five years after its construction. People come from around the world to view it and discuss collaborations; in 2008, we hosted over 300 international delegates from countries including China, New Zealand, Germany, Denmark, Vanuatu, USA, India, Japan, Italy, Vietnam, Chile, Malaysia, Peru, Spain, France, Singapore, Norway, Scotland, the Netherlands, England, Switzerland, Pakistan, Greece, Fiji, Zimbabwe and Zambia.
NEW GROUP LEADERS FOR IMB

Dr Brett Collins joined the IMB in 2008 after a stint as a Senior Research Associate at the Cambridge Institute for Medical Research in the United Kingdom. Originally part of Dr Robyn Rasbash’s group, Dr Collins was promoted to running his own laboratory in 2008. His lab focuses on defining the structures of the retromer complex, a protein coat found on the endosome, an intracellular structure that transports proteins into cells.

Dr Kirk Alexandrov joins the IMB from the Max-Planck Institute of Molecular Physiology in Dortmund, Germany. He will conduct research and share his expertise in protein engineering and production.

Dr Dagmar Wilhelm focuses on understanding how gene expression is controlled, particularly in embryonic development and to related diseases. Dr Wilhelm received her PhD from the German Cancer Research Centre in Heidelberg. She worked at the Institute for Genetics at the Research Centre, Karlsruhe, and at the Biocentre at the University of Wulzburg, both in Germany, before joining the IMB in 2008.

Dr Nick Hamilton will develop new methods of analysing cellular data, made necessary by the growing amount of information that researchers create in the course of their work. Dr Hamilton has a PhD in Pure Mathematics from the University of Western Australia. He held several positions at The University of Queensland and one at the University of Gent in Belgium before joining the IMB in 2004.

KNOCKING THE SOX OFF CANCER AND LYMPHATIC DISORDERS

Scientists have identified a gene critical for the development of the lymphatic system in a discovery that will have implications for the treatment of cancer and lymphatic disorders and other diseases. The team, led by Professor Peter Koopman and Dr Mat Francois from the IMB, found that a single gene – Sox18 – triggers the development of the lymphatic vessels.

“The rate at which new lymphatic vessels can form is thought to be one of the key factors in determining how quickly a tumour can spread and thus how severely a patient will be affected by cancer,” Professor Koopman said. “The lymphatic vessels also play a central role in maintaining fluid balances in the body and carrying infection-fighting white blood cells, so greater knowledge about the lymphatic system can offer insights and suggest therapies for a range of diseases.”

SCIENTISTS IDENTIFY HIDDEN LAYER IN BRAIN FUNCTION

Hundreds of molecules that are likely to be important for brain function, and ultimately human development, have been identified by scientists from the IMB. The molecules, known as long non-coding RNAs, are derived from parts of the genome that do not encode proteins and until recently have been largely regarded as non-functional or ‘junk’ DNA.

The researchers, including Dr Marcel Dinger and Dr Michael Wainwright of IMB and Dr Robert Wechsler-Shalita from the Institute of Anatomy and Neurobiology at the Hebrew University of Jerusalem, identified more than 80,000 non-coding RNAs that do not encode proteins and until now have been largely ignored by the scientific community. The team’s findings may provide additional avenues for the development of drugs to treat neurological conditions such as Alzheimer’s Disease and dementia.

Dr Marcel Dinger from the IMB has pioneered a new approach to studying gene content and activity that stands to revolutionise the future of genetics. The international team showed that it is now possible to sequence the DNA code of every gene in a biological sample in just one experiment.

“The completion of the Human Genome Project took worldwide effort, an estimated US$2.7 billion and 13 years to complete. In testing this new approach, we were able to sequence four times the sequence content of the entire human genome in our laboratory at only a fraction of the cost,” Dr Dinger said.

MEDICAL RESEARCH TO BE QUICKER AND CHEAPER WITH NEW GENE SEQUENCER

A research team led by Associate Professor Sean Grimmond from the IMB has pioneered a new approach to studying gene content and activity that stands to revolutionise the future of genetics. The international team showed that it is now possible to sequence the DNA code of every gene in a biological sample in just one experiment.

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GENETIC BLUEPRINT REVEALED FOR KIDNEY DESIGN AND FORMATION

IMB researchers were among a team that generated the first comprehensive genetic blueprint of a developing mammalian organ, shielding light on the genetic and molecular dynamics of kidney formation. The detailed genome-based atlas will serve as a resource for understanding healthy and abnormal kidney development and disease.

IMB GENE TECHNOLOGY LAUNCHED IN US

A new gene expression analysis platform developed in collaboration between Australian scientists and Infinium Corporation to help other researchers understand fundamental aspects of human development has been launched in the US market. Professor John Mattick and Dr Marcel Dinger from the IMB developed the technology for Infinium to Invitrogen for the first commercially available high-density microarray chip, the NCodex™ Human and Mouse non-coding RNA microarray, which can be used by researchers to profile both messenger and non-coding RNAs.

FEAR AND BACTERIA: POSSIBLE WAYS OF CONTROLLING THE CANE TOAD

They found a range of potential control strategies that could selectively target and reduce the survival of cane toad eggs, tadpoles and adults. These include exposing them to an alarm chemical which causes tadpoles to turn into toads prematurely, resulting in underweight toadlets with lower chances of survival, and targeting the bacteria that expand the range of toad toxins and influence the toads’ behaviour.

CHILDHOOD OBESITY STUDY LAUNCHED

The KOALA Childhood Obesity study was officially launched on Saturday, January 12, 2008, with an activity day for kids at Brisbane’s Riverlife Adventure Centre. The study is a one-year pilot being conducted by UQ and Mater Children’s Hospital researchers and will investigate the social, behavioural and genetic reasons behind childhood obesity. Dr Gary Loong, who works at both the IMB and the Mater Children’s Hospital, is leading the study.

PROFESSOR MARTIN IN SYNC WITH REMOTE ACCESS

Professor Jenny Martin, who was the first Queensland researcher to use the Australian synchrotron, became the first user to access the facility remotely. Professor Martin sent her samples to Melbourne via courier, but instead of following them down, she loaded a special program on her computer and ran the experiment from aRastering room at the IMB.

Remote access has saved time for Professor Martin’s group and is much more efficient, as they no longer have to send postie to Melbourne every time they have beamtime allocated at the synchrotron. “It’s changed the way we do science, and many other researchers are wanting to learn how to run their experiments in this way...” Professor Martin said.

Dr Michelle Hill and Professor Rob Parton.

IMB 2008 HIGHLIGHTS

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ANNUAL REPORT 2008

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GENE PIONEER GIVES MEMORIAL LECTURE

Associate Professor Josef Gecz, from the Women’s and Children’s Hospital and University of Adelaide, presented the Dr Toshiba Yamada Memorial Lecture on Thursday, March 13. His seminar was titled, “The genetic landscape of learning and memory: what do we learn from naturally occurring mutations?” It was the fourth Dr Toshiba Yamada Memorial Lecture, established to commemorate an IMB researcher who passed away suddenly in 2001, and co-hosted by the IMB and the Queensland Brain Institute.

Grants

$2.5 MILLION TO EXPAND CANCER RESEARCH FACILITY

IMB researchers will have access to even more cutting edge cancer research equipment after being awarded a $2.5 million grant from the Australian Cancer Research Foundation (ACRF). The grant, whose application was led by Professor Jenny Stow and Associate Professor Alpha Yap, will allow the expansion of the ACRF Dynamic Imaging Facility for Cancer Biology currently in place at IMB.

CONES SNAILS AND PLANTS USED TO DEVELOP ORAL DRUG FOR PAIN

Molecules from cone snail venom and plants are being used by Queensland researchers as a blueprint to develop an oral drug to treat chronic pain. Professor David Craik and Dr Richard Clark received $218,275 from the Australian Cancer Research Foundation (ACRF) to investigate using peptides, the building blocks of proteins, to form the basis of a new type of stable therapeutic.

“MY project will focus on fusing unstable peptides to a circular protein framework that will overcome their stability problems, and result in a drug with far fewer side effects than existing anti-cancer drugs,” Dr Daly said.

HIGH-PERFORMANCE COMPUTING TO POWER SYSTEMS BIOLOGY INVESTIGATION

A consortium of eight researchers, seven of whom are from the IMB, won a $400,000 Australian Research Council Linkage Infrastructure, Equipment and Facilities grant, which they will use to establish an advanced computational platform to study biological processes at a systems level. Systems biology is the study of the organism as a whole and provides a deeper understanding of biological processes than is possible by studying components separately.

“I am excited that this project will enable us to investigate key biological processes at a systems level,” said IMB Director Associate Professor Ben Hankamer.

INDUSTRY AND RESEARCHERS JOIN FORCES TO DEVELOP BETTER BIOPELTS

Associate Professor Ben Hankamer will lead a collaboration between researchers and industry that aims to develop biofilms that don’t compete with food production and that can use saline water sources.

“The platform’s hardware and specialised software will allow Australian researchers to examine complex pathways involved in animal and human health and disease, as well as in biotechnology and environmental processes,” Professor Mark Ragan said. “It will provide unique capabilities not currently available in Australia, and help us to remain internationally competitive.”

US $1.3 MILLION INTERNATIONAL GRANT SHAPED BY IMB CELL BIOLOGY

Associate Professor Alpha Yap and three international collaborators have been awarded a grant from the Human Frontier Science Program worth US$450,000 per annum for three years.

“If these interactions go wrong, diseases such as cancer and inflammation can occur.”

STATE GOVERNMENT BOOST FOR PhD FOCUS ON CANCER

Four IMB PhD students tackling the problems of disease and obesity have received Queensland State Government scholarships. The students are: Mrs Lattin is studying beta-amylase, proteins involved in the regulation of the body’s immune response. Eight IMB students were named on the 2007 Dear’s Commendation List, recognising the outstanding quality and exceptionally innovative nature of the research performed for their PhD thesis. Fewer than 15 percent of PhD graduates are recognised in this way each year.

Awards

IMB SCIENCES ELECTED TO TOP NATIONAL BODY

Two IMB researchers have been acknowledged as being among the country’s top scientists after being elected Fellows of the Australian Academy of Science. Professor Peter Koopman and Professor John Mattick, AO, were recognised by the Academy for significantly advancing, and continuing to advance, the world’s scientific knowledge.

“Peter and John have been leaders in establishing their fields of expertise, and their work has had a significant impact on the scientific community both within Australia and world-wide,” said IMB Director Associate Professor Ben Hankamer.

AMGEN AWARD

Pia Cingoli (Regine) Low from the Stow lab won the Amgen Award for being the best overall honours student at the IMB in 2007. The award was presented during 2008, when Ms Low was in her first year of PhD, also in the Stow lab. Ms Low’s honours project involved establishing and optimising a high-content screening assay for Tnf trafficking and secretion in macrophages. It has already been used to screen molecules including natural product libraries and drugs.

VALENCYTOR FROM IMB

A honours student at the IMB was named 2008 Valedictorian of the UQ Bachelor of Science. Elanor Wainwright, who completed her honours thesis under the supervision of Dr Dagnar Wilhelm, was ranked first out of over 300 graduating students. Ms Wainwright is now employed as a research assistant in the Wilhelm group.

SPECIAL AWARD FOR YOUNG RESEARCHER

Andrew Noakie, a PhD student from the Marsh group, presented a talk titled, “Using reconstruction and analysis of whole mammalian cells by new tomographic and computational approaches” at the Queenstown Molecular Biology meeting. The organisations were so impressed with his presentation, declaring it one of the best of the meeting, that they created a special Young Investigator Award in recognition.

Award for Miracle Worker

Dr Amanda Garzotto, IMB’s Postgraduate Administrative Officer, was awarded a UQ Miracle Worker’s Award. The award acknowledges staff who continually go above and beyond expectations, inspire, deliver and are generally outstanding. In nominating Dr Garzotto, PhD student Jonathan Robson said, “Her enthusiastic attitude towards aiding students of the IMB as well as our positive outside on all IMB students make her an ideal recipient for this prestigious reward.” Mr Robson, who is President of the IMB student association, also lauded Dr Garzotto for being “a source of sound advice on matters relating to PhD management and financial support”. “My project will focus on fusing unstable peptides to a circular protein framework that will overcome their stability problems, and result in a drug with far fewer side effects than existing anti-cancer drugs,” Dr Daly said.

Awards

IMB 2008 HIGHLIGHTS

Associate Professor Ben Hankamer with microalgae.

Left: Cone snail.
Below left: Associate Professor Ben Hankamer with microalgae.

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Professor Paul Greenfield, AO, is Vice-Chancellor of The University of Queensland. Professor Greenfield graduated with first-class honours in Chemical Engineering from the University of New South Wales (UNSW) and worked in the private sector before completing a PhD at UNSW. He then worked at CSIRO before winning an inaugural Executive Dean in 1997. From 2000 to 2007, he served as UQ Senior Deputy Vice-Chancellor, before becoming Vice-Chancellor in 2008. Professor Greenfield has extensive experience as a Board Director and has consulted and worked widely with industry. His interests lie in biotechnology, environmental management, and R&D management and commercialisation. He is currently Chair of the Scientific Advisory Group of the South East Queensland Waterways Partnership. He is also Chair of the Riversymposium Strategic Planning Committee, the Thess International Riverscapes Committee and the International Water Centre. In 2008 he was appointed an Officer in the Order of Australia for his contribution to environmental management, biotechnology and tertiary education. In 1995, he won the Chimeca Medal, awarded jointly by The Institution of Chemical Engineers and the Institute of Engineers Australia for outstanding contribution to the profession.

Professor Brandon Wainwright was appointed Director of the Institute for Molecular Bioscience in late 2006. Previously, he was the Deputy Director (Research) of the IMB from 2002. Professor Wainwright completed his undergraduate and postgraduate studies at the University of Adelaide, after which he took up a postdoctoral fellowship at St Mary’s Medical School, the University of London. He remained at St Mary’s for six years, eventually becoming a Medical Research Council Senior Research Fellow. In 1990, he moved back to Australia, joining the Centre for Molecular and Cellular Biology (CMCB) at The University of Queensland. Professor Wainwright stayed with the CMCB when it was merged with another UQ Centre (the Drug Design and Development Centre) in 2003 to create the Institute for Molecular Bioscience. In addition to being Director of the IMB, Professor Wainwright continues his research into the use of genomic approaches to dissect the basis of common genetic disease. In 2008 he led a team that discovered the origins of the often-fatal brain tumour medulloblastoma.

Dr Howard is CEO of Maxygen and one of the company’s founders. Since the creation of Maxygen in 1997, its core technologies have been used to create several independent businesses. Today, Maxygen is focused on optimisation and development of significantly-improved proprietary versions of several marketed protein pharmaceuticals. Originally trained in biochemistry and chemistry at the University of Melbourne, Dr Howard spent over 20 years studying infectious diseases, primarily malaria. Before joining Maxygen, Dr Howard served at research institutes, biotechnology companies and a pharmaceutical company both in Australia and overseas. In addition to numerous patents, Dr Howard has over 140 publications in peer-reviewed journals.

Dr Peter Isdale, AM, is the CEO of IMBcom Pty Ltd, The University of Queensland’s commercialisation company for the IMB. He is a former Business Director at the Australian Institute of Marine Science (AIMS), Australia’s national marine research agency. He is also a former Principal Research Scientist at AIMS, and authored or co-authored more than 30 papers in his field of marine and climate research. He has 25 years of experience in the operation and governance of private, public and ASX-listed companies in Australia, Asia and the Pacific Rim. He is a Member of the Australian Institute of Company Directors. Dr Isdale currently holds five non-executive directorships in biotech companies, senior positions on Foundations around the world and is an Adjunct Professor at Texas A&M University. He holds a PhD in Marine Geomorphology (1982) from James Cook University of North Queensland. In 2008 he was awarded an Order of Australia (AM) for service to marine science through research and as a contributor to the development and commercialisation of biotechnology.

Bob McCarthy is the Director-General of the Queensland Department of Tourism, Regional Development and Industry. He leads a staff totalling more than 800 people, and is responsible for delivering the Smart Industry Policy, which will improve productivity levels across key Queensland priority industries, and rolling out the Centres of Enterprise initiative, which will build the economic strength of regional areas by focusing on their particular industry strengths. As Director-General, Mr McCarthy chairs or co-chairs several state and national committees including Queensland Water Infrastructure Board, Aviation Australia, the Knowledge Based Research and Business (KBRE) CEO Steering Committee, the Aviation Industry Advisory Board, and the Tourism Queensland Board. He is also the Queensland Government’s Champion for Napanum, a remote settlement located 13 kilometres south of Weipa.

Mr McCarthy has extensive experience and understanding of agribusiness and resource management and structural change, and regional economic development gained from over 30 years working in the private sector and state and federal governments. He has previously held positions as Director-General of the Department of Natural Resources, Mines and Water, and Deputy Director-General of the Department of State Development and Innovation.

