The Ramaciotti Centre is a high throughput genomics facility, offering expertise in sequencing and microarray technology. It supports genomics research throughout UNSW and Australia-wide by offering a range of services and access to equipment.

**Mission**
To delivery internationally competitive genomic services to the Australian research community.

**Objectives**
The Ramaciotti Centre for Gene Function Analysis aims to

- Provide our users with enabling technology and services, to facilitate internationally competitive research.
- Provide genomics and related services of the highest possible quality
- Provide support for bespoke and niche projects.
- Provide services at competitive rates.
- Build the genomics community in the state of NSW and beyond.
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2012 was another successful year for the Centre. This has only been possible through the hard work of all Centre staff. I would like to warmly thank them for their dedication, ongoing enthusiasm and (it has to be said) their tireless patience with researchers in the community we serve. I would also like to thank the Centre Steering Committee for their continued input, thoughtful suggestions and support.

Almost all activities of the Centre have experienced growth this year. Of note is the number and type of analyses undertaken by next-generation sequencing; a total of 976 samples were analysed in 2012 – up from 282 in 2011. This is particularly impressive given the degree of competition that exists internationally in the next-gen sequencing area. Due to a large NHMRC-funded genotyping study, our microarray service also had a record year, having analysed a total of 7,675 samples. In addition to the above, 44,823 samples were analysed by Sanger capillary sequencing and 1,114 samples analysed on the Bioanlayzer. Whilst we had anticipated a reduced use of some older technology platforms, such as the Roche GS FLX+ or microarrays, we are yet to see these platforms become obsolete.

The Centre has continued to acquire new technology. A second HiSeq platform, which became operational in August 2012, was acquired through a combination of EIF Super Science (Bioplatforms Australia) and ARC LIEF funding. A MiSeq platform, which has longer read lengths than the HiSeq but generates less data per lane, was installed, having been funded from the UNSW MREII Scheme. A DataSend facility, to allow Centre users to securely and remotely download their analytical results, was established. These platforms have increased our analytical breadth and depth and thus our ability to support a wide range of genomic, transcriptomic and other specialty projects.

2012 saw the Centre participate in its first large-scale human genome sequencing project. As part of the Melanoma Institute’s 500 genome sequencing project, the Centre sequenced approximately 50 human genomes. Genomes from cancer samples were sequenced at 70x coverage whilst paired normal tissue genomes were sequenced at 50x coverage. The data, whilst still in analysis, looked outstanding and we look forward to further substantial projects of this type in the future. Special thanks must go to Centre staff Dr. Helena Mangs and Tonia Russell for their dedication and skill in this flagship project.
The finances of the Centre continue to be sound. We acknowledge continued support from the Federal Government EIF Super Science Initiative, administered by Bioplatforms Australia, from the NSW State Government, ARC LIEF and from the University of New South Wales. We also look forward to activating funds in 2013 from successful new LIEF and UNSW MREII grants. Grant funding, together with income generated from Centre activities, has allowed us to slightly expand our technical staff. I thank Dr. Helen Speirs, Centre Manager, for her skills and effort in looking after Centre activities whilst keeping a watchful eye on the bottom line.

Last, but by no means least, it is with some sadness that I announce that the Chairperson of the Ramaciotti Centre Steering Committee, Prof. Peter Bergquist, will step down at the end of 2012. Peter has served as the Committee Chair for over 10 years, and helped enormously with many aspects of the Centre and its smooth management. Peter also helped maintain a wonderful collegial culture in the steering committee. We thank Peter for his contributions and wish him the very best. Prof. Ian Dawes has agreed to take up the role of Chair in 2013.

Professor Marc Wilkins
Director
The Facility

Core Facility
The Ramaciotti Centre for Gene Function Analysis is located in the School of Biotechnology and Biomolecular Sciences at the University of New South Wales.