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PROFESSOR NICOS NICOLA, AO

Professor Nicos Nicola is an ex officio member of the IMB Board, as he serves as the Chair of the IMB Scientific Advisory Council. He is Assistant Director of the Walter and Eliza Hall Institute, where he also serves as Head of the Cancer and Haematology Division. Professor Nicola completed both his undergraduate and postgraduate degrees at the University of Melbourne, before working for a year at Brandeis University in Massachusetts, USA. He then joined the Walter and Eliza Hall Institute in 1977. He is responsible for major discoveries including the purification of mouse G-CSF, the definition of the human equivalent of G-CSF and the purification of Leukaemia Inhibitory Factor. Professor Nicola has published over 200 journal articles and has 17 patents.

PROFESSOR DAVID SIDDI

Professor Siddiq is the Deputy Vice-Chancellor (Research) of The University of Queensland. He is responsible for enhancement of the University’s research and research training profile, and development of research collaborations. Areas under his direct management include the six research Institutes (including IMB), the Research and Research Training Division, the Graduate School and UQ Biological Resources. He became DVD (Research) in 2002 following his September 2001 appointment as the University’s Pro-Vice-Chancellor (Research). Previously he was Pro-Vice-Chancellor (Research) at the University of Sydney 1997-2001 and Dean, Postgraduate Studies at The University of Queensland 1993-1997. Professor Siddiq is a Director of the Australian Synchrotron Company and Australian Synchrotron Holding Company; AHURI Queensland Research Centre Ltd; CDMAx and this Australian Genomics Research Facility Ltd. Professor Siddiq is an experimental psychologist with interests in the areas of orienting, attention and conditioning. He has published two books and more than 100 book chapters and journal articles, and was Editor of Biological Psychology for five years. He has worked at the University of London and the University of Southampton, both in the United Kingdom, and the University of Ottawa in Canada. He has held positions at Macquarie University, the University of Tasmania, and the University of Sydney in Australia, as well as The University of Queensland.
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Assistant Director
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 Brandeis University, USA

PROFESSOR MARINO ZERIAL
Max Planck Institute of Molecular Cell Biology
Dresden, Germany
IMB RESEARCHERS

The IMB is a highly collaborative environment where researchers from different fields combine to contribute to strategic research programs investigating the basis of growth and development at the genetic, molecular, cellular and organ levels. Only by understanding the complex molecular and cellular events that occur throughout a normal human life can scientists understand anomalies responsible for many common human diseases and to find treatments for them.

RESEARCH FOCUS

This program includes the ARC Centre of Excellence in Bioinformatics and the Queensland Facility for Advanced Bioinformatics. It intersects with the Department of Mathematics and the School of Information Technology and Electrical Engineering. It focuses on understanding the genetic programming of humans, specifically, comparative mammalian and vertebrate functional genomics, rnomics, and computational modelling of genetic and cellular regulatory networks (i.e. the Visible Cell® project).

Research Group Leaders
Tim Bailey
Kevin Burrage
Sean Grimmond
Nick Hamilton
John Mattick
Mark Ragan
Rohan Teasdale
My research develops and applies computational methods to extract knowledge and understand biological processes from large datasets. My approach is to use computer algorithms to reveal patterns in high-throughput data that provide insights into gene expression and control transcriptional processes. We have developed novel algorithms for pattern discovery and modelling, especially those that combine non-sequence data about genome structure and the role of transcription factors. We have also refined our computational model for gene expression regulation in novel species. Our work on discovering patterns in high-throughput data can greatly improve the accuracy of computational methods for predicting the places in the genome where transcription factor proteins bind to DNA and control gene transcription. We extended our “evolutionary motif model” of binding sites to allow the use of non-sequence data such as “binding intensities” data from chromatin immunoprecipitation experiments. This year my group studied combining multiple types of high-throughput data for predicting the places in the genome where transcription factor proteins bind to DNA to control gene transcription. We extended our “evolutionary motif model” of binding sites to allow the use of non-sequence data such as “binding intensities” data from chromatin immunoprecipitation experiments.

In the coming year, we will apply the tools we developed this year to study the role of DNA-RNA triplex formation in gene regulation. We will also continue to develop novel algorithms for pattern discovery and modelling, especially algorithms that combine additional types of non-sequence data for discovering the targets of transcription factors and other interacting factors. We will also initiate a project to analyze the role of DNA-RNA triplex formation in gene expression.

**KEY PUBLICATIONS**


This group works on developing computational and visualisation methodologies for understanding the behaviour of complex cellular processes, both on the plasma membrane, in the cytosol, and at the genetic regulatory level. The simulation models take into account stochastic effects, while the visualisation focuses on two or three-dimensional display. In microscopic systems formed by living cells, we are using the new classes of stochastic models that more accurately and effectively reflect the underlying cellular models.

We are also focusing on some new methods for both large-scale kinetic and spatial models that more faithfully capture complex kinetic and transport processes within the cell.

**RESEARCH PROJECTS**

- Developing new Monte-Carlo Simulation techniques in conjunction with the group of John Hancock and researchers at Oxford University (Dan Nicolau Jr.) that allow us to model the behaviour of lipid rafts and to investigate the effects of anomalous diffusion and the linking of kinetics on the plasma membrane with cascading reactions such as MAPK cascade activation.

- Developing the effects of transcriptional and translational delays in genetic regulatory systems.

- Building mathematical models from imaging data, with the Teasdale, Study of RAID, and translational delays in genetic reaction cascades such as MAPK cascade activation.

**KEY PUBLICATIONS**


**LAB MEMBERS**

Research Officers: Dr John Hawkins, Dr Philip Machanick
PhD Students: Denis Bauer, Tom Whittington, Robert Molyay

**LAB MEMBERS**

Research Officers: Dr Shoaib Sehgal, Dr Shih MacNamara, Dr John Balward, Dr Fawang Liu, Dr Pamela Burunge
PhD Students: Shih MacNamara, Alhadi Bustanami, Duncan Mortimer
Expression Genomics

The central focus of the IMB’s expression genomics lab is to globally survey genomic, transcriptomic and epigenomic information and then use these data to define the underlying molecular networks controlling key biological processes (such as cell division and differentiation) and pathological states (breast and pancreatic cancer). These systems-wide studies give us the opportunity to identify both the key genes driving specific phenotypes and also the chance to recognise the different layers of control guiding biological states. It also provides a strong foundation from which to study novel genome biology (such as the role of miRNAs, non-coding RNAs, retrotransposons, RNA editing etc). As the capturing of “omic” data is a key component of our research, we are actively pursuing the use of microscopy-based profiling, automated in situ hybridisation screening and next-generation sequencing technologies for these studies. For more information on our research and details of the research projects listed below, please see our webpage at: www.imb.uq.edu.au/index.htm?id=11679

RECENT PUBLICATIONS


High throughput screens for applications such as drug and genetic discovery are leading to massive image sets in need of new methods of analysis. Further, live cells may now be imaged in 3D over time with the interactions and dynamics of multiple proteins observed at high resolution. The core of my group’s research is to develop the methodologies and tools needed to enable the full benefit of these rich data sources to be realised. Recent research has focused on automated classification, clustering and visualisation of high throughput microscopy imaging. Towards this, the Automated Subcellular Phenotype Classifier (ASPC) was developed by combining novel image statistics created in the group with machine learning methodologies to enable rapid classification of high throughput imaging with near-perfect accuracy. The approach will enable whole-proteome imaging to be analysed in days rather than months. Building on this, the Cluster methodology currently being developed allows the clustering, differentiation and visualisation of high throughput image sets to enable sense to be made of the vast sets being generated. A recent highlight has been the creation of a more sensitive statistical test to enable the automated detection of subtle differences between treated and untreated cells. Towards the analysis of 3D and 4D bio-imaging, the group has been developing two streams of research. The first is in quantification, to extract the key parameters that describe the systems being observed. In this area we have developed the Object Based Co-localisation (OBCoL) system to segment and quantify individual structures from 3D and 4D video-cell imaging. This approach has enabled the detailed analysis of spatial distribution of proteins on individual subcellular structures and their true diversity to be seen for the first time. The second is in building mathematical models of the subcellular systems observed based on the quantification methodologies of first stream. For instance, dynamic geometric models based on live cell imaging have provided surprisingly detailed information and insights into the systems observed and have been used to predict biologically relevant and experimentally verifiable quantities such as pH change and solute concentration. Other areas of interest include modelling of recruitment and expulsion of proteins from membrane surfaces.

The group is strongly multidisciplinary and collaborative, with a focus on delivering methodologies and tools to be used by researchers. This year has seen the public release of iCluster and OBCoL, both available under open-source license via institute-hosted websites.

KEY PUBLICATIONS


Rnmos: RNA in mammalian evolution and development

We are exploring the thesis that the genetic programming of higher organisms has been fundamentally misunderstood for the past 50 years, because of the assumption that most genetic information is transcribed by proteins. It is now clear, despite the fact that only a small fraction encodes proteins, that the majority of the genomes of mammals and other complex organisms is transcribed in a developmentally-regulated manner, and that most complex genetic phenomena are RNA-directed. Working in conjunction with collaborators in the United States, Europe and Japan, we are working to characterise and understand the functions of the mammalian transcriptome, and to validate the prediction that most genetic information in mammals is conveyed by RNAs that control differentiation and development. This includes the identification of small RNAs that regulate gene expression at various levels, including transcription, and to determine the expression patterns and function of the tens of thousands of longer noncoding RNAs that are dynamically expressed during differentiation in mammalian cells, including embryonic stem cells. Among our recent findings we have shown that it is possible, it not likely, that most of the mammalian genome is under evolutionary selection, and demonstrated that the majority of long noncoding RNAs are expressed in the brain, in many precise cellular and subcellular locations, some of which are novel. We use advanced computational, visual and experimental methods, integrating in silico, in vitro and in vivo approaches. The outcomes of our research will be to expand our understanding of human evolution, genetics and development, with important practical implications in medicine, genetic engineering and programming of self-assembling systems.

RESEARCH PROJECTS

- Bioinformatic prediction and experimental validation of new classes of small RNAs in animals
- Analysis of the dynamic expression of long noncoding RNAs during the differentiation of embryonic stem cells, neural stem cells, muscle, macrophages, T-cells and developing tissues such as the male and female genital ridge, as well as the alteration of noncoding RNA expression in pathological states such as cancer
- Analysis of the subcellular location of noncoding RNAs to expand knowledge of existing cellular compartments and discover new ones
- Targeted functional analysis of selected non-coding RNAs involved in developmental processes and neurogenesis
- Analysis of the conservation patterns of noncoding regions in the mammalian genome and alignment on the basis of RNA structural rules
- Deep sequencing of the small and large RNA transcriptome in embryonic stem cells, and various tissues in mouse and human, as well as of RNAs associated with chromatin modification complexes, transcription factors, RNA editing enzymes and DNA-RNA triplex structures in chromatin.

KEY PUBLICATIONS


Computational genomics

We use advanced computational and data management methodologies to investigate similarities and differences among genomes and the gene product evolutionary record. Our goal is to make rigorous quantitative inferences, at both global and fine scales, about how genomes, gene and protein families, regulatory networks and cellular functions have evolved and diversified. We are particularly interested in scalable approaches, including those based on the Semantic Web technologies, approaches that let us interrogate diverse data types including molecular sequences and structures, signalling pathways, regulatory and molecular interaction networks, gene expression patterns, subcellular localisation and cellular function. Genomes have diversified, both structurally and functionally, from shared ancestral states. We develop methods and employ analytical pipelines to reconstruct the paths of descent (phylogenetics) and to study processes of change through time (evolutionary genomics) in bacterial pathogens, teleosts and mammals. Within the Nuclear Receptors in Breast Cancer consortium we are responsible for expression informatics and network inference. We also collaborate in the Visible Cell®-based project.

For more information on our group and our research projects, please see: www.ibs.tohoku.ac.jp/index.html?/page/11671

RESEARCH PROJECTS

- Automatic inference of vertical and lateral gene transmission, genetic recombination breakpoints, and molecular interaction networks in prokaryotic bacteria
- Genome dynamics and the evolution of new protein functions in lizards
- Fine-scale mapping of orthologous and paralogous regions of mammalian genomes
- Ubiquitously protein-protein interaction networks in cellular context

- Computation discovery of novel miRNA targets in mammalian genomes
- Integration and querying of molecular network and cellular structure information, and querying-over these data, using Semantic Web technologies
- Software and data infrastructure for the Visible Cell®

KEY PUBLICATIONS


The endosomal/lysosomal system of mammalian cells is a highly dynamic organelle, and the trafficking pathways within the endosomal system are fundamental for a wide variety of key cellular processes. My group is developing cellular and computational approaches to identify novel mammalian proteins associated with the endosomal system.

The regulated movement of membrane receptors and ligands between the cell surface and intracellular compartments is vital to many cellular operations, including communication between cells and their environment. A major current focus of the group is the characterisation of the mammalian retromer complex. We have implicated this complex, using real-time microscopy and molecular interaction techniques, in the sorting of numerous membrane receptors, including EGFR, within the endosomal system.

Macropinocytosis is a regulated form of endocytosis that mediates the non-selective uptake of extracellular material. Macropinocytosis is highly relevant to many aspects of both normal cell function and disease with particular importance in tumour progression and metastasis and in many infectious diseases. Our recent work has focused on characterising macropinocytic pathways and the molecular machinery associated with macropinosomes. We have determined that the regulation of phosphoinositides is central to macropinocytosis and leads to the recruitment of key effector proteins including the PtdIns(3)P-binding PX-domain family of proteins. This emerging protein family performs a range of critical biochemical actions within the mammalian endosome and we are keenly interested in the roles these proteins play. Currently we are undertaking a systems biology approach to examine the distinct stages of macropinocytosis.

Numerous infectious pathogens exploit specific endocytic pathways to invade the host. Characterisation of pathogen entry pathways is essential for understanding infectious diseases but has also proven to be a powerful tool for gaining insight into normal cellular processes. We are currently investigating the molecular details of these pathways and how they are modulated in response to infection with Salmonella, a leading cause of human gastroenteritis.

RESEARCH PROJECTS
- Host-pathogen interactions during Salmonella infection
- Maintaining and updating LOCATE: A Protein Subcellular Localisation Database - http://locate.imb.uq.edu.au
- Developing computational approaches to analyse image and real-time microscopy data
- Studying endosome dynamics, macropinocytosis and retromer
- Systems biology of the mammalian endosome

KEY PUBLICATIONS


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KEY PUBLICATIONS

How genes regulate embryo development

Our group studies genes controlling the formation of various organs in the developing embryo. In particular we are striving to understand the events that regulate the development of functional male and female gonads and the formation of the blood and lymphatic vessels. The gene SRY, which acts as a single switch to initiate the male pathway of development, was discovered over a decade ago. However, the genetics and cellular events leading to testis development and male sex determination remain elusive. Our lab specialises in the identification and characterisation of sex development genes using techniques such as microarray screening and transgenic mouse models. Further projects are focusing on identifying the timing and mechanism of sex determination in cattle and canoe toads, in an effort to manipulate sex ratios and population numbers respectively.

We are also interested in how germ cells come to develop as sperm in males or eggs in females. The recent discovery in our lab that retnicotic acid controls germ cell malascia entry in the female gonad has provided a pivotal point to understanding this process. A third major focus in our group includes investigating the function of Sox genes in mouse development, was discovered over a couple of years and is expected to lead to better ways of investigating the function of Sox genes in mouse development.

RESEARCH PROJECTS

• Sex Determination and Gonadal Development
• Development of Male Germ Cells
• Sox Gene Function and Evolution
• Molecular Genetics of Lymphatic Development
• Sexual Development in Canine Toads
• Pilot Study for Male-Only Offspring Production in Bovine Cattle

KEY PUBLICATIONS


Kidney development, damage, repair and regeneration

Each of us has a pair of kidneys that play an important role in maintaining fluid balance, blood volume and electrolyte balance. On top of this, they regulate blood pressure, blood density and number of red blood cells via the production of specific growth factors. As a result of the many complex roles played by the kidneys, kidney diseases have a profound effect on the patient. Chronic kidney disease (CKD) is a devastating disease and is expensive one to treat. Once this condition has reached and stage renal failure, it can only be treated with dialysis or transplantation. Each year, more than 4000 Australian adults will be diagnosed with CKD, which cost the health system $1.8 billion in 2006. This cost is likely to escalate to $4.7 billion by 2010. There is an urgent need to develop novel therapies as the rate of CKD is rising at 6-8 percent per annum, primarily due to increasing rates of Type II diabetes and obesity, and as only one in four patients will be lucky enough to receive a kidney transplant.

As for other organs, there are many conditions, both experimental and genetic, that result in impaired kidney function. Perhaps more surprising is the fact that the risk of kidney failure during our lives is now known to be linked to what happens during the development of our kidneys.

Our laboratory is acknowledged internationally for our work in defining the genes involved in normal kidney development and in integrating this understanding with an understanding of how the adult kidney responds to damage. In this way, we hope to develop novel approaches to the diagnosis and treatment of both acute and chronic kidney disease. Such therapies will grow out of our understanding of the processes involved in normal kidney development.

RESEARCH PROJECTS

• Creating an atlas of gene expression during urogenital development
• Characterising the molecular basis of nephron formation
• Locking for stem cells in the adult kidney
• Investigating the link between the processes of development and the normal repair in the kidney
• Reinstituting kidney development to repair an adult kidney
• Characterising the process of vascular development in kidney

KEY PUBLICATIONS


Nuclear receptors, skeletal muscle and metabolic disease

**Nuclear Hormone Receptors (NRs)** control lipid, glucose and energy homeostasis in metabolic, cardiovascular and endocrine organs. The importance of NRs in human health is underscored by the therapeutic utility of medications that target dysfunctional hormone signalling in the context of inflammation, cancer, endocrine and metabolic diseases. NRs function as agonist-dependent DNA-binding factors that translate metabolic and pathophysiological signals into gene regulation. Proteins have been identified that belong to the NR superfamily on the basis of homology, but the molecules that regulate their activity have not yet been identified and are denoted as ‘orphan’ NRs. The orphans provide a platform for the unravelling of new signalling cascades that may have potential therapeutic utility. Many orphan NRs are expressed in skeletal muscle, a peripheral tissue that accounts for ~40 percent of the total body mass and energy expenditure, and is a major site of fatty acid and glucose oxidation. Accordingly, muscle has an important role in insulin sensitivity, the blood lipid profile, and energy balance. Thus, the tissue has a significant role in the development of metabolic disease. Not surprisingly, NRs are emerging as targets against obesity and type II diabetes.

Surprisingly, the function of these orphan NRs in skeletal muscle metabolism has not been examined. In this context, our group has provided evidence for crosstalk between beta-adrenergic and Nuclear Receptor (NR) 4A signalling in skeletal muscle in the regulation of metabolism. Secondly, we have utilised mouse models to demonstrate that dysfunctional NR/HR (ROAroma) expression leads to reduced adiposity, dyslipidaemia and resistance to diet-induced obesity. Muscle-specific perturbation of ROAroma signalling leads to aberrant insulin signalling in this lean tissue. In the context of understanding crosstalk between NRs and other signalling pathways in obesity, we have utilised the Sfi transgenic mouse model to investigate the role of sfi and NR crosstalk in mediating reduced adiposity, and increased fatty acid oxidation. Collaboratively, we have shown regulatory crosstalk between melanocortin 1 receptor (MC1R) and NR4A signalling in melanocytic cells. We have identified that NR4A is an important step in MC1R-mediated DNA repair in melanocytes. Furthermore, impaired NR4A induction in melanocytes harbouring homozygous red hair colour variant MC1R alleles may underlie an increase in melanoma susceptibility. In the context of cancer, we are also involved in an NIBM program to completely profile NR and coactivator expression in normal, estrogen receptor (ER) positive, and ER negative breast cancers.

**RESEARCH PROJECTS**

- the role of ROR and COUP-TF subgroups in lipid homeostasis
- the role of the NR4A subgroup (Nur77 and NR0B1) in skeletal muscle energy balance and adrenergic signalling
- Determining the role and function of the Sfi gene in body composition and metabolism via modulation of NR4A dependent metabolism in skeletal muscle, fat and liver
- Profiling NR and coactivator expression in normal, estrogen receptor (ER) positive and ER negative breast cancers

**KEY PUBLICATIONS**


Blood development

**Our group is interested in the transcriptional regulation mediating specification. We are primarily concerned with transcriptional hierarchies and how key regulatory factors work within biochemical and genetic pathways, and also how deregulation of such programs leads to cancer. Our group uses mouse and zebrafish model systems to examine gene function in vivo, and a wide variety of biochemical assays to examine gene function in vitro.**

**We have four primary focus areas:**

1. Transcriptional hierarchies which are active during embryonic stem (ES) cell differentiation into mesoderm-derived tissues such as the kidney and blood. The methodologies used include directed differentiation of ES cells in various recombinant growth factors, gene targeting and BAC recombineering for generating reporter ES cell lines and mice in which stem cells can be followed by epifluorescence and FACS, expression profiling and chromatin immunoprecipitation.

2. Transcriptional regulation of erythropoiesis. Mutations in the globin genes are the most common genetic mutations worldwide. These mutations are responsible for thalassemia and sickle cell disease, which cause serious morbidity and mortality. We are interested in trying to decipher the complex process of haemoglobin switching at a molecular level. The long term goal is to design new drugs that target key regulators of this process and thereby reestablish fetal haemoglobin in adults.

3. Zebrafish are used as a vertebrate model for dissection of some of the earliest transcriptional events which underpin morphogenetic movements which lead to the generation and ‘education’ of stem cells within the mesoderm germ layer. Once again we are concerned primarily with the activities of master regulator transcription factors of key gene and developmental classes. We have established expression profiling in zebrafish and have established assays and systems for study of morphogenesis.

4. The role played by the Kruppell-like factor (KLF) family of zinc finger genes in normal differentiation and human skin, colon and blood cancers.

**RESEARCH PROJECTS**

- Studying transcriptional hierarchies active during ES cell differentiation into mesoderm-derived tissues
- Investigating the transcriptional regulation of erythropoiesis
- Studying morphogenesis using zebrafish models
- Researching role of KLF in differentiation and cancer

**KEY PUBLICATIONS**


We have utilised primary cultures of human melanocytes and melanoblasts, as well as numerous melanoma cell lines grown as adherent cultures or induced to form non-adherent spheroids, in our investigations into melanocytic cell growth and transformation. Recent publications have suggested that melanoma may arise from the malignant transformation of melanocytic precursor cells resident in the skin. Our proposal is to study potential differences in the transcriptional and signalling network of skin-derived precursor (SKP) cells, when grown in vitro as spheroids and differentiated into melanocytes. We aim to identify the differentiation and regulatory pathways active in normal melanocyte growth that differs to those responsible for melanoma development, and the formation of spheroids from melanoma cell lines.

Fine mapping association of blue-brown eye colour-related SNPs in an adolescent twin collection from South-East Queensland has been performed within the intergenic region upstream of the OCA2 and within the neighboring HERC2 genes. We reported that a single SNP in intron 66 of HERC2, rs12913832, predicted eye colour with almost perfect correlation. Comparison of sequence alignments of multiple species showed this SNP lies in the centre of a short highly-conserved sequence, and the blue-eye associated allele breaks up this conserved sequence, part of which forms a consensus binding site for the helicase-like transcription factor (HLTF). We have identified the induction of the NR4A nuclear receptor transcription factors as an important step in MC1R-mediated DNA repair in melanocytes. Furthermore, impaired induction in primary human melanocytes harbouring homozygous RHC variant MC1R alleles may underlie an increase in melanoma susceptibility in these individuals.

**RESEARCH PROJECTS**

- Understanding skin cancer risk phenotypes through studying the interaction of genes involved in skin, hair and eye colour.
- Undertaking parallel genetic and cellular analysis of human melanogenesis.
- Investigating eye colour as a genetic trait.
- Researching melanocyte spheroids as a model for melanoma development and metastasis.
- Role of NR4A nuclear hormone receptors in melanocytic cells.

Further information and publications are available at www.imb.uq.edu.au/index.html?id=11690
Using genomic approaches, our group mapped and isolated the gene for the heritable cancer disorder, naevoid basal cell carcinoma syndrome (NBCCS). The patched gene, discovered from our studies on NBCCS, has defined a signalling pathway known as the "hedgehog pathway", which appears to be mutated or perturbed in a wide range of tumour types, including lung, gastro-intestinal, skin, pancreatic, prostate, brain and ovarian cancer. This has led us to focus on the role of hedgehog signalling, not only in cancer but also on the regulation of stem cell compartments. Increasingly it appears that in some tumour types there are cells known as "cancer stem cells" which reside within the tumour and are responsible for the overall phenotype. Currently such cells can be partially defined functionally but their molecular signature remains elusive. We believe that the patched/hedgehog pathway defines many of the characteristics of such stem cells and is a powerful starting point for understanding tumour biology and the development of new therapeutics.

Given that cancer represents a state of unregulated cell growth, it is likely that the pathways that lead to cancer are also involved in the normal process of tissue repair and regeneration. The two most common cancer types in NBCCS patients are basal cell carcinoma of the skin and medulloblastoma, a common brain tumour occurring predominantly in children. In the example of both tumour types we are examining how activation of the hedgehog pathway causes the tumour, and defining the cell of origin of the tumour using a combination of molecular genetics and cell biology. We are also defining the interaction of the hedgehog pathway with other genetic pathways such as Notch signalling in order to understand the normal development of the skin and the cerebellum, but also what therapeutic strategies might be useful to treat the tumours. In addition to studying known pathways, we are seeking new interactions through genomic approaches to discovering new genes and pathways in model systems such as mice and zebra fish. The IMB has a well-developed drug discovery platform and we are using our knowledge of the biology of these tumours to look for potential new therapeutics.

As part of our experimental approach our laboratory makes extensive use of transgenic and knockout mice. However at all points we refer back to the human diseases under study and have major activities based around mutation analysis, transcriptomics and proteomics of human material, integrating the data from all systems.

As a result of these studies we have a particular interest in the interface between developmental cell biology and human genetics, and in therapeutic interventions such as gene or cell therapies.
Towards a new understanding of the reproductive system: from non-coding RNAs to disease

Our group focuses on the elucidation of regulatory mechanisms that control gene expression during embryonic development. One of the most amazing biological processes is the development of a fertilised egg into a complex organism. It involves the orchestration of cellular processes such as cell proliferation, migration, differentiation and apoptosis, which is controlled by a delicate network of gene regulation and interaction. Disturbance of this network caused by gene mutation or misexpression during development results in malformation and malfunction of organs, diseases such as cancer and often lethality. Therefore, each of these processes must involve a large number of regulatory mechanisms. Until recently our work centred around the conventional dogma, which states that gene activity is controlled by transcription factor binding to proximal promoters and/or enhancers adjacent to genes. We are now extending these studies to include the fact that gene activity is also regulated post-transcriptionally by non-coding RNAs (ncRNAs), such as microRNAs. In addition to investigating the role of microRNAs during development, we have discovered a new class of ncRNAs, UAI-RNAs (3'UTR-associated non-coding RNAs) that display a highly regulated stage- and sex-specific expression pattern during embryogenesis.

Our research uses mouse as a model system and integrates molecular, developmental, and cancer biology to study mechanisms of gene regulation by transcription factors as well as ncRNAs during embryonic development, concentrating on sex determination and gonadal development but extending to other developmental systems such as chondrogenesis.

The aims of our research are to address the interactions of the following questions:

1. What are the regulatory mechanisms underlying the development of the reproductive system with emphasis on ovarian development?
2. What are the roles of ncRNAs, specifically UAI-RNAs and microRNAs, during the development of testes and ovaries, and in tumour formation?
3. How does testicular and ovarian cancer develop?

RESEARCH PROJECTS
• Characterising the role of miR-202 during embryonic development
• Identification and analysis of upstream regulators and downstream target genes of miR-202
• Functional characterisation of UAI-RNAs during embryonic development and possible implications in cancer
• Studying the cellular and molecular regulation of foetal ovary development

KEY PUBLICATIONS
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RESEARCH PROJECTS

- Characterising the role of miR-202 during embryonic development
- Identification and analysis of upstream regulators and downstream target genes of miR-202
- Functional characterisation of uaRNAs during embryonic development and possible implications in cancer
- Studying the cellular and molecular regulation of foetal ovary development

KEY PUBLICATIONS


Biochemistry of protein prenylation

Over the past 15 years, it has become increasingly clear that post-translational modification with isoprenoids is a widespread phenomenon, affecting up to 2 percent of proteins in eukaryotic cells. In all cases that have been studied, such a modification has been shown to be crucial for protein function by modulating protein–lipid or protein–protein interactions. Most of the prenylated proteins are GTPases that have key functions in signal-transduction pathways. Much of our attention is focused on the understanding of prenylation of Rab GTPases — the largest group of prenylated proteins. Rab GTPases are modified by Geranylgeranyltransferase type II (RabGGTase) — a 100 kDa heterodimer that catalyzes the transfer of two 20-carbon geranylgeranyl groups from geranylgeranyl pyrophosphate (GGPP) onto C-terminal cysteine Rab’s C-terminus GTPases.

The remarkable feature of RabGGTase is its ability to interact with more than 70 different Rab proteins. At the same time, the enzyme is strictly specific for the Rab family and no unspecific activity could be detected. RabGGTase is composed of tightly associated alpha and beta subunits and belongs to the family of protein prenyltransferases together with farnesyl transferase (FTase) and geranylgeranyl transferases, together with farnesyl transferase (FTase) and geranylgeranyl transferases. RabGGTase-substrate/product complexes provide insights into the evolution of protein prenylation. 

**KEY PUBLICATIONS**


The endosome at atomic resolution: structural studies of the endosomal trafficking machinery

Our lab is focused on understanding the basic processes of intracellular membrane trafficking within the secretary and endocytic systems of the human cell. We do this by using a multidisciplinary approach that integrates high-resolution structural characterisation of essential membrane trafficking machinery by X-ray crystallography with biochemical and cell biological experiments guided by these mechanistic details. We concentrate primarily on the process of protein sorting within the dynamic organelles known as endosomes, which are key sorting stations for regulated exo- and endocytosis of cell-surface receptors, signaling molecules and many other cellular components. The regulated trafficking of proteins and their ligands between membrane-bound endosomal compartments, the plasma membrane and other internal organelles is a fundamental process in human cells, and indeed in all eukaryotes. Defects in the endosomal membrane transport system are linked to many different human diseases, including a number of cancers, lysosomal storage disease and hypercholesterolaemia, and it is also exploited by bacteria toxins and virus pathogens such as HIV to gain entry into the cell. Membrane sorting between secretory and endocytic organelles is predominantly controlled by small carrier vesicles and tubules that are laid on their cytoplasmic faces by specific protein machineries. The roles of these protein coats are threefold: (i) to select transmembrane and lipid cargo to be packaged into vesicles at the donor membrane, (ii) to control vesicle budding and scission and (iii) to specify the final destination of the transport intermediates. Using a multidisciplinary structural biology/biochemistry/cell biology approach, our goal is to reveal how these machineries assemble, how they control receptor trafficking at the molecular level. Current work focuses on the multi-subunit retromer protein complex with a central role in directed transport of endosomal cargo proteins, the sorting nexus (SNX) family of proteins involved in membrane remodeling, and a novel family of amrin-related trafficking proteins.

**RESEARCH PROJECTS**

- Structure and function of the retromer protein complex
- Analyzing the interaction of retromer with cargo proteins and regulatory molecules
- Membrane remodeling by the SNX protein family
- Structural studies of PX-domain proteins and complexes with effector molecules
- Structure and function of amrin-related proteins

**KEY PUBLICATIONS**


Plasma Membrane Nanostructure and Signal Transduction

Our group studies mammalian intracellular signalling. We are especially interested in the function of Ras proteins. These small GTP-binding proteins operate as molecular switches in signal transduction pathways and are present in a mutant, activated state in many human tumours. Understanding the basic biology of Ras has major implications for the development of novel anticancer therapeutics.

Specifically, we are investigating how the Ras membrane anchors cooperate with the G-domain and peptide sequences flanking the anchor to drive lateral segregation. Our work suggests new models are needed to explain how lipidated proteins interact with, and use, the plasma membrane to generate signalling platforms.

We remain interested in how confinement of signalling complexes onto a 2D surface in general, and in plasma membrane nanodomains in particular, regulates the kinetics and sensitivity of Raf/MEK/Erk signal output. Similarly, as we develop our spatial and proteomic maps of the plasma membrane, we can address how the composition and organisation of the membrane alters in response to specific growth factors. The integration of complex spatial, kinetic and biochemical data sets increasingly requires mathematical modelling to generate and test our novel hypotheses of nanodomain structure and function.

We also have a major interest in characterising the K-Ras ER to plasma membrane trafficking pathway and studying the biology of Ras prenyl binding proteins such as DFE delta.

RESEARCH PROJECTS

- Molecular mapping of the proteins and lipids of plasma membrane nanodomains
- Electron microscopic visualisation and quantitative characterisation of surface nanodomains to build up a high-resolution 2D map of the nanodomains of the inner plasma membrane
- Investigating the dynamic regulation of nanodomain localization of Ras and Ras interacting proteins in response to physiological stimuli
- Characterising the mechanisms whereby K-Ras is transported to the plasma membrane
- Mathematically modelling Ras signal transduction
- Monte Carlo modelling of plasma membrane nanodomain dynamics

Structure-function studies of the endocrine pancreas — comparative studies of mouse and human pancreatic islet biology

The β-cells of the endocrine pancreas are the sole source of insulin in mammals. Death of the β-cells, or their abnormal processing, trafficking and secretion of insulin, results in the disease commonly known as diabetes. This disease is one of Australia’s national health priority areas and represents the fastest-growing epidemic internationally. More than 230 million people worldwide currently live with the disease, but this number is expected to rise to 350 million within 20 years. In 2007, the world spent an estimated US$215-375 billion to care for diabetes and its complications. In particular, type 1 diabetes is one of Australia’s fastest-growing chronic diseases, and represents a life-long autoimmune disease that usually begins in childhood and results in premature death through health complications. Type 1 diabetes cannot be prevented, and a cure remains to be found.

Our group’s research is focused on understanding the basic mechanisms related to β-cell function and dysfunction from a structural cell biology perspective, so that we can precisely identify how and where defects in these steps occur. By necessity, this work has led us to develop or advance techniques for the improved preservation and imaging of pancreatic β-cells in situ within pancreatic islets of Langerhans isolated from both mice and humans, so that we are positioned to reliably elucidate the basic cell biology and physiology of the β-cell and islet biology more generally — through comparative studies of islet cell structure-function.