Partners
The Ramaciotti Centre is affiliated with other universities and medical research institutes in the Sydney region. Representatives from each sit on the Centre’s Steering Committee.

University of Sydney
University of Newcastle
Macquarie University
University of Technology, Sydney
Kolling Institute
Victor Chang Cardiac Research Institute

Steering Committee

Professor Peter Bergquist
Independent Chair

Professor Marc Wilkins
(Director)
University of New South Wales

Professor Ian Dawes
(Deputy Director)
University of New South Wales

Professor Ian Charles
University of Technology, Sydney

Professor Merlin Crossley
University of New South Wales

A/Prof Debbie Marsh
Kolling Institute of Medical Research

Professor Ian Paulsen
Macquarie University

Professor Rodney Scott
University of Newcastle

Dr Catherine Suter
Victor Chang Cardiac Research Institute

Professor Peter Waterhouse
University of Sydney

Alternates
Professor Nick Packer
for Professor Ian Paulsen

Professor Claire Wade
for Professor Peter Waterhouse
Staff

Director
Professor Marc Wilkins

Deputy Director
Professor Ian Dawes

Centre Manager
Dr Helen Speirs

Microarray
Dr Bronwyn Robertson
Dr Erika Becker
Dr Hannah Ginn
Dr Kristin North

Research
Dr Ruby Lin (Postdoctoral Fellow)

Sequencing
Dr Helena Mangs
Tonia Russell
Jason Koval
Jackie Chan

IT
Robin Herron

< From left
Dr Helen Speirs
Dr Bronwyn Robertson
Dr Erika Becker

< From left
Dr Hannah Ginn
Dr Kristin North
Dr Helena Mangs

< From left
Tonia Russell
Jason Koval
Jackie Chan
The Ramaciotti Centre is a not-for-profit facility, which provides service and expertise in the use of microarrays, sequencing and other high-throughput genomic technologies. The Centre has a strong track record in the provision of services in transcriptomics and genomics with users Australia-wide and overseas.

**Microarray Service**
The Ramaciotti Centre has been providing a high quality microarray service to the research community since 2000. We offer a comprehensive range of services on three different technology platforms: Affymetrix, Agilent and Illumina.

**Affymetrix GeneChip®**
The Centre is an Authorized Affymetrix Service Provider. We offer a full processing service on all types of Affymetrix GeneChips®, in both cartridge and peg array plate format. These include:
- gene expression
- microRNA
- exon (alternative splicing)
- promoter (gene regulation)
- genotyping (SNP)
- copy number variation (CNV)

Equipment supporting this service includes:
- Affymetrix GeneTitan™ for processing array plates
- Affymetrix GC3000 4 colour scanner with autoloader for processing cartridge arrays
- 4 X Affymetrix FS450 fluidics stations
- Affymetrix GCAS robotics
- 3 X Affymetrix hybridisation ovens

**Agilent Microarrays**
The Centre offers a full processing service on all types of Agilent arrays. These include:
- gene expression
- microRNA
- CGH
- CNV & SNP
- DNA methylation
- custom array design

Equipment supporting this service includes:
- Agilent HD microarray scanner
- Agilent hybridisation oven

**Illumina BeadChips**
The Centre provides a full processing service on all Illumina gene expression BeadChips and CytoSNP BeadChips.

Equipment supporting this service includes:
- Illumina BeadAarray scanner
- 2 x Illumina hybridization ovens
Sequencing Services
The Ramaciotti Centre has been providing sequencing services to the research community since 1995. With the acquisition of next-generation sequencers the Centre has remained at the forefront of genomic research in Australia. We offer a range of next generation sequencing (NGS) services and a Sanger sequencing service.