To complement our move toward an integrated or holistic approach to understanding cells as examples of complex systems, we have undertaken a multi-scale/multi-resolution approach whereby we have started reconstructing entire mammalian β-cells in 3D at both high (admiral) and intermediate (15-20nm) resolutions. These approaches underpin the Visible Cell® project (www.visiblecell.com) coordinated by the JMB and the Australian Centre of Excellence in Bioinformatics (ACEB) at The University of Queensland. Our group’s data will uniformly inform advanced in silico studies of 3D cell and molecular organisation in mammalian cells that are focused on developing the capacity to model and predict cellular differentiation during normal development, as well as the pathophysiology of chronic diseases like type 1 diabetes.

New Research Project: Correlative structure-function studies of cis- and trans-Golgi membrane traffic in mammalian cells

This project combines imaging by light and electron microscopy with additional techniques for studying protein function at the molecular level, to elucidate how changes in the 3D organisation of cellular machinery can lead to fundamental changes in the function and health of mammalian cells. Although this work includes detailed investigation of the ‘insulin factory’, it has the potential to modify established concepts on membrane traffic and protein secretion well beyond the field of diabetes.

KEY PUBLICATIONS


Plasma Membrane Nanostructure and Signal Transduction

Cholesterol depletion also causes the lipid raft marker protein (GPI-T), imaged on intact plasma membrane sheets by immunogold labelling to de-cluster...
The cell surface in health and disease

Our group is interested in the organisation, dynamics, and functions of the plasma membrane. The properties of the plasma membrane rely on the specialisation of the plasma membrane into microdomains of specific function. We have particularly focussed our attention on caveolae, a specialised domain of the cell surface with a distinct structure. Caveolae have been implicated in regulation of cell growth and in maintaining the balance of lipids in the cell. In addition, caveolae and caveosomes, the major proteins of caveolae, have been implicated in a number of disease states including tumour formation, atherosclerosis, and muscular dystrophy. To study caveolae function and, in particular, the link between lipid regulation and cancer, we are using caveola-null cells, lacking caveolins, and zebrafish embryos. These systems are also being used to study the role of caveolin in muscle and the molecular changes associated with muscular dystrophy. We have recently discovered a family of caveolin coat proteins that regulate caveola formation and function. An additional aim of our work is to understand the link between caveolae and lipid-filled organelles termed lipid droplets, which are major storage organelles involved in obesity. We have shown that caveolins are essential for the formation of lipid droplets during liver regeneration.

RESEARCH PROJECTS

- Characterisation of the structure and function of a new family of caveolin coat proteins
- Caveolae and obesity: dissecting the role of caveolins and Rab proteins in lipid droplet formation and function in adipose tissue and during liver regeneration
- Caveolae and caveolin-3 in muscle: analysing the role of caveolin-3 and caveolin in muscle development and in muscular dystrophy
- Caveolins and caveolin-interacting proteins in zebrafish: using zebrafish as a model system to understand the role of caveolins during development and the effect of muscular dystrophy mutants of caveolin-3 on muscle structure and function
- Clathrin-independent endocytosis: characterising the structure and function of a novel endocytic pathway in mammalian cells and the zebrafish
- Caveola formation and structure: studying caveola biogenesis and caveola structure in health and disease using electron tomography and novel cell systems
- Caveola formation in i.e. cell: characterising novel nanocaveolae

KEY PUBLICATIONS


The cell surface in health and disease

Protein trafficking in human disease

Our research group studies protein trafficking in human and animal cells with the aim of mapping the cellular organelles and molecules that function in the secretion and endocytosis of disease-related proteins. In this work we use a range of cellular, molecular and biochemical approaches. Trafficking is a highly-dynamic process and studies in this field have been greatly enhanced by the development of fluorescent probes and microscopic techniques for imaging in living cells. Live cell imaging, combined with other forms of microscopy, has thus become a major core technology for the research in our group. In epithelial cells we are studying E-cadherin, an essential adhesion protein and a vital tumour suppressor. E-cadherin is trafficked to and from the cell surface to regulate cadherin-based cell-cell adhesion and cell polarity. A main goal of this work is to understand how E-cadherin trafficking functions in morphogenesis and cancer progression. As a model system we grow epithelial cells in mini-organs cultures where the effects of gene expression or gene silencing can be analysed.

Cells of the immune system secrete tightly orchestrated arrays of cytokines to control immune responses. In macrophages we are studying the secretion of pro-inflammatory cytokines that contribute to the onset and progression of chronic inflammatory diseases. Understanding how they are trafficked and secreted may lead to the development of new therapeutic strategies in inflammation. Gene expression arrays, live cell imaging, FACS and biochemical approaches are used to map out intracellular pathways for cytokine trafficking and secretion. Recent progress has shown that we can manipulate cytokine secretion in mice and current efforts are focused on using this approach in the treatment of arthritis and inflammation of the stomach and bowel. Based on recent findings, we are now also studying the pathways for phagocytosis or ingestion of different microbes by macrophages.

RESEARCH PROJECTS

- Imaging live cells to create 3D and 4D maps of trafficking pathways: fluorescence imaging and computer modelling
- E-cadherin trafficking in epithelia: morphogenesis and tumorigenesis in cyst cultures
- E-cadherin and growth factor signalling in cancer cells
- Secretion of inflammatory cytokines in macrophages
- Secretion of cytokines in mouse models of inflammatory disease
- Phagocytosis and trafficking of microbes

KEY PUBLICATIONS


Role of growth hormone and related cytokines in growth, cancer, diabetes and obesity

Adult height is determined by the actions of growth hormone (GH) during childhood and adolescence. In the adult, growth hormone is an important metabolic agent regulating body composition, opposing the actions of insulin. In old age, growth hormone status determines lifespan, at least in animal models. We study the means used by growth hormone to achieve these changes, using a variety of approaches directed to the growth hormone receptor, from high-resolution protein structures to genetically-engineered animals.

The growth hormone receptor determines the degree of the cell response to growth hormone, which we originally cloned collaboratively with Genentech. Through FRRT, BiRT, cryospectroscopy and targeted mutagenesis we have developed a new model of how the GH receptor is activated by GH, involving realignment of receptor subunits within a constitutive dimer. An extension of this model describes how a rearrangement of an extracellular b-loop of the GH receptor selectively controls ERK activation without influencing STAT5 activation through the use of an alternate: Src kinase.

By creating targeted knock-in mutations to signalling domains within the GH receptor cytoplasmic domain, we have shown that enhancement of postnatal somatic growth by GH is dependent on its ability to activate the transcription factor STAT5. Because these mice become strikingly obese after 6 months of age, we are currently investigating the mechanism of activation of the Src kinase constitutively bound to the receptor

Elucidating the role of the growth hormone receptor in the cell nucleus in relation to proliferation, oncogenesis and stem cell proliferation

Determining the role of GH-dependent Stats 3/5/11 in lipid and carbohydrate metabolism, including insulin secretion and action

Establishing the molecular basis for GH-dependent liver regeneration

Investigating the feasibility of using GH receptor antagonists to block breast and prostatic cancer

KEY PUBLICATIONS
Conway-Campbell, B.L., et al. (2008). The extracellular domain of the growth hormone receptor interacts with coactivator activator to promote cell proliferation. Molecular Endocrinology 22: 2190-2202.


Cells are the building blocks of our bodies. Interactions between different cells are important to shape our developing bodies, and a range of diseases occur when those interactions are disturbed, including cancer and inflammation. My laboratory studies one set of cell-to-cell interactions, those that occur when cells attach to one another. We focus on the cadherin family of cell-cell adhesion receptors. Those critically determine the ability of cells to recognise one another and organise into coherent tissues. The importance of these receptors is emphasised by the fact that loss of cadherin function promotes cancer progression in epithelial tissues (such as the breast and colon) – the commonest form of human cancers. By understanding the basic biological mechanisms of cadherin-mediated cell recognition we thus hope to provide vital insights into the basis of developmental patterning and common human diseases.

We currently focus on understanding how cadherins cooperate with the actin cytoskeleton, long believed to be central to cadherin function. Our experience makes it increasingly clear that this cooperation involves a complex interplay between adhesion receptors and diverse distinct states of the cytoskeleton that are coordinated by a variety of signalling pathways at the cell membrane. In particular, our work demonstrates that cadherin function as an actin-activated cell signalling receptors that stimulate pathways to regulate the actin cytoskeleton, thereby influencing cell shape, adhesion, and cell-cell cohesion. Relevant signals include the Rho family GTPases and Src family kinases. These affect a range of cytoskeletal regulators, including actin nucleators, cross-linking proteins, scaffolds and the myosins II and VI.

RESEARCH PROJECTS
• Regulation of the actin cytoskeleton by E-cadherin
• Cooperation between cadherins and myosin motors at cell–cell contacts
• Cooperativity between cadherins and microtubules
• Cadherin signalling to Src family kinases: defining the pathway(s)
• The morphogenetic consequences of cadherin-activated cell signalling and cooperation with the actin cytoskeleton

KEY PUBLICATIONS


‘(Equal contributions)’
Design and discovery of bioactive peptides and proteins

The overall focus in the group (www.uq.edu.au/alewood) is the identification of bioactive molecules that have the potential to play important roles in human health and wellbeing. Some specific interests include: the discovery and total synthesis of potent and selective peptides (toxins) from Australia’s venomous creatures; the chemical synthesis of proteins and bioactive peptides; the development of new synthetic and analytical chemistry; and protein structure and function. Special emphasis is placed on determining the structure-function relationships of natural and designed molecules. Current research programs involve: the discovery, isolation and characterisation of toxins from snakes, spiders, cone snails, platypus, ticks and scorpions; mimetics of calcium-binding proteins; elucidation of the chemical synthesis of proteins and small bioactive proteins; and enzymes (up to 200 residues).

**RESEARCH PROJECTS**

- Identification and characterisation of novel peptides from Australian animals that target ion channels, transporters and receptors
- Dissecting chronic neuropathic pain pathways with receptor-selective toxins
- Protein mimetics
- Development of new enabling synthetic chemistry to access disulfide-rich peptides and small bioactive proteins and enzymes (up to 200 residues)
- Design and synthesis of novel small molecules that mimic peptide structure and function (peptidomimetics)

**KEY PUBLICATIONS**


Our research centres on the detection, isolation, characterisation, identification and evaluation of novel bioactive metabolites from Australian marine and terrestrial biodiversity. These metabolites span all known biosynthetic structure classes including many molecules new to science, and their study requires the use of sophisticated chromatographic, spectroscopic and chemical technologies. Natural products uncovered during our investigations represent valuable new leads in the search for drugs with application in the fields of human and animal health and crop protection, have potential as molecular probes to further investigate and understand living systems, and could find application as biological control agents.

The research group coordinates an extensive network of collaborations across many scientific disciplines, in industry, academia and government, both in Australia and overseas, which allows us to target such therapeutic indications as infectious and neurodegenerative diseases, cancer, inflammation, pain, diabetes and obesity, as well as invertebrate animal and pest control through chemical ecology, and gene-activated microbial biodiscovery.

**RESEARCH PROJECTS**

- Marine biodiscovery: discovering new drugs to control neurodegenerative diseases
- Cephalosporin biodiscovery: exploring chemical ecology as a source of new pain drugs
- Microbial biodiscovery: Exploring the microbial genome for bioactive metabolites with application against infectious and neurodegenerative diseases, diabetes, obesity, atherosclerosis, inflammation, pain and cancer
- Chemical synthesis: Developing “natural” alkaloids to combat parasitic infection in livestock
- Chemical ecology: Developing new “natural” strategies for controlling cane toads
- Biomimetic synthesis: Developing new “natural” routes into bioactive chemical space

**KEY PUBLICATIONS**


Our group uses NMR spectroscopy to determine the structures of proteins that are important in drug design programs and in agriculture. By elucidating the structures of biologically-active proteins we are able to identify regions crucial for activity and can use this information to design new drugs. The proteins we study come from a range of animal and plant sources but are often involved in host defence. Examples include the conotoxins (venom components from marine snails) and the cyclotides (novel circular proteins from plants).

We have an interest in the discovery and structural characterisation of novel protein topologies. In particular we aim to determine the mechanisms of biosynthesis and evolutionary origin of circular proteins and to apply protein-engineering principles to explore applications of circular proteins in drug design and agriculture.

We undertake protein-engineering studies in which we modify protein frameworks either by “grafting” new biologically-active epitopes onto them, or by stabilising them by cyclisation. We also study the protein-folding problem, i.e., how do proteins fold into the complex shapes that determine their functions?

Amongst the highlights of last year included our isolation and characterisation of a pair of key cyclic peptide-processing enzymes (asparaginyl endoprotease and peptide disulfide isomerase) and our identification of potential common processing mechanisms of circular proteins across divergent plant families.

To read more details about other projects we are working on, please see: www.imb.uq.edu.au/index.html?id=11695
Chemistry and human therapeutics

Our group works at the interface of chemistry, biology and disease. Our researchers study chemistry, biology or chemistry and biology to better understand the detailed processes of life, ageing, disease and death.

Our chemistry researchers develop expertise in organic, medicinal or drug design; solid and solution phase synthesis; structure determination using 2D NMR; and interactions between small molecules, proteins, DNA and RNA. Outcomes are new chemical reactions/mechanisms/compounds/structures, enzyme inhibitors, protein agonists/antagonists, and structural mimics of protein surfaces.

Our biology researchers use our new compounds to interrogate human protein and cell function and to elucidate mechanisms of protein activation, biological/physiological processes, disease development, and drug action. Researchers gain insight to processes pivotal to human physiology or aberrant in disease, and develop interdisciplinary skills in enzymology, biochemistry, pharmacology, immunology, oncology, parasitology, virology and neurobiology.

**Research Projects**
- Designing and discovering drugs (e.g. for GPCRs, proteases, enzymes)
- Synthetic organic or medicinal chemistry (solution & solid phase)
- Determining structure using 2D NMR spectroscopy
- Enzymology & protein–protein interactions
- Pharmacology: molecular (cellular) and experimental (animal models)
- Structural and functional mimicry of protein surfaces by small molecules
- Mechanisms of disease development & drug action in human inflammatory disorders, cancers, viral and parasitic infections, neurodegenerative and cardiovascular diseases

**Key Publications**

Determining the structures of membrane proteins, macromolecular assemblies and viruses is one of the great challenges of cell and structural biology. Using advanced high-resolution cryo-electron microscopes it is now possible to capture atomic-resolution information of biological macromolecules. However, as the captured images are inherently ‘noisy’, this information must be recovered by aligning many copies of the protein (~10^7 individual molecules) either computationally (by single particle analysis), or biochemically (via crystallography).

As part of the IMB’s Visible Cell® project we have established a powerful single particle analysis pipeline, as well as new biotechnologies for template assisted 2D crystal production. The single particle process involves merging large numbers of 2D projection images of randomly-oriented molecules to calculate 3D reconstructions. Our current benchmark resolution is ~10 Å at which individual α-helices begin to be resolved, and we are actively developing processes to improve this further. In parallel we have developed detergent-resistant 2D templates that chisle N at the surface, to facilitate the systematic production of 2D crystals of tethered His-tagged membrane proteins. Using those twin approaches we are studying a wide range of important membrane proteins (e.g. photosynthetic membrane protein complexes, ATPas, mechanosensitive channels), macromolecular assemblies (AAA ATPases and related proteins, ferritin, NE1) and icosaedral viruses. These structures provide fundamental new insights into many fascinating molecular machines and feed into the Visible Cell® project. These technologies are also being used to develop novel bio-fuel production systems within the Solar Bio-fuels consortium.

The Solar Bio-fuels consortium (www.solarbiofuels.org), co-directed by Ben Hankamer, has brought together an international team of about 70 specialists to develop high-efficiency 2nd-generation bio-fuel production systems using microalgae. This represents a rapidly expanding area of biotechnology of global significance. Our specialisation is the structural biology and biochemistry of the photosynthetic machinery, which drives the first step of converting solar energy into chemical energy (fuels). Consequently its optimisation offers significant downstream benefits for all bio-fuel production systems (bio-ethanol, bio-diesel, BTL diesel, bio-H2 and bio-methane). With colleagues, we are now taking the ‘Visible Cell®’ approach to develop a 3D atlas of the photosynthetic machinery within the cellular context. This 3D atlas will assist in the fine-tuning of the light capture and conversion processes of photosynthesis, just as a manual is required to tune the engine of a car.

**Research Projects**
- High-Resolution Single Particle Analysis: biology, physics and software development
- The Visible Cell® Project: resolving the 3D structure of the macromolecular assemblies
- Template mediated 2D crystallisation: towards streamlined membrane protein crystallisation
- 2nd-generation micro-algal biofuel systems: development of bio-fuel systems for bio-H2, bio-diesel and BTL diesel production that are coupled to CO2 sequestration

**Key Publications**

**Lab Members**
Research Officers: Dr Ian Ross, Dr Michael Landsberg
Research Assistant: Rosalia Rothnagel
PhD Students: Evan Stephane, Erin Aarni, Drew Rumschmit, Emily Krauth, Winnie Vazaitou, Matthew Timmins
MSc Student: Mattia Kock
Honours Student: Hong Wai Tham
Research in my laboratory is aimed at the development of novel pharmaceutical agents and environmentally-friendly insecticides. Approximately half of the group is studying bacterial cytokinesis or signalling by bacterial histidine kinases in order to provide a molecular understanding of these key biological processes and to establish a platform for the development of novel anti-microbial agents. The remainder of the group is focused on developing novel anti-coagulants and environmentally-friendly insecticides by harnessing the remarkable chemical diversity encoded in the venoms of spiders and scorpions. Most research projects are highly interdisciplinary and the experimental techniques employed range from molecular biology through protein chemistry to structure determination using NMR spectroscopy and X-ray crystallography. Research in the lab is currently funded by three ARC and five NHMRC research grants.

My research focuses on the discovery and characterisation of venom peptides, especially the conotoxins produced by the predatory cone snail. These highly structured peptides or mini-proteins act selectively at a wide range of ion channels, G-protein coupled receptors and transporters found in the membranes of cells. Interestingly, several conotoxins have been taken into the clinic including Xonotoxin Gi2174 for chronic neuropathic, post-surgical and cancer pain, which was developed from α-MaIA, originally discovered by my group.

A major focus of the group is to discover novel peptide targets and develop new peptides able to act at these targets to reduce pain sensation. This research involves the assay-guided isolation of venom peptides, peptide synthesis, tissue pharmacology, high-content imaging, radioligand binding, receptor mutagenesis, homology modelling, and finally co-crystal structures and docking simulations of the peptide target interaction.

**RESEARCH PROJECTS**

- Developing novel antibiotics targeted against Gram positive pathogens
- Investigating the architecture and function of the bacterial cell division machinery
- Using tarantula toxins to characterise ion channels involved in sensing pain
- Developing environmentally-friendly insecticides based on spider venom peptides

**KEY PUBLICATIONS**


**LAB MEMBERS**

**Senior Research Officers:** Dr Susan L. Rowland, Dr Meli Mobli

**Research Officers:** Dr Volker Herzog, Dr Riikko Hoorup, Dr David Willow, Dr Brit Winnen

**Research Assistants:** Lindsay Long, Alysha Elliott

**PhD Students:** Margaret Ganitz, Sandy Gonzalez, Jonas Jansen, David Morgenstern, Natalie Saiz, Kimberly Wadswood

**MSc Students:** Radhika Seshadri, ViraJitha Rajagopalan

**Undergraduate Interns:** Tomas Mijenovic, Darshani Rapasinge, Mitchell Sullivan

**RESEARCH PROJECTS**

- Developing novel antibiotics targeted against Gram positive pathogens
- Investigating the architecture and function of the bacterial cell division machinery
- Using tarantula toxins to characterise ion channels involved in sensing pain
- Developing environmentally-friendly insecticides based on spider venom peptides

**KEY PUBLICATIONS**


Protein structure and drug design

Our work aims to better understand the role of proteins in disease and to develop novel chemicals to modify the functions of disease-causing proteins. We use a range of techniques to investigate the structure, function, and interactions of proteins. Our research has been enhanced enormously through the recent ARC LIEF-funded automation upgrade of the UQ ROCX Facility.

A major outcome over the past years has been the advance in our understanding of insulin-stimulated trafficking of the GLUT4 glucose transporter. This process, which is critical to the regulation of blood glucose levels, is affected in Type II Diabetes. Our recent results, in collaboration with Professor David James (Garvan Institute), show that the Munc18c protein binds to a short N-terminal peptide of the SNARE syntaxin4 protein, and that this interaction stimulates SNARE ternary complex formation thereby promoting vesicle fusion (Latham et al. Traffic 2006). We determined the structure of the Munc18c: Sx4 peptide complex showing that the N-peptide interaction is evolutionarily conserved in almost all SNARE systems (Hu et al. PNAS 2007). This work has been recognised by the award of a 2009 NH&MRC program grant between James and Martin and other diabetes researchers at the Garvan Institute.

Our long-running interest in bacterial redox folding factors has led us to focus our attention on developing inhibitors of DsbA as potential antibacterial agents, using the technique of fragment-based screening. We have already successfully applied this approach to the study of inhibitors of PNMT.

using our new automated UQ ROCX facility, PNMT crystals were used to screen 400 drug-like fragments: 12 hits were identified and confirmed by isothermal calorimetry. Six elaborated compounds were designed and synthesised and these are currently being tested for inhibitory activity. This whole procedure from first crystal to final chemical synthesis step has taken one PhD student just 18 months, demonstrating the strength of structure-based approaches for drug lead discovery.

**RESEARCH PROJECTS**
- Studying the structure, function and interactions of SNARE proteins associated with insulin action
- Studying the structure, function and inhibition of redox folding factors involved in disease
- Investigating novel inflammation drug targets using high-throughput structure approaches
- Studying the structure, function and inhibition of transferase enzymes involved in disease

**KEY PUBLICATIONS**


Our research focuses on advancing drug design and synthetic organic and peptide chemistry to discover novel biologically-active molecules. We are applying these new drug design and discovery methodologies to discover drugs to treat unmet medical needs or provide better therapeutic solutions to existing marketed drugs.

Using a combination of mathematics, software development, drug design, combinatorial chemistry and phage display, we are developing new approaches to identify biologically-active molecules. Thus, projects are multidisciplinary and focused on achieving medical outcomes.

**RESEARCH PROJECTS**
- Modulating hematopoietic prostaglandin D2 synthesis for allergic disease
- Studying antagonists of Myb for treatment of leukaemia
- Designing SHP-1 inhibitors to boost haematopoiesis
- Developing antipathogenic compounds to treat microbial infections
- Developing structure-based phage display
- Developing new computational algorithms and strategies for sampling biologically-relevant chemistries
- Developing a synthetic process for the combinatorial synthesis of biologically-relevant compounds
- Developing in vitro and cell-based assays for screening arrays of compounds

**KEY PUBLICATIONS**


Molecular dynamics of biomolecular systems

The group, with members based both at The University of Queensland (UQ) and the University of Groningen (RUG), The Netherlands, concentrates on modelling the structural and dynamic properties of biomolecules such as proteins, nucleic acids and lipid aggregates. In particular, we use computer simulations to understand and predict the macroscopic (experimentally observable) behaviour of complex biomolecular systems based on the interactions between atoms. We develop the software, atomic force fields and theoretical models needed to address a range of fundamental questions.

First, how do proteins fold? Understanding how proteins fold is one of the grand challenges of modern biology and a critical test of our ability to accurately predict interactions in protein systems. The failure of proteins to fold correctly is also linked to a range of debilitating diseases including Alzheimer’s Disease, BSE and some forms of Type II diabetes where misfolded proteins form destructive aggregates called amyloid fibrils. Currently, it is not possible to directly simulate the folding of proteins in atomic detail. Dramatic progress has, however, been made in the de novo folding of small peptides and the refinement of some proteins. Research on folding is conducted at multiple levels. Small model systems are used to refine force fields and simulation techniques. On a larger scale we are simulating how multiple copies of certain peptides aggregate in order to understand how amyloid fibrils form.

Second, how do cell surface receptors transmit a signal through the cell membrane? Receptor proteins of the surface of cells play a vital role in cellular communication. However, little is known in regard to the mechanism by which the binding of a molecule to an extracellular receptor transfers a signal across the cell membrane or even how changes in the environment can activate certain cell surface receptors. On one hand we are investigating the mechanism by which low pH triggers the activation of the Dengue E protein, which plays a critical role in the entry of the virus into cells. We are also investigating the structural changes associated with the binding of human growth hormone to the growth hormone receptor.

Third, how do membrane proteins assemble? Cell membranes are the archetypal self-organised supramolecular structure. Membrane protein complexes also represent a new frontier in structural biology. Using simulations, we are able to directly investigate how by layers and vesicles form. We are also investigating the assembly of functional structures such as the assembly of anti-microbial peptides into transmembrane pores. This in turn is being used to understand the mechanism by which larger complexes form in heterogeneous environments.

**RESEARCH PROJECTS**
- Simulating peptide folding and assembly
- Pore-forming peptides as models for protein assembly
- The nucleation and growth of amyloid fibrils
- Mechanism of activation of the human growth hormone receptor
- New methods in drug design

**KEY PUBLICATIONS**

Applied statistics and bioinformatics

My research in applied statistics is in the related fields of classification, cluster and discriminant analyses, data mining, image analysis, intelligent systems, machine learning, neural networks, and pattern recognition, and in the field of statistical inference. The focus in the latter field has been on the theory and applications of finite mixture models and on estimation via the Expectation-Maximization algorithm. I am also actively involved in the field of bioinformatics with the focus on the development of methods and software for the analysis of data from high-throughput genomics projects, with particular emphasis on gene-expression profiles. The limitations of conventional methods of cancer classification and diagnosis based on the site and appearance of the tumour or organ are well-known. With microarrays allowing genome-scale measures of gene expression, attention has turned to using differences in the activity of the gene expressions (gene profiling) to classify and diagnose tumours. However, the complexity of tumours makes it likely that a diagnostic test will be based on marker profiles rather than individual markers. But the identification of relevant subsets of the genes has its challenges, because typically thousands of gene expression levels are available from only tens of patients. It means that off-the-shelf methods of statistical analysis cannot be implemented, at least not without serious modifications. Thus, there is a need for new methodologies to be able to process thousands of genes with the aim of finding those genes that are biologically heterogeneous and therefore potential markers for cancer type, treatment therapies, or clinical outcomes.

Research projects

- Statistical modeling via finite mixture models, including methods for the detection of differentially expressed genes in different treatment classes or in time-course studies
- Analysing the statistics of microarray gene-expression data for the development of disease diagnostics
- Developing diagnostic methods for cancer using multiple molecular indices in conjunction with clinical factors
- Developing statistical methodology for the next generation of high-throughput technology with fast sequencing platforms

Key publications


IMBcom Pty Ltd is The University of Queensland’s company for commercialisation of valuable discovery research of the IMB. It is responsible for the protection and development of the University’s IMB intellectual property portfolio. Established in 2000, IMBcom has a skilled, independent Board of Directors and operates as a separate commercial entity, but with a charter of service to the University’s commercialisation objectives.

The company has fifteen employees who provide the specialist skills to commercialise the results of IMB researchers’ discoveries. IMBcom uses a model of cooperative integration with the discovery activities of the research labs. IMBcom staff are involved from the earliest disclosure stages with the planning and delivery of ways to add value to the emergent innovations. The company manages the IMB’s Intellectual Property as custodians, developers and drivers, resulting in licences, contracts and the formation of start-up companies to take discovery to products and services into markets.

IMBcom has had a historical strategic focus on developing new companies. During the first five years, IMBcom has established 11 new biotechnology startup companies, two in conjunction with UniQuest. These companies have raised more than $50 million through private sector investment, $16 million in federal and state government commercial grants and currently employ, or contract over 50 individuals in R&D and commercialisation. These spinouts have gone on to develop strategic relationships in their own right with many other Australian and international biotechnology and pharmaceutical companies, and have encouraged the growth and establishment of service providers, adding to the fabric and critical mass of the industry in Queensland. The companies continue to mature under their own management once substantial investment is raised.

IMBcom has exited its interest in one of the companies developed in partnership with UniQuest, Xenome, and the funds generated for the IMB and IMBcom are being used to provide the “proof-of-concept” funds for future IP and product development.

The IMB has a commitment to the training of high-quality graduate students in the molecular biosciences and aspires to provide a more holistic training with the inclusion of commercial and ethical dimensions. IMBcom delivers this objective through the provision of workshops throughout the training period. These “bootcamps”, or BioBusiness Retreats, incorporate elements of career preparation, understanding and working in a commercial environment, and working in teams to produce outcomes. The training engages experienced professionals from the pharmaceutical, biotechnology, investment and research industries, and has provided one of the building blocks of the commercial culture emerging in the IMB. These programs have provided commercial, project and team management skills to over 330 individuals to date, some of whom have adopted careers in the industry, being placed in Queensland biotechnology companies and IMBcom itself. The IMBcom model is widely offered by organisations that recognise that the preservation of value in intellectual property is the key to building assets upon which industry develops.

IMBcom provides assistance to Queensland and Commonwealth government departments and agencies with respect to biotechnology industry development, and is well regarded as an effective advocate for Queensland’s consistent promotion of the Smart Queensland agenda. IMBcom showcases not only the IMB and the University to industry and investment, but also Queensland as an industry destination.
It has been another productive year for the IMB postgraduate program! Our number of RHD students has stabilised at around 130 students and, again, over 20 students completed their PhD degree in 2008 (for a full list see page 64). An additional 15 students submitted their theses for assessment in 2008 and we are looking forward to a high number of graduations in 2009. While some of our graduates have remained within IMB throughout the year to complete research projects, many have taken up positions both locally and overseas, in locations such as Europe and the States (for details see page 64). As noted in the previous report, the number of international students within our cohort is growing, with approximately 38 percent of our current students being international students representing 20 different countries! This year we welcomed students from Guatemala, Turkey, Israel and Poland as well as Malaysia, India, France, Denmark, USA, Egypt and Singapore.

The Dean’s list for 2007 was announced in the first half of 2008, further verifying that our graduates are producing high-quality research outcomes. Of the 22 students who had their degrees conferred in 2007, eight appeared on the Dean’s list, which is particularly impressive as this represents the top 10 percent of theses for any given year. Congratulations must go to Melissa Davis (Teasdale group), Christian Gruber (Craik group), Julitta Imperial (Alewood group), David Hird (Hankamer group), Jason Kay (Stow group), Marian Loughnan (Lewis group), David Ireland (Craik group), Jason Kay (Stow group), Ranjala Ratnayake (Capon group) and David Woodford (Hankamer group) for their outstanding theses.

A number of other students also received accolades throughout the year. Some of the highlights are given in table 2 on page 65. Of particular note were the achievements of Ms Maggie Gentz from King group. Mid-year, she was chosen to become a “2008 Young Science Ambassador” by the Australian Academy of Technological Sciences and Engineering and in this role has already visited Rosewood, Cunnamulla and Charleville (State High Schools to bring her research to the next generation of young scientists. Together with Michael Tallack (Perkins group), she was chosen as an IMB finalist in the inaugural UQ Graduate School “3 Minute Thesis” competition and together with Caroline Hopkins (Little group) was a “Women in Technology” award finalist for the Griffith Biotech PhD Career Start Award. In July this year she was an invited speaker at the International Congress on Entomology, Durban, South Africa and in November was an invited speaker at the Entomological Society for America, receiving the Fair Graduate Student Award in Insect Physiology, Biochemistry, or Molecular Biology. In addition, she was instrumental in instigating the IMB Science Ambassadors Program, which will have its pilot year in 2009. Twenty-four Early Career Researchers (ECRs) at IMB have been chosen to take part in this program, which aims to both develop a training program for ECRs to heighten communication skills, useful when dealing with both the media and members of the public, and provide a vehicle for formally acknowledging those young researchers who regularly assist in showcasing the IMB’s research to the community. There will be more about this exciting new initiative in the 2009 annual report.

Our honours cohort was again smaller than usual for 2008 and, as with our RHD students, was distributed such that nearly half the students commenced their honours study mid-year. We had 15 students commencing in February 2008, six students who carried over from July 2007 and six others who commenced July 2008.

As in previous years, 80 percent of those students completing their year in 2008 obtained a grade of First class honours. The Amgen Award, for the most outstanding honours student at the IMB in 2007, was presented in 2008 by Ms Bronwyn Shanahan from AMGEN Australia Pty Ltd to Ms Pa Ching Regina low from Professor Jenny Stow’s group, Regina, whose honours project involved establishing and optimising a high-content screening assay for TNF trafficking and secretion in macrophages, completed her honours year in mid-2007 and commenced a PhD in the Stow group later that year. Apmen Australia has been presenting our honours students with this award for over a decade and we are thrilled by their continued support of our young researchers.