Next-Generation Sequencing
The Centre offers next-generation sequencing services on Illumina HiSeq 2000, Illumina MiSeq and Roche GS FLX+ platforms. These include:
- genome sequencing
- transcriptome sequencing
- ChIP sequencing
- small RNA discovery
- amplicon sequencing
- targeted sequencing

Equipment supporting this service includes:
- Illumina HiSeq 2000 sequencer
- Illumina HiSeq 2500 sequencer
- Illumina c-bot, cluster system
- Illumina MiSeq sequencer
- Roche GS FLX+ sequencer
- Covaris E220
- Computing cluster

Sanger DNA Sequencing
Using ABI 3730 technology, the Centre offers Sanger sequencing services including:
- DNA sequencing
- DNA fragment analysis including microsatellites, AFLP’s, RFLP’s and SNP’s

Other Services
Agilent Bioanalyzer
An Agilent Bioanalyzer quality control service is run by the Centre for:
- RNA
- small RNA
- DNA

Consumable Sales
The facility also reduces costs to users by procuring consumables at bulk rates and on selling them to our users. These consumables can be purchased through our online store.

Access to Equipment and Software
In addition to the core equipment required to operate the microarray and sequencing services, the Ramaciotti Centre maintains a number of items of equipment, which are available for use by the wider academic community. A full list of Centre equipment assets, can be found on our website. The Centre also has a current software license for Partek’s Genomics Suite which customers can access free of charge.

Bioinformatics
The Centre has continued its longstanding collaboration with the NSW Systems Biology Initiative (the SBI) for the bioinformatics analysis of data. The SBI has expertise in:
- genome assembly and annotation
- comparative genomics
- transcriptomics data analysis from next-gen and microarray platforms
- pathway, network and systems-level analysis of transcriptomic data
- network visualization
- integrative analysis of transcriptomic and proteomic data

The SBI works with users of the Ramaciotti Centre collaboratively and also encourages researchers to work inside the SBI on a ‘research hotel’ basis.

The Centre also continues to collaborate with the Peter Wills Bioinformatics Centre (PWBC) at the Garvan Institute. The PWBC houses all of the microarray data generated by the Ramaciotti Centre.
Summary of services provided to the research community in 2012.

- 7,675 samples analysed by microarray
- 976 samples analysed by next generation sequencing
- 44,823 sequencing analyses on the AB capillary sequencer
- 1,141 samples analysed on the Bioanalyzer

Microarray

**Affymetrix array service**
A full processing service was offered for all available GeneChips®, including gene expression, genotyping and copy number arrays.

In 2012 the Centre processed 6,693 Affymetrix arrays, an increase of 392% from 2011. The majority of these were for a Genome Wide Association Study (GWAS), for the NHMRC Clinical Trials Centre, University of Sydney. This study, known as the FIELD (Fenofibrate Intervention and Event Lowering in Diabetes) study, is investigating the use of fenofibrate to modify blood lipids and reduce the risk of coronary heart disease in people with type 2 diabetes. In total, 5,760 genotyping arrays were processed for this study on the GenTitan™ robot. The remaining arrays processed were mostly gene expression arrays. The Affymetrix array processing summary is presented in Table 1.

New arrays for whole-transcriptome analysis of model and applied research organisms were released in 2012. These arrays allow researchers to obtain a more complete view of gene expression than if using traditional 3’ biased arrays. Customers performing research in dogs and Arabidopsis were among the first to access these new arrays.

There was an increase in demand for our low input gene expression service. A total of 10 array projects were completed in 2012 where starting amounts were less than 5ng of total RNA.

**Agilent array service**
A total of 545 Agilent arrays were processed during 2012, an increase of 7% from 2011. The Agilent microarray service continues to support a diverse range of life science research. In 2012 this included tomato, zebrafish, bovine, sheep and custom array designs. The Agilent array processing summary is presented in Table 1.

**Illumina array service**
A total of 437 Illumina BeadChips were processed in 2012, an increase of 135% from 2011. The Illumina array processing summary is presented in Table 1.