The IMB continued the Undergraduate Research Scholarship Scheme (URSS) in 2008, placing 22 second-and third-year students in laboratories within one of our divisions for eight hours per week during semester. Additionally, a number of third-year students completed mini-research projects as part of the “Introduction to Research” module of their degrees and several Advanced Studies students completed research projects as part of their program. We also placed 12 students in summer projects of 6-10 weeks duration as part of newly launched UQ Summer Vacation program, which attracted students from as far afield as New Zealand to the IMB. Once again, we hosted many international students who joined IMB for up to one year as occupational trainees, undertaking overseas research placements as part of their degree requirements within their home institution. We also welcomed a number of year 10 and 11 students from schools throughout Queensland to undertake a brief period of work experience within research laboratories.
Our IMB Student Association, SIMBA, continued to organise a host of social events and bonding exercises, which reinstate our student body’s cohesive identity within the institute. These included the SIMBA- and IMBcom-sponsored “Great Debate” which, much to everyone’s delight, positioned whether we should “Bring the science sexy back into science”. The affirmative team, comprising PhD student Rohan Wirajudith and his PhD supervisor, Professor Andrew King, and Dr Matt Sweet namely defeated the negative team of PhD student Kate Ewan, group leader Professor Jenny Martin and the IMBcom’s Zachary King. Many thanks to Andrew Nissoke (2007 SIMBA secretary) and Dr Pieter Isido (CDE IMBcom) for instigating the debate, which we hope now will become an annual event! Just prior to this, SIMBA ushered in a new Executive at their AGM in July and we welcomed to the helm: Jonathan Robson (President), Ruth Thiagarajan (Vice-President), Erin Aherne (Secretary), Lena Constantin (Treasurer), Emily Knauth (SIMBAzine Editor-in-Chief) and Robert McLeay (Webmaster). This Executive continued with the energy of the last, and the second annual IMB/ABRI inter-institute Trivia Evening, this year sponsored by IMVigor (which ABRI won) and providing opportunities to collect the Calamity Olivia and the Halloween Olaf. They also became involved with the honours recruitment session held in September: running tours and providing information for prospective students. The IMB Early Career Researcher (ECR) Committee continued to organise the Institute-wide Monday Midday Meetings and arranged for ECRs to lunch with speakers after their Friday Seminar Series as part of a new IMB-funded initiative. During 2008, the members of the ECR committee were postdocs Dr Johanna Barley, Dr Michael Hanley-Bayer, Dr Mathias Francois, Dr Andrew Brooks, Dr Richa Dave, Dr Kari Khassani, and PhD students Evan Stephen and Simon Wurkhin.

The Postgraduate Program continued to run a set of workshops designed to assist students in overall career development. These included IMBcom’s three-day “Biobusiness Retreat” for the third-years, which was held in 2008 from April 2 to April 4 at Noosa Springs Resort, Noosa Heads. Once again, feedback from the retreat was extremely positive, with students really enjoying the mentoring sessions, the networking opportunities and career advice. We ran both a basic and advanced statistics course with Carl Shawed and the Bioethics Workshop for first-years, run by Dr Lucy Carter and Ms Angela Wallace, which this year discussed “Tissue Engineering, a some ethical considerations”. An information session covering fellowship applications was conducted by our Grants Officer, Michelle Foley, in November, and Bromyn Adams, our Communications Officer, organised a half-day workshop on communication skills and media training, run by Ms Jan King, the UQ Communications Manager, and her team.

2008 continued to be a time of change for the UQ Graduate School, with the RHD offices initiating further changes in practices, which are set to continue in 2009. One of the biggest changes for 2008 was the move to compulsory electronic thesis submission, a first for an Australian university. Students now lodge their thesis for assessment in electronic form only and the final approved copy, housed by UQ, is also kept in this form (no longer hard copy). Assessors may of course request a hard copy of the thesis for examination, which is supplied from the Theses Office, but the student is no longer required to supply this at any stage during the assessment process. Other noted changes impacted positively on our International students. Due to a change in the way UQ handles international student costs, it has become more straightforward for schools to apply for fee-waiver scholarships (UQRTA) for students of callibre who are in receipt of merit-based stipend scholarships. In the past, because the number of IPRS and UQRTA scholarships was restricted to a total of 50 university-wide and assigned as part of the annual IPRS round, many gifted students were not funded by this scheme. The ability of a school to apply for an UQRTA, through a nomination process, has relieved research budgets from the cost of student fees for many of our best students. In addition, as of September 2008, the IPRS/UQRTA scholarships round became continuous. Students can apply for scholarships at any time throughout the year provided they have a unconditional offer of entry into the RHD program. This is in line with changes made to the APA/UQRTA scheme in late 2007. Another major change, which will be in effect by 2009, is the introduction of the Candidate Milestones, which are set to replace annual progress reports. During 2008, after much discussion at the Academic Board’s UQ RHD Committee, in which our Postgraduate Coordinator, Professor Rob Capon, took an active role, UQ policies were formulated to cover both the Milestones and RHD recruitment. A letter from SIMBA was lodged with (and well received by) the committee as part of the ongoing debate during the development process. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports. Schools are now developing guidelines defining how the Milestones will be set to replace annual progress reports.

The IMB, once again, has been extremely fortunate to have Professor Rob Capon continue in his role as the IMB Postgraduate Coordinator and IMB representative on the UQ RHD Committee of the Academic Board. Rob’s commitment to and vision for the UQ RHD Program has ensured that it continues to move forward in a proactive and directed way to help deliver to our students the best possible research experience.

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VISITING SPEAKERS

PROFESSOR TED BAKER
University of Auckland, New Zealand
“Crystallography and the world around us”

DR SUJESH-KUMAR BALASUBRAMANIAN
School of Integrative Biology, The University of Queensland
“Exploiting natural variation to dissect the genetic basis of complex developmental traits”

DR GARY BROOKE
Mater Medical Research Institute, Brisbane
“Mesenchymal stem cells: from bench to clinic!”

ASSOCIATE PROFESSOR BERNIE CARROLL
School of Land, Crop and Food Sciences, The University of Queensland
“Intercellular RNA signalling in plants”

PROFESSOR ROBERT FREEDMAN
Warwick University, Coventry, United Kingdom
“Protein disulphide-isomerase – still trying to find how it works!”

DR BRYAN FRY
OEI Research Fellow, Department of Biochemistry and Molecular Biology, Bio21 Institute, Melbourne, Victoria
“Central role for venom in predation by the Komodo Dragon and extinct giant Megalania”

PROFESSOR JOHN FUNDER AO
Prince Henry’s Institute of Medical Research, Melbourne, Victoria
“Translational research goes both ways: lessons for basic biology from clinical studies”

DR MAXIMILLIAN FÜRTHAUER
University of Geneva, Switzerland
“Cell division and signalling: a relationship in development”

DR BEN HOGAN
Norwich Research Park, United Kingdom
“The secret life of salmonella in epithelial cells: unexpected insights from a transcriptional approach”

DR BEN JOKAN
Hubrecht Institute for Developmental Biology, Utrecht, The Netherlands
“Embryonic lymphangiogenesis: new insights from zebrafish”

DR PAUL HORTON
Computational Biology Research Centre, Tokyo, Japan
“Mitochondrial beta-signal: the end of the story?”

DR LEVON KHACHIGIAN
University of New South Wales, Sydney
“A role in pathogenesis for the transcription factor NmIR: oxidative and nitrosative stress response”

DR STEPHEN KIDD
Walter and Eliza Hall Institute, Melbourne, Victoria
“The molecular regulation of platelet life span”

PROFESSOR LEVON KHACHIGIAN
Centre for Vascular Research, University of New South Wales, Sydney
“Immediate-early genes as master regulators of angiogenic, inflammatory and proliferative disorders”

PROFESSOR JAY HINTON
Victor Chang Cardiac Research Institute, Sydney, New South Wales
“Molecular pathways in heart developmental and congenital heart disease”

DR LAURA HOPKINS
University of Melbourne, Victoria
“Iron is hot: the molecular basis of iron regulation and its disorders”

DR BENJAMIN KILE
Walter and Eliza Hall Institute, Melbourne, Victoria
“The molecular regulation of platelet life span”

DR LUKE GIUDDAT
School of Molecular and Microbial Sciences, The University of Queensland
“Branch chained amino acid biosynthesis- structural studies”

DR MICHAEL J. KELSO
University of Wollongong, New South Wales
“Combating antimicrobial drug resistance – looking to nature for clues”

ASSOCIATE PROFESSOR JEAN-PIERRE LEVESQUE
Mater Medical Research Institute, Brisbane
“Behaviour of haematopoietic stem cells is governed by their niches”

PROFESSOR ROB LEWIS
Director, Monash Centre for Synchrotron Science, Monash University, Melbourne
“The use and importance of synchrotrons in biomedical research”

PROFESSOR CHRISS MARSHALL
Institute of Cancer Research, Chester Beatty Laboratories, London, UK
“Who family GTPases, actomyosin contractility and cell migration”

DR BERNARD MATHEW
John Curtin School of Medical Research, Australian National University, Canberra, Australian Capital Territory
“Genetically manipulated mos: providing all the answers, or just more problems?”

DR ALBERT S. MELLICK
University of Sydney, New South Wales
“Out on a LIM: protein interactions in disease and development”

DR BETH McGRAW
School of Integrative Biology, The University of Queensland
“Beyond the gonads: a broader view of the Wolbachia by insect host interaction”

DR ALBERT S. MELLIUK
School of Medical Science, Griffith University, Brisbane
“Small non-coding RNAs, bone marrow stem cells and cancer”

PROFESSOR CHRISTINA MITCHELL
Head, Department of Biochemistry, Monash University, Melbourne, Victoria
“Regulation of PI3-kinase signalling in macrophages”
Further underlining the Institute’s commitment to research excellence, IMB Group Leaders collaborate extensively with partners both within Australia and internationally. The IMB is a core partner and participant in many research centres around the country, including three Major National Research Facilities (MNRFs) and two Cooperative Research Centres (CRCs). These programs are integral to building Australia’s national and international research capabilities. They aim to create the scale and focus necessary to maintain and develop Australia’s world-class standing in priority areas through highly innovative research that addresses challenging and significant problems. CRCs and COEs make vital contributions to Australia’s research landscape and produce outcomes with economic, social and cultural benefits to the country. Involvement in these ventures reflects very highly on the participating researchers, indicating the value of their work in both scientific and commercial terms.

**ARC SPECIAL RESEARCH CENTRE FOR FUNCTIONAL AND APPLIED GENOMICS**

The ARC Special Research Centre for Functional and Applied Genomics was funded in 2000 to provide and develop technologies that enable world-class research in the field of genomics. An integrated network of core technology units was established and their services have supported the research of local and national researchers and biotechnology companies for the past nine years. Funding for the SRC ended on 31st December 2008 but several of the more established facilities including the Microarray Facility, the Protein Expression Facility, the Biodiscovery Unit, the Mass Spectrometry Facility and TASQ (the Transgenic Animal Service Queensland) will keep operating, allowing researchers continued access to state of the art infrastructure and expertise in these areas.

**AUSTRALIAN PHENOMICS FACILITY**

The Australian Phenomics Facility (APF) is based at the John Curtin School for Medical Research and is a Major National Research Facility (MNRF) formed by support from the IMB, the Australian National University and the Garvan Institute for Medical Research. The APF is focused on the use of mouse genetics to discover novel genes that influence traits of medical relevance. Large populations of mice are exposed to a mutagen, traits are identified and selected and then genetic mapping is used to locate the general regions where the genes reside. The mutagen used to create the mutants leaves a particular genetic fingerprint that can be discerned by sequencing candidate genes, thus identifying the gene responsible for the trait under consideration. This is a powerful approach to biology, enabling gene function to be elucidated based upon the high-throughput analysis of phenotypes ("phenomics").

**ARC CENTRE OF EXCELLENCE IN BIOTECHNOLOGY AND DEVELOPMENT**

The ARC Centre of Excellence in Biotechnology and Development (CBD) was established in 2003 to focus on the biology of male germ cells – embryonic stem cells that eventually produce sperm cells in man. A review of the Centre in 2007 confirmed its status as a Centre of Excellence, and extended its funding for a further three years. Collaborating institutions include the IMB, the Universities of Queensland, Melbourne, and Newcastle, Monash University and the Australian National University. Unlike many other types of stem cells, germ cells represent a truly "blank slate" that can develop into any tissue in the body. Understanding their specification and programming is central to contemporary efforts to harness stem cell technologies. Since male fertility depends on generating sperm cells in vast numbers, and since genetic and environmental factors commonly disturb the quantity and quality of sperm produced, the research will further impact on understanding and possible treatment of infertility, a distressing condition that represents a massive healthcare burden in Australia and worldwide. Disorders of germ cells are often accompanied by testicular cancer, and so the potential medical significance of this research is profound. It has become increasingly clear that manipulating the quantity and/or quality of germ cells, particularly male germ cells, presents powerful opportunities in the pest management arena, and in other biotechnological pursuits such as the management of endangered wildlife species.

**ARC CENTRE OF EXCELLENCE IN BIOINFORMATICS**

The ARC Centre of Excellence in Bioinformatics, with headquarters at IMB, brings Australian and overseas researchers together into interdisciplinary programs designed to explore how information in the
In the establishment of the Queensland node of the ASCC at The University of Queensland and with the aid of a grant from the Australian Cancer Research Foundation (ACRF), the Centre was formed as a collaboration between the CRC and the Queensland State Government. Professor Melissa Little and Professor Rob Capon have also received revenue from both the ASCC and the Queensland State Government to establish high content screening of embryonic stem cells using the unique chemical compound libraries within the IMB.

The IMB is a core participant in the CRC for Chronic Inflammatory Diseases (CRC-CID), whose partners are Monash University, The University of Melbourne and AstraZeneca. The major objective of the CRC is to discover new molecular targets involved in the pathogenesis of chronic inflammatory lung and joint disease and use this information to develop novel treatments for these disorders. The CRC is using gene microarrays, proteomics, cell-based assays and genetically-modified animal models of disease to understand how macrophages cause chronic inflammation. The CRC is structured to facilitate the entire drug discovery cycle: primary target identification using functional genomics; and proteomic approaches, target validation in disease models and human tissues; high-throughput cell-based assay development, lead target screening, generation of therapeutic and research antibodies, and the development of macromolecule-targeted drug delivery strategies.

Australasian Invasive Animals CRC

Australasian Invasive Animals CRC is a venture aiming to counteract the impact of invasive animals through the development and application of new technologies and integrating approaches across agencies and jurisdictions. It is the first time that research, industry, environmental, commercial and government agencies have combined to create and apply solutions for invasive animal threats, which cost Australia at least $270 million per annum. This unique partnership will deliver the means to deal with existing high-profile invasive animal pests as well as those that have the potential to cause catastrophic impacts in the future. Professor Peter Koopman from the IMB currently serves on the advisory board for the Daughtercell Car Program of the AARCC. This program, based at CSIRO fisheries in Hobart, uses innovative technologies with a view to skewing the sex ratios of wild populations of the common carp, one of the most widespread threats to indigenous fish species in our large waterways. Professor Koopman’s laboratory is also expanding this program, under the auspices of the CRC, to develop a similar management strategy for the cane toad, currently ecological public enemy number one in Queensland.

Australian Microscopy & Microanalysis Research Facility

The Advanced Cryo-Electron Microscopy Laboratory – the Queensland node of the Australian Microscopy & Microanalysis Research Facility – is housed in a purpose built facility at IMB. This MNRF was formed as a collaboration between the Universities of Queensland, Western Australia, Melbourne, New South Wales and Sydney. The facility, which includes a 300kV Technical microscope, is currently the only one in Australia or New Zealand capable of collecting and processing atomic resolution images at low temperature, as well as undertaking a 3D electron microscopy (EM) tomography of organelles, cells and tissues at both ambient and low temperatures. Only a handful of international and no other Australian laboratories can offer researchers equivalent state-of-the-art research tools for high-resolution 3D imaging of cells and tissues. The AMMRF is a successor to the Nanostructural Analysis Network Organisation (NANO).

Australian Stem Cell Centre

The Australian Stem Cell Centre (ASCC) is a national Biotechnology Centre of Excellence funded by the federal Department of Industry, Innovation and Science and the Australian Research Council and initially created in 2001. While establishing laboratories at Monash University, it has now expanded to create a node of activity at The University of Queensland. The ASCC funds research in both adult and embryonic stem cells, with the long term aim of translating this research to outcomes. The IMB has very close links with the ASCC. Professor Melissa Little was seconded to the ASCC in 2007 as its Chief Scientific Officer, where she was responsible for scientific strategy, scientific review and management. She was also instrumental in the development of the QFAB. This program has shifted focus towards the elucidation of transcriptional control networks. Both activities have involved the establishment of large international consortia, firstly the FANTOM consortium (Functional Annotation of Mouse), and more recently the Genome Network consortium. The consortium has previously published a comprehensive analysis of the human and mouse transcriptomes, resulting in a series of papers in Nature Genetics, PLoS Genetics, PLoS Computational Biology, Genome Biology and Genomics.

The Australian Genome Research Facility (AGRF) is an MNRF of the Commonwealth Government and was established in 1996 through a government appropriation by Professor John Mattick, who served as the inaugural director until 2002, and Board Member until 2004. Professor Brandon Wainwright currently serves on the AGRF Board. The AGRF is a state-of-the-art facility for the collection of molecular genetic information covering large-scale DNA sequencing, genotyping, microarrays, agricultural genomic services and other resources for the genetic and physical mapping of chromosomes, mutation detection and associated bioinformatics analysis. It serves several hundred research groups across all states and territories of Australia from nodes at The University of Queensland, the Walter and Eliza Hall Institute of Medical Research in Melbourne, and the Walter and Eliza Hall Institute of Medical Research in Melbourne, and the Walter and Eliza Hall Institute of Medical Research in Melbourne. The Qiagen’s international expertise in wet and dry lab equipment and technology allows researchers to dissect cancerous and non-cancerous cells and reconstruct them in 3D, revealing much greater detail about their inner workings. Researchers can now also examine a vast range of proteins at the same time and examine their dynamic in live cells over time.

Riken

Riken is the Institute for Physical and Chemical Sciences of the Japanese Science and Technology Agency, and a major site of genomics research in Japan. Professor John Mattick has a visiting scientist appointment at Riken. The Riken Genome Sciences Center is based at Yokohama and Tokyo. In the late 1990s, Riken established a program aimed at elucidating the complete transcriptional output of the mouse. More recently, the program has shifted focus towards the elucidation of transcriptional control networks. Both activities have involved the establishment of large international consortia, firstly the FANTOM consortium (Functional Annotation of Mouse), and more recently the Genome Network consortium. The consortium has previously published a comprehensive analysis of the human and mouse transcriptomes, resulting in a series of papers in Nature Genetics, PLoS Genetics, PLoS Computational Biology, Genome Biology and Genomics.

Queensland Facility for Advanced Bioinformatics (QFAB)

QFAB was established in 2006 with a $1.9 million Queensland State Government grant and is based at the IMB. It is rapidly becoming a leader in supporting the bioinformatics requirements of research-intensive universities, institutions and companies, beyond the capability of any single organisation in Australia or the Asia-Pacific region. It provides the bioinformatics, ICT, research biology and clinical community with secure access to the tools and the knowledge to efficiently deliver relevant solutions. Its projects cover: programmatic access to large data sets and tools, data integration and workflow technology for biological and health data, mirror site for genome browsers, annotation pipelines and workflows for biological and health data, genome and proteome linkages, analysis and visualisation of biological data and building and using web-based tools.

Network for Pancreatic Organ Donors With Diabetes (NPOD)

NPOD is an initiative of the Juvenile Diabetes Research Foundation International (JDRF) and brings together organ procurement organisations, academic researchers and leading diabetes researchers from Europe and America. The only Australian node is at the IMB, led by Professor Thomas Kay at St Vincent’s Institute and Peter Colman at the Royal Melbourne Hospital. One goal of the NPOD program is to establish a similar initiative among groups leading type 1 diabetes research within Australia.
The IMB website remains the main source of information about the Institute for external stakeholders. When “molecular bioscience” is searched in Google, the IMB is the number one response, a position it has held consistently throughout the past few years. In 2008, the website received over 260,000 visits, resulting in over 1.25 million page views. The IMB website is also a repository for all of IMB’s media releases and newsletters. These provide another avenue for disseminating information about the Institute, and during 2008, substantial donations were received to the Institute as a result of media coverage.

IMB researchers volunteered at several events organised by UQ throughout the year, notably UQ’s Open Day and the Ekka. St Lucia Open Day attracted nearly 16,000 people to the St Lucia campus of the university. IMB staff were on hand to give information to prospective students, and PhD students Pahan Villani (Wairwright group) and Adam Costin (Marsh group) conducted tours of the IMB. An encouraging sign was the fact that tour numbers doubled from the 2007 figures. IMB students also volunteered at the Ekka, or the Royal Brisbane Show as it is officially known, with Denis Bauer (Bailey group), Conor Sicily (Farina group), Brooke Gardiner (Glirmond group) and Britt Winnan (King group) helping children extract DNA from strawberries at the UQ stand. IMB staff made up “showbags” for stand visitors to take home, containing IMB merchandise, handouts with science activities and information for parents, which proved to be very popular.

Open Day was not the only time that people toured through the IMB. Various interest groups, including primary and high school classes, international university representatives, industry members, dignitaries and politicians came through the facility. IMB welcomes enquiries from groups wishing to tour the Institute; please email imb@imb.uq.edu.au in the first instance.

IMB researchers engaged with the community in a number of ways in 2008. Maggie Gentz from the King group was chosen as an Australian Academy of Technological Sciences and Engineering Young Science Ambassador. In this role, she visited Charleville State High School, Cunnamulla State High School and Rosewood State High School, as well as attending a Science-in-Parliament workshop on nanotechnology and speaking at the ATSE Queensland Annual Meeting.

Five IMB scientists participated in the “Scientists in Schools” program, which pairs scientists with teachers and brings real-life science in the classroom. Dr Brad Marsh joined classes at Gracemere State School and Richmond State School; Adi Irids went to Wooloowin State School, Dr Horst Schirra teamed with Junction Park State School, Andrew Noske went to Wilston State School and Peter van der Heide partnered with Mansfield State High School.

The Queensland State Government launched a program called “Talking Scientists” which aimed to link up community groups looking for interesting speakers with scientists. Sixteen IMB researchers signed up for this program, and Professor Brandon Wairwright was asked to give a talk to a Rotary group in Townsville. 2009 should present further opportunities for these scientists to give talks, with Maggie Gentz already scheduled for a talk in Toowoomba.

In the past, IMB has usually engaged with others through existing channels, such as those outlined above, rather than duplicating the efforts of valuable existing programs. However, it was decided in 2008 that the Institute had reached a level of maturity where it would be useful to have its own ambassadors, and to engage proactively with the community. As a result, the IMB Science Ambassadors program was created.

Science Ambassadors will receive training in media and community engagement, and will serve the IMB in a number of ways, for example, participating in outreach activities, taking tours, supervising work experience students and creating educational resources. The pilot cohort of ambassadors will also help shape the program, and make suggestions on how it can be developed in the future. Applications were called for late in 2008 and the first cohort of 24 early career researchers has been chosen. They will begin training early in 2009, and their activities and achievements will be outlined in next year’s report.
Kimberly Wadsworth  
Level 5 Floor Manager  
PhD Student

Wendy van Zuylen  
Research Officer  
Undergraduate Intern

Mitchell Sullivan  
Group Leader

Rohan Teasdale  
Research Officer

Brandon Wainwright  
PhD Student

Liam Town  
Undergraduate Student

Ernest Tee  
Research Assistant

Shivangi Wani  
Honours Student

Elanor Wainwright  
Research Assistant

Terje Svingen  
Group Leader

Mike Waters  
Research Officer

Andrea Vernal  
Honours Student

Winne Waudo  
Kathryn Tunny  
Group Leader  
Research Assistant

Matt Sweet  
Research Officer  
Masters Student

Rathi Thiagarjan  
Level 6 Floor Manager

Jane Weber  
Research Officer  
Receptionist

Ronda Turk  
Research Officer

Irina Vetter  
Research Officer

Piers Walser  
Research Officer

Irene Vissers  
Research Officer

Ryan Taft  
Research Officer

Jack Wang  
Research Officer  
PhD Student

Nicola Waddell  
Research Officer

Nicole Wheatley  
Research Officer

Zakir Tnimov  
Research Assistant

Jan Westermann  
Research Assistant

Tom Taguchi  
Research Assistant

Chia-Chia Tan  
Research Officer

Mark Tallack  
Research Officer

Chung-Wei (Jimmy) Wu  
Research Officer

Danielle Wilson  
Research Officer

Kellie Broderick  
Officer  
Manager, Infrastructure

David Wood  
PhD Student

Stephanie Wood  
Research Officer

Simon Wilkins  
Research Officer

Karen Yong  
Undergraduate Student

Zheng Yuan  
Research Officer

Danielle Wilson  
Research Officer

Jodie McNab  
Company Accountant

Leah Creed  
Research Officer

Aijun Yang  
Research Officer

David Wilson  
Research Officer  
PhD Student

Jenny Zhang  
Company Accountant

Chung-Wei (Jimmy) Wu  
Research Officer

Chen Yang  
Research Officer

Chris Price  
Executive Assistant

Lyn Rosen  
Executive Assistant

Ujjwal Dua  
Officer  
Commercialisation & Education Manager

Chris Price  
Chief Executive Officer

Diana Schaeffer  
Systems Administrator

Amanda Smith  
IP & Operations Manager

Leigh Lambert  
Senior Research Systems Administrator

Karen Soxsmith  
Systems Administrator

Noi Inthasan  
Senior Research Systems Administrator

Karen Saxby  
Postdoctoral Research Investigator

Leanne Sander  
PhD Student

Leanne Samson  
Research Officer

Rebecca Saxby  
Research Officer

Lisa Schiffler  
Research Officer

Shirley Sayler  
Research Officer

Susan Sayler  
Research Officer

Karen Sayler  
Research Officer

Susannah Sayler  
Research Officer

Leigh Schiffler  
Research Officer

Beth Schiffler  
Research Officer

Katie Schiffler  
Research Officer

Catherine Schiffler  
Research Officer

Karen Sayler  
Research Officer

Leigh Schiffler  
Research Officer

Beth Schiffler  
Research Officer

Katie Schiffler  
Research Officer

Catherine Schiffler  
Research Officer

Karen Sayler  
Research Officer

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Research Officer

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Research Officer

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Research Officer

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Research Officer

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Research Officer

Katie Schiffler  
Research Officer

Catherine Schiffler  
Research Officer

Karen Sayler  
Research Officer

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Research Officer

Beth Schiffler  
Research Officer

Katie Schiffler  
Research Officer

Catherine Schiffler  
Research Officer

Karen Sayler  
Research Officer

Leigh Schiffler  
Research Officer

Beth Schiffler  
Research Officer

Katie Schiffler  
Research Officer

Catherine Schiffler  
Research Officer

Karen Sayler  
Research Officer

Leigh Schiffler  
Research Officer

Beth Schiffler  
Research Officer

Katie Schiffler  
Research Officer

Catherine Schiffler  
Research Officer

Karen Sayler  
Research Officer
### Statement of Operating Income and Expenditure – Year ended 31 December 2008

#### Income:

<table>
<thead>
<tr>
<th>Source of Income</th>
<th>2004</th>
<th>2005</th>
<th>2006</th>
<th>2007</th>
<th>2008</th>
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</thead>
<tbody>
<tr>
<td>University of Queensland (Operating Grant)</td>
<td>1,687,000</td>
<td>7,205,765</td>
<td>10,267,311</td>
<td>11,547,942</td>
<td>11,982,919</td>
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<tr>
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<td>259,323</td>
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<td>193,291</td>
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<td>10,170,000</td>
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<td>10,857,603</td>
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<tr>
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<td>4,261,849</td>
<td>4,744,519</td>
<td>5,218,279</td>
<td>6,010,239</td>
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<td>Arthritis Foundation of Australia</td>
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<tr>
<td>Australian Cancer Research Foundation</td>
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<td>600,000</td>
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<td>0</td>
<td>0</td>
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<td>79,757</td>
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<td>159,780</td>
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<td>772,965</td>
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<td>Close and Near Rainforest Foundation</td>
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<td>0</td>
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<tr>
<td>Community Health &amp; Tuberculosis Australia</td>
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<td>120,216</td>
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<tr>
<td>CRC for Discovery of Genes for Common Human Diseases</td>
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<td>CRC for Chronic Inflammatory Diseases</td>
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<td>1,367,457</td>
<td>1,326,058</td>
<td>1,462,776</td>
<td>1,214,510</td>
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<td>Dairy Australia</td>
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<td>203,765</td>
<td>167,644</td>
<td>700,321</td>
<td>333,084</td>
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<td>200,000</td>
<td>135,000</td>
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<td>Department of Primary Industries</td>
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<td>0</td>
<td>50,000</td>
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<tr>
<td>Department of Industry Science and Technology</td>
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<td>0</td>
<td>45,000</td>
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<td>Human Frontiers Science Program</td>
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<td>51,486</td>
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<td>The John Trivett Foundation</td>
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<td>Juvenile Diabetes Foundation International</td>
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<td>177,814</td>
<td>176,645</td>
<td>147,708</td>
<td>115,723</td>
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<td>0</td>
<td>0</td>
<td>0</td>
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<tr>
<td>The Merck Genome Research Institute</td>
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<td>0</td>
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<td>0</td>
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<td>The Murdoch Institute</td>
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<td>0</td>
<td>0</td>
<td>0</td>
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<td>National Health and Medical Research Council</td>
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<td>5,218,279</td>
<td>11,554,142</td>
<td>12,445,654</td>
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<tr>
<td>New Zealand Dept Science &amp; Technology</td>
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<td>0</td>
<td>0</td>
<td>40,738</td>
<td>0</td>
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<td>Novartis</td>
<td>0</td>
<td>0</td>
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<td>0</td>
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<td>Post Graduate Scholarships</td>
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<td>140,237</td>
<td>261,263</td>
<td>305,355</td>
<td>234,520</td>
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<td>140,000</td>
<td>215,100</td>
<td>148,700</td>
<td>310,000</td>
<td>554,520</td>
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<td>Sylvia and Charles Viertel Charitable Foundation</td>
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<td>0</td>
<td>0</td>
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<tr>
<td>University of Newcastle (Re Arc Centre)</td>
<td>127,893</td>
<td>47,727</td>
<td>252,562</td>
<td>128,218</td>
<td>153,218</td>
</tr>
<tr>
<td>University of Newcastle (Re Arc Centre)</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
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<tr>
<td>Wellcome Trust</td>
<td>140,376</td>
<td>152,311</td>
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<td>0</td>
<td>0</td>
</tr>
<tr>
<td>University of Newcastle (Re Arc Centre)</td>
<td>1,473,905</td>
<td>1,856,012</td>
<td>2,018,054</td>
<td>4,880,234</td>
<td>4,585,965</td>
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<tr>
<td>Cross-institutional Contributions to List or Facilities</td>
<td>192,800</td>
<td>60,000</td>
<td>529,472</td>
<td>188,000</td>
<td>50,000</td>
</tr>
<tr>
<td>University of Newcastle (Re Arc Centre)</td>
<td>127,893</td>
<td>47,727</td>
<td>252,562</td>
<td>128,218</td>
<td>153,218</td>
</tr>
<tr>
<td>GRP Passovers</td>
<td>312,979</td>
<td>260,382</td>
<td>256,680</td>
<td>4,000</td>
<td>40,738</td>
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<td>Shared Investigator</td>
<td>128,764</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
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<tr>
<td>Conference Income</td>
<td>25,501</td>
<td>72,608</td>
<td>66,185</td>
<td>184,340</td>
<td>70,508</td>
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<td>GRD $/Kau</td>
<td>44,021</td>
<td>247,890</td>
<td>274,819</td>
<td>314,057</td>
<td>326,215</td>
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<tr>
<td>QMB Research Institute</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>18,423</td>
<td>0</td>
</tr>
<tr>
<td>Miscellaneous Income</td>
<td>355,652</td>
<td>416,707</td>
<td>369,887</td>
<td>357,293</td>
<td>341,778</td>
</tr>
<tr>
<td><strong>TOTAL INCOME</strong></td>
<td>36,349,512</td>
<td>41,265,778</td>
<td>43,338,729</td>
<td>52,967,307</td>
<td>52,580,186</td>
</tr>
</tbody>
</table>

#### Funds brought forward from previous year:

<table>
<thead>
<tr>
<th>2004</th>
<th>2005</th>
<th>2006</th>
<th>2007</th>
<th>2008</th>
</tr>
</thead>
<tbody>
<tr>
<td>6,746,999</td>
<td>6,557,150</td>
<td>9,050,612</td>
<td>11,441,270</td>
<td>15,641,004</td>
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<tr>
<td><strong>TOTAL FUNDS AVAILABLE</strong></td>
<td>43,096,511</td>
<td>47,822,929</td>
<td>52,389,341</td>
<td>64,408,577</td>
</tr>
</tbody>
</table>

#### Expenditure:

<table>
<thead>
<tr>
<th>Category</th>
<th>2004</th>
<th>2005</th>
<th>2006</th>
<th>2007</th>
<th>2008</th>
</tr>
</thead>
<tbody>
<tr>
<td>Salaries - Research</td>
<td>16,195,354</td>
<td>18,430,158</td>
<td>20,110,376</td>
<td>22,878,237</td>
<td>24,750,517</td>
</tr>
<tr>
<td>Salaries - Administration</td>
<td>1,243,375</td>
<td>1,343,782</td>
<td>1,205,466</td>
<td>1,349,056</td>
<td>1,345,709</td>
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<tr>
<td>Salaries - Infrastructure</td>
<td>3,137,860</td>
<td>2,383,622</td>
<td>1,942,902</td>
<td>3,280,429</td>
<td>2,940,237</td>
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<tr>
<td>Research Services</td>
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<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Education Programs</td>
<td>4,418,784</td>
<td>375,177</td>
<td>369,445</td>
<td>332,919</td>
<td>380,735</td>
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<tr>
<td>Administration</td>
<td>5</td>
<td>379,357</td>
<td>522,612</td>
<td>521,743</td>
<td>486,666</td>
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<tr>
<td>Corporate Services (UD)</td>
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<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Infrastructure</td>
<td>6,172,940</td>
<td>1,287,442</td>
<td>1,290,139</td>
<td>1,862,013</td>
<td>2,160,062</td>
</tr>
<tr>
<td>Capital Expenditure</td>
<td>7,531,215</td>
<td>2,339,215</td>
<td>2,688,825</td>
<td>5,156,825</td>
<td>5,484,525</td>
</tr>
<tr>
<td><strong>TOTAL EXPENDITURE</strong></td>
<td>36,317,300</td>
<td>36,372,016</td>
<td>40,560,071</td>
<td>49,767,273</td>
<td>49,765,430</td>
</tr>
</tbody>
</table>

#### Funds carried forward:

| 2008 | 8,957,150 | 9,050,612 | 11,441,270 | 15,641,004 | 16,495,763 |
Explanatory Notes to Statement of Income and Expenditure

1/ A) IN-KIND CONTRIBUTIONS

Figures do not include the following salaries for affiliate appointments paid annually or by other departments:

<table>
<thead>
<tr>
<th>Location</th>
<th>Percentage</th>
</tr>
</thead>
<tbody>
<tr>
<td>K. Burrage</td>
<td>50</td>
</tr>
<tr>
<td>G. McManus</td>
<td>90</td>
</tr>
<tr>
<td>A. Mark</td>
<td>80</td>
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</tbody>
</table>

2/) GROSS INCOME & CORPORATE SERVICES CHARGE

The 2006 Annual Report showed University of Queensland Operating Grant Income as a gross amount and Corporate Services charge shown separately under expenditure. Subsequent years have reverted to the previous method for better direct comparison. 2006 figures have been adjusted accordingly and none show the charge.