The number of arrays the Centre processes per annum has remained more or less steady since 2009. This year however, has been remarkable. We processed our largest single study to date, the FIELD study, which has lead to a spike in array numbers (Figure 1). We also had an unexpected 18% increase in our gene expression array business (Figure 2). The anticipated drop in demand for gene expression arrays due to the increased uptake of next-generation sequencing technology did not come in to effect this year.
Sequencing

**Illumina HiSeq NGS service**

The Centre continued to focus its sequencing business on the application of next generation technology. With funding from Bioplatforms Australia, the Centre acquired a second HiSeq 2500 doubling our sequencing capacity. This allowed the Centre to become part of the Bioplatforms Australia Melanoma Biomolecular Datasets project and sequence its first whole human genomes. As expected, demand for Illumina sequencing data increased with a jump of 250% in the number of samples processed this year. The service sequenced 724 samples for 58 different customers whose research projects ranged from Tasmanian devil and wheat transcriptome sequencing to whole human genomes. The type of sequencing applications requested included genomic, transcriptomic and chromatin immunoprecipitation (ChIP) sequencing. The Illumina HiSeq sequencing summary is presented in Table 1.

**Illumina MiSeq NGS service**

A successful MREII grant application in November 2011, allowed us to acquire an Illumina MiSeq. The MiSeq is a bench top sequencer with a modest output of ~8Gb and a fast run time. It enables the rapid sequencing of amplicons, targeted genomic regions or smaller genomes. The service was up and running in June 2012. The Illumina MiSeq sequencing summary is presented in Table 1.

**Roche GS FLX+ service**

The longer read lengths of Roche GS FLX+ remained in demand. The service processed 205 samples an increase of 173% from 2011. The type of sequencing applications requested included genomic, transcriptomic and amplicon sequencing. A drop in demand for this technology is anticipated as the read length increases in other platforms that have a lower cost per base. The Roche GS FLX sequencing summary is presented in Table 1.

Table 1: Core Facility Processing in 2012 compared with previous years

<table>
<thead>
<tr>
<th>Platform Service</th>
<th>2012 Sample Total</th>
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<tr>
<td>Affymetrix array Gene Expression</td>
<td>1,173 955 1,303 1,124</td>
</tr>
<tr>
<td>Genotyping &amp; Cytogenetics</td>
<td>5,520 404 409 935</td>
</tr>
<tr>
<td>Agilent array Gene Expression</td>
<td>469 476 354 319</td>
</tr>
<tr>
<td>Cytogenetics</td>
<td>76 32 52 40</td>
</tr>
<tr>
<td>Illumina array Gene Expression</td>
<td>312 186 NA NA</td>
</tr>
<tr>
<td>Cytogenetics</td>
<td>125 0 NA NA</td>
</tr>
<tr>
<td>Illumina GAIIx/HiSeq 2000 DNA/RNA/ChIP/small RNA</td>
<td>724 207 168 59</td>
</tr>
<tr>
<td>Illumina MiSeq DNA/RNA/amplicon</td>
<td>47 NA NA NA</td>
</tr>
<tr>
<td>RocheGS FLX+ DNA/RNA/amplicon</td>
<td>205 75 225 110</td>
</tr>
<tr>
<td>Sanger Sequencing Sequencing</td>
<td>37,006 40,421 66,616 63,717</td>
</tr>
<tr>
<td>Fragment Analysis</td>
<td>7,817 11,881 18,881 21,236</td>
</tr>
<tr>
<td>Agilent Bioanalyzer RNA QC</td>
<td>1,141 1,325 1,073 585</td>
</tr>
</tbody>
</table>
With the acquisition of the latest next generation sequencers the Ramaciotti Centre has remained at the forefront of genomic research in Australia. The number of NGS samples sequenced and the number of sequencing runs increased massively in 2012, Figure 3 and Figure 4 respectively. This demand is driven by the continuing decrease in the cost per base, and the ability to sequence any organism, opening up genomic research in areas that were previously unavailable to most biologists.

**Sanger sequencing service**

The Sanger sequencing service continued to experience a reasonable level of demand and processed 44,823 samples. This figure is down 14% from 2011 (Table 1). Sequencing accounted for 83% of the samples processed and Genescan fragment analysis for the remaining 17%. The Sanger sequencing service has experienced a gradual drop in demand due to customers moving towards using next-generation sequencing technology. Nevertheless it continues to provide a continuous stream of revenue.
Our Customers

A Australian Institute of Marine Sciences
Australian Museum
Australian National University
Australian Nuclear Science and Technology Organisation
Australian Wine Institute
Agricultural Institute Camden
ANZAC Research Institute
ARC Centre of Excellence in Plant Energy Biology
Australian Antarctic Division

B Baker IDI Heart and Diabetes Institute

C Centenary Institute
Centre for Environmental Stress and Adaptation Research, University of Melbourne
Centre for Marine Bio-innovation, UNSW
Centre for Immunology
Charles Darwin University
Children’s Cancer Institute Australia
Children’s Hospital at Westmead
Children’s Medical Research Institute
CSIRO Food and Nutritional Sciences
CSIRO Land and Water
CSIRO Livestock Industries
CSIRO Molecular & Health Technologies
CSIRO Plant Industry
Curtin University

D Department of Primary Industries

F Flinders Medical Centre
Flinders University

G Garvan Institute of Medical Research
Griffith University

J John Curtin School of Medical Research

K Kolling Research Institute

L La Trobe University

M Macquarie University
Melbourne University
Monash University
Murdoch Children’s Research Institute

N Nepean Hospital Neuroscience Research Australia

P Peter MacCallum Cancer Center
Princess Alexandra Hospital
Prince of Wales Hospital
Prince of Wales Medical Research Institute

Q Queensland Institute of Medical Research

R Reproductive Health Sciences
Royal Botanic Gardens
Royal Children’s Hospital
Royal North Shore Hospital
Royal Prince Alfred Hospital

S Schizophrenia Research Institute
South Australian Museum
Southern Cross University
St George Clinical School
St George Hospital
St Vincent’s Centre for Applied Medical Research
St Vincent’s Hospital
St Vincent’s Institute

T Telethon Institute for Child Research

U University of Adelaide
University of Auckland
University of Ballarat
University of Canberra
University of Newcastle
University of New South Wales
University of Queensland
University of Padova
University of Sydney
University of Technology, Sydney
University of Western Sydney
University of Western Australia

V Vialactica
Victor Chang Cardiac Research Institute

W Walter and Eliza Hall Institute
Westmead Millennium Institute
By type

- University
- Research Lab
- Hospital
- Government
- Commercial
- Other

By discipline

- Biomedical
- Diagnostics
- Environmental
- Agriculture
- Veterinary
- Plant Biology
- Other

Internal vs External

- UNSW
- Non-UNSW
The Ramaciotti Centre’s mission to deliver internationally competitive genomic services to the Australian research community depends on the acquisition of the latest technology and the provision of services using this technology to the research community.

Acquisition of Second Illumina HiSeq 2000
As the demand for sequencing data continued to grow the Centre focused on the application of next-generation sequencing technology. With funding from the Education Investment Fund Super Science Scheme, the Centre purchased a second Illumina HiSeq 2000 sequencer, doubling our sequencing capacity. We continue to provide a number of services on the Illumina platform for an increasingly diverse range of customers. Research projects ranged from human transcriptome sequencing to metatranscriptome sequencing of coral from the Great Barrier Reef.

New Technology – MiSeq Personal Sequencer
The School of BABS and the Ramaciotti Centre were successful in their application to the UNSW Major Research Equipment and Infrastructure scheme for an Illumina MiSeq. The MiSeq is a personal sequencer that provides a fast turnaround on small scale sequencing projects. The MiSeq facilitates rapid, cost effective sequencing of amplicons and small genomes such as those from viruses and bacteria.