3/) FELLOWSHIP/PROJECTS FROM GOVERNMENT AGENCIES

- Postgraduate scholarships 303,623
- Postgraduate recruitment and training 77,110
- Total Education Services 380,733

# Of this, $1.8m is to carry forward on IMB Group Leader core accounts & $0.7m relates to outstanding 2008 equipment commitments. There is also a significant commitment regarding orders placed in 2008 which payment has been deferred to 2009 due to the introduction of a new financial system. This is also the reason for the significantly higher activity in 2008 through Grants.

4/) FINANCIAL STATEMENTS


5/) ADMINISTRATION

<table>
<thead>
<tr>
<th>Item</th>
<th>Amount</th>
</tr>
</thead>
<tbody>
<tr>
<td>Annual Report</td>
<td>9,773</td>
</tr>
<tr>
<td>Marketing</td>
<td>48,954</td>
</tr>
<tr>
<td>Personnel Recruitment and Training</td>
<td>74,824</td>
</tr>
<tr>
<td>Visiting Scientists/ Seminars</td>
<td>36,293</td>
</tr>
<tr>
<td>Fees</td>
<td>9,499</td>
</tr>
<tr>
<td>Quarterly/Annual Review</td>
<td>50,555</td>
</tr>
<tr>
<td>Photocopying</td>
<td>114,879</td>
</tr>
<tr>
<td>Postage and Freight</td>
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</tr>
<tr>
<td>Printing and Stationery</td>
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</tr>
<tr>
<td>Telephone</td>
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</tr>
<tr>
<td>Travel Expenses</td>
<td>15,921</td>
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<tr>
<td>Board Fees</td>
<td>25,240</td>
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<tr>
<td>Total Administration</td>
<td>499,665</td>
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</tbody>
</table>

6/) INFRASTRUCTURE

<table>
<thead>
<tr>
<th>Item</th>
<th>Amount</th>
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</thead>
<tbody>
<tr>
<td>Building Maintenance</td>
<td>199,836</td>
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<tr>
<td>Rental Storage</td>
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</tr>
<tr>
<td>Safety Equipment</td>
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</tr>
<tr>
<td>Laundry</td>
<td>4,562</td>
</tr>
<tr>
<td>Minor Equipment &amp; Furniture</td>
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<tr>
<td>Equipment Maintenance</td>
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<td>Animals</td>
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<tr>
<td>Computer Services</td>
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<tr>
<td>Glass washing and replacement</td>
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<td>Refrigerated rooms, food and dry ice</td>
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<tr>
<td>Cost Recovery</td>
<td>140,823</td>
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<tr>
<td>Stores</td>
<td>742,802</td>
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<tr>
<td>Total Infrastructure</td>
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</table>

7/) CAPITAL EQUIPMENT

<table>
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<th>Item</th>
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</thead>
<tbody>
<tr>
<td>Scientific Equipment</td>
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</tr>
<tr>
<td>Total Capital Equipment</td>
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</table>

9/) FUNDS CARRIED FORWARD TO 2009

<table>
<thead>
<tr>
<th>Item</th>
<th>Amount</th>
</tr>
</thead>
<tbody>
<tr>
<td>University of Queensland Operating Grant</td>
<td>7,468,461</td>
</tr>
<tr>
<td>University of Queensland Research Grants</td>
<td>53,647</td>
</tr>
<tr>
<td>Post Graduate Scholarships</td>
<td>84,768</td>
</tr>
<tr>
<td>State Government</td>
<td>3,036,834</td>
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<td>IRC Grant</td>
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</tr>
<tr>
<td>Fellowships (as approved by funding bodies) 541,548</td>
<td></td>
</tr>
<tr>
<td>Overseas Grants funded mid year</td>
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<tr>
<td>Contract Research</td>
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<tr>
<td>Project Grants (as approved by funding bodies) 1,814,376</td>
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<tr>
<td>Total</td>
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</tbody>
</table>

10/) FUNDS CARRIED FORWARD TO 2009

<table>
<thead>
<tr>
<th>Item</th>
<th>Amount</th>
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</thead>
<tbody>
<tr>
<td>University of Queensland Operating Grant</td>
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<tr>
<td>University of Queensland Research Grants</td>
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<tr>
<td>State Government</td>
<td>53,627</td>
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<tr>
<td>IRC Grant</td>
<td>1,972,609</td>
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<tr>
<td>Fellowships (as approved by funding bodies) 41,502</td>
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</tr>
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<tr>
<td>Contract Research</td>
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</tr>
<tr>
<td>Project Grants (as approved by funding bodies) 3,018,644</td>
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</tr>
<tr>
<td>Total</td>
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</tr>
</tbody>
</table>

GLOSSARY OF TERMS

Ab initio: A calculation made from “first principles”, rather than experimental data.

Actin: A protein, along with myosin, responsible for muscle contraction.

Actin Nucleators: Proteins that increase the rate of growth of actin filaments.

Adipose: Fat or fatty tissue.

Agonist: A molecule that interacts with a receptor, triggering a cellular response.

Allele: One of a number of possible versions of a gene. Each person inherits two alleles per gene, one from each parent.

Antagonist: A molecule that blocks a chemical from binding to its receptor.

Antithetics: Anything that risks the body of parasitic intestinal worms.

Antinociceptive: Counteracts the effect of anything causing pain, in response to pain.

Aptosis: Programmed cell death.

ARC: Australian Research Council.

Assay: Qualitative or quantitative analysis of a substance performed in order to determine its components.

Atrophersis: The process whereby arteries harden and narrow over time.

Bioinformatics: The collection, organisation and analysis of large amounts of biological data using networks of computers and databases.

Bistayer: Two layers of molecules.

Biocatalysis: An effect on a living organism.

Bioinformatics: The use of computational resources in the study of biological information.

Biomimetic synthesis: The use of synthetic methods to synthesise numerous, related chemical compounds.

Compeptide: Peptides found in the marine cone snail.

Conotoxin: A group of toxic peptides isolated from the venom of the marine cone snail.

Cytokine: A molecule that carries the genetic instructions for making a protein.

Dyspepsia: A disorder that occurs when there is an excess of acids in the stomach.

Effector molecules: A molecule that alters the activity of a protein by binding to it.

EPGR: Equal growth rate factor receptor.

Enzyme: A protein produced by living organisms that catalyses chemical reactions of other substances without being altered by the reactions.

Endocytosis: Uptake of material into a cell.

Endosome: An organelle involved in protein trafficking.

Epigenetic: Any technology that uses “first principles” to create something new.

Epifluorescence: A type of microscopy using a very bright light source. This light is used to energise the sample into emitting light (or “fluorescing”) at various wavelengths, which allows researchers to produce an image of the sample.

Epidemic: The collection, organisation and analysis of large amounts of biological data using networks of computers and databases.

Enzymatic synthesis: An artificial process for synthesising chemistry that is inspired by biochemical processes.

Bioscience: Any of the branches of science dealing with the structure and behaviour of living organisms.

Biomimetic synthesis: The use of computational resources in the study of biological information.

Biomimetic synthesis: An artificial process for synthesising chemistry that is inspired by biochemical processes.

Biotechnology: Any technology that uses biological systems or living organisms to make or modify products or processes.

BIPET: Bioluminescence resonance energy transfer. A cell-based assay allowing the direct study of complex protein-protein interactions in living cells.

BSE: Bovine spongiform encephalopathy.

Caveolin: A small pocket extending from the outside to the inside of a cell. Shells of uptake and expulsion of materials into and out of the cell.

Cephalopods: Organisms in the class Cephalopoda, which includes octopuses and cuttlefishes.

Cerebrum: The part of the brain that co-ordinates voluntary movement.

Chelate: An organic molecule that has bonded to a metal to form a ring-shaped structure.

Chromodynamics: The development of cartilages.

Chromatin: The complex of DNA and proteins that form a chromosome.

Chromatography: A method of separating chemical compounds into their base constituents by transporting the compound in liquid form through a porous substance. The different rates of absorbency of the constituents mean that as they pass through the substance they will separate.

Clathrin: The protein that largely forms the vesicle responsible for transportation of proteins into and out of the cell.

CNS: Central/Nervous System.

Combinatorial Chemistry: Methods used to synthesise numerous, related chemical compounds.

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**Glossary of Terms**

**Erythropoiesis** The development of mature red blood cells.

**Eukaryotes** Organisms whose genetic material is enclosed in a membrane-bound nucleus. Includes all organisms except viruses and bacteria.

**Exocytosis** The discharge of material from the cell.

**FACS** Fluorescence-activated cell sorting. A method of sorting a heterogeneous group of cells using the light scattering and fluorescent characteristics of each cell.

**Factor** A sequence of DNA involved in producing a polypeptide chain.

**FRET** Fluorescence Resonance Energy Transfer. A method of quantifying molecular dynamics such as protein-protein interactions.

**Gene** Considered the basic unit of heredity, a gene is a segment of DNA that encodes all of the information to make a protein.

**Genome** All DNA contained in an organism or cell.

**Genomics** The study of genes and their functions.

**Glucose** A six-carbon sugar that is a major energy source for the body.

**GPCRs** G-protein-coupled receptors, the largest family of membrane receptors.

**Histidine** A type of amino acid, which binds to a larger molecule.

**Histone** A protein found in red blood cells that carries oxygen around the body.

**Heterodimer** An organic molecule formed by combining two smaller, different molecules.

**Homologous recombination** Composed of more than one element.

**Histidine** A type of amino acid, which binds to form proteins. Histidine is found in proteins involved in the repair and growth of tissue.

**Homeodomain** A protein motif in a homeobox (a highly-conserved DNA sequence) found in genes that regulate embryonic development.

**Homeostasis** A condition where the body uses negative feedback processes to maintain its systems at a constant equilibrium.

**Homology** Similarity due to common ancestry.

**Homogametic** Refers to a gene in which both copies of an allele are the same.

**Homozygous** Refers to a gene in which both copies of an allele are the same.

**Hypothesis** The multification of cells beyond that which is normal.

**Immunoaffinity chromatography** A process whereby an antigen is formed in a solution using a specific antibody.

**In silico** A process that has been simulated on a computer.

**In situ** In its natural place.

**In vitro** A process occurring in an artificial environment that would normally occur in an organism.

**In vivo** A process occurring within an organism.

**Insulin** A hormone that regulates sugar concentration in the blood.

**Intact Chromosome** Proteins that act as gates in order to control the flow of ions across cellular membranes.

**Irat Cluster** A group of cells in the pancreas that secrete insulin.

**Iosporon** Naturally occurring organic molecules.

**Isothermal calorimetry** A technique of measuring the heat and heat capacity of chemical reactions; often used to characterise potential drug candidates.

**Keratinocyte** Cells that make keratin, a substance found in hair and nails (hard keratin) and skin (soft keratin).

**Kinesin** An enzyme that catalyses the transfer of a phosphate group from a donor to a target molecule.

**Knockdown** A technique in which specific genes are made inactive, so scientists can determine their effect.

**Ligand** A chemical that binds to a larger molecule/receptor.

**Lipid** Any of a group of heterogeneous fat or fat-like compounds that are insoluble in water.

**Loxos** The location of a gene on a chromosome.

**Lymphatic** Pertaining to the circulatory network of vessels that produce and store the cells that fight infection.

**Lymphedema** A condition that occurs when excess lymph fluid collects in a localized area.

**Lysosome** An organelle capable of digesting microorganisms and cellular debris.

**MacroPhage** A large cell that engulfs and detects waste material, harmful microbes or other foreign bodies in the bloodstream and tissues.

**Macropinocytosis** The formation of fluid-filled macropinosomes, large heterogeneous, dynamic vesicles.

**Mass spectrometry** A method of studying the structure and composition of molecules.

**Mechanosensitive channels** Proteins in the membrane that open and close in response to mechanical forces.

**Melanin** The process by which cells divide to produce eggs and sperm.

**Melanoblast** A precursor of a melanocyte.

**Melanocyte** Cells that produce melanin, the pigment that gives skin, hair and eyes their colour.

**Melanogenesis** The production of melanin.

**Membrane** A thin layer of tissue surrounding a cell and separating it from the rest of the environment.

**Mesoderm** The middle layer of cells in the early embryo.

**Metabolism** A chemical involved in or produced during metabolism.

**Metabolic** Relating to all of the metabolites in a sample at any given time.

**Metastasis** Migration of cancer cells from their original site to other parts of the body.

**Microarray** A technique for studying how large numbers of genes interact and how a cell’s regulatory network controls vast amounts of genes simultaneously.

**Microtubules** Tiny tubes found in most cells.

**Mitochondria** A molecule involved in the formation and growth of tumours.

**Monoclonal** A protein involved in the formation and growth of tumours.

**Ontogeny** The formation and growth of a cell, tissue, organ or organism.

**Organelle** A subcellular structure with a specialised function.

**Ornithine** A type of amino acid, which binds to a larger molecule.

**Organic** A molecule composed of one or more carbon atoms. An example is the sugar glucose.

**Organism** The complete set of proteins being translated at a site. The organism delivers DNA’s message to the site of protein synthesis.

**Organism** The complete set of proteins being translated at a site. The organism delivers DNA’s message to the site of protein synthesis.

**Paralogous** Two genetic sequences that have evolved from a common ancestor.

**Pathogen** A disease-causing organism.

**Pharmcoligand** A compound of two or more amino acids.

**Phage** A virus that infects bacteria.

**Phagocytosis** The process by which cells engulf material in order to destroy or digest it.

**Pharmacology** The study of drugs and their effect on organisms.

**Pharming** engineered animals and plants to produce drugs.

**Phenotype** The characteristics of an organism resulting from the interaction between its genotype and its environment.

**Phosphatase** An enzyme that removes a molecule containing phosphorus acid from a nucleic acid or protein.

**Phosphoproteins** A class of enzymes that transfer energy from ATP to other molecules. An example is the ATPase that pumps sodium ions into the cell.

**Phosphoregulators** A chemical that regulates gene expression.

**Phosphorylation** The process by which a molecule containing phosphorus acid is transferred to a nucleic acid or protein.

**Phosphorylase** An enzyme that catalyses the production of adenosine triphosphate.

**Polymer** A large molecule consisting of repeated subunits.

**Polymerase** The enzyme involved in synthesizing new DNA.

**Population** The formation of multiple forms of a gene or DNA sequence.

**Polyphenol** A class of bony vertebrate fish.

**Phosphorylation** The process of forming a series of detailed pictures of areas inside the body, created by a computer linked to an X-ray machine.

**Protein** A chemical similar to a single strand of DNA, except that DNA contains ribose instead of deoxyribose and uracil instead of thymine. RNA delivers DNA’s message to the site of protein synthesis.

**Protamine** A protein that regulates gene expression.

**Protease** Any enzyme that causes the interior peptide bonds of a protein to split.

**Proteoglycan** A large molecule composed of one or more chains of amino acids in a specific order. Proteoglycans are required for the structure, function and regulation of the body’s cells, tissues and organs, and each protein has a unique function. Examples are hormones and antibodies.

**Proteome** The complete set of proteins being expressed at any one time by a cell, tissue or organism.

**Quantitative** An attribute that is clearly measurable.

**Radioligand** A radioactive substance injected into tissue that binds to receptors and allows researchers to study its behaviour.

**Redox** A reduction/oxidation reaction, where the oxidation number of an atom changes.

**Retrotransposon** Segments of DNA that can move around the genome and amplify themselves.

**RNA** An RNA similar to a single strand of DNA, except that RNA contains ribose instead of deoxyribose and uracil instead of thymine. RNA delivers DNA’s message to the site of protein synthesis.

**Scanning** Determining the order of nucleotides in a DNA or RNA strand.

**Somatic** Relates to any of the non-reproductive parts of the body, also used to mean a condition that is non-inherited.

**Spectroscopy** The study of the interaction between light and matter (eg. light, sight).

**Stathm** A protein that regulates gene expression.

**Stochastic** A process that is governed by random chance.

**Teleosts** A class of bony vertebrate fish.

**Tertium** The process of creating a series of detailed pictures of areas inside the body, created by a computer linked to an X-ray machine.

**Transform** The formation of RNA from a DNA template.

**Transcription** The formation of transgenes from genes within a given genome.

**Transgene** An organism that has a transferred gene (transgene) incorporated into the chromosome of all its cells.

**Triplex** Consisting of three parts.

**Tumourigenesis** The formation of a tumour.

**Upregulated** When the production of a substance, or the rate of a process, is increased.

**Vascular** Pertaining to anything related to or involving the transport of blood to or from the body.

**Vesicle** A closed membrane shell.


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