Melanoma Sequencing Project
As part of the Bioplatforms Australia Melanoma Biomolecular Datasets project, the Centre sequenced its first complete human genomes. The project aims to sequence both normal and cancer samples from 75 individuals to 40x and 70x coverage respectively. It is a collaborative project utilising sequencing capacity across Australia, with contributions from all three nodes of Genomics Australia (ANU, AGRF & RAMAC).

FIELD Trial – Genome Wide Association Study
The Centre completed a genome-wide association study for the NHMRC Clinical trials Centre. The study aimed at discovering genetic factors that predict complications in type 2 diabetes used the Centre’s GeneTitan robot to genotype 5,760 individuals. This is the largest single array study the Centre has ever undertaken.
Bioinformatics and IT
The Centre continued its collaboration with the NSW Systems Biology Initiative (the SBI) in the analysis and contextualization of data. Notable projects in 2012 included network-based analysis of transcriptomes from good versus bad outcome melanoma patients, network-based analysis of the transcriptomes of cancer cachexia-affected cardiac tissue, along with the assembly and analysis of 6 genomes of Campylobacter, of 2 genomes of Lactobacillus.

For IT, the Centre established a DataSend facility to allow large next-gen files to be securely downloaded by end users via the internet. This obviates the need for the shipping of data on hard drives.

Biosecurity Breakthrough – Queensland Fruit Fly Genome Project
The Queensland fruit fly (QFF) is a significant threat to a wide range of horticultural crops, and can have a major impact on Australia’s export market. Using sequence data generated by UNSW’s Ramaciotti Centre for Genomics Dr Stuart Gilchrist and colleagues from the University of New South Wales have assembled the genome of the QFF and identified over 9,000 genes. This data will be used to develop a reliable method to identify unknown larvae in fruit for export and in the longer term develop more effective lures and baits.

Therapeutic inhibition using synthetic oligonucleotides in an in vivo mouse model of heart failure.
In collaboration with Dr Julie McMullen, Dr Ruby Lin, a senior research fellow based at the Ramaciotti Centre for Genomics, utilised locked nucleic acid (LNA)-modified antimiR to provide therapeutic benefits in mice with pre-existing pathological cardiac remodelling and dysfunction (Bernardo et al., Proc Natl Acad Sci U S A. 2012;109:17615-20). This project provided evidence that silencing entire family of miR-34 is cardiac protective and the team continues to investigate using LNA-antimiRs in the development of new therapeutics for heart failure.
Promotional activities throughout the year sought to raise our profile within the genomics community. Our main promotional activities include: organisation of educational workshops and seminars, exhibits, presentations and production of promotional materials and communications.

The Centre organised workshops and seminars in the areas of microarray and sequencing. It also hosted seminars on new emerging technology. As in previous years the Centre’s 2012 workshop and seminar program focused on education in the technologies central to its core business.

Workshops

17th July 2012
Quantitative RT-PCR & Sequencing Workshop
The Centre organised and hosted a one-day workshop to train UNSW Science Faculty students and staff in quantitative RT-PCR and sequencing. Staff from the Centre and field applications specialists from supporting companies presented on a range of topics including sample QC, primer design, data analysis, troubleshooting and introduction to next-generation sequencing. The workshop was sponsored by Life Technologies.

13th September 2012
Partek Data Analysis Workshop
The Centre hosted a one-day workshop on the use of Partek Genomics Suite software. Presentations were made by Erwin Tantoso and Hsiufen Chua from Partek. Topics covered included gene expression microarray data analysis, NGS read alignment QAQC, RNA-Seq, variant detection analysis and visualisation.

Seminars

31st May 2012
Snapshot of Services at Ramaciotti Centre – Overview of NGS
Dr Helen Speirs

7th June 2012
Bio-Rad ddPCR
Bio-Rad presented data from the QX100 droplet digital PCR system and how it measures small differences in gene expression, performs copy number determination and detects rare target sequences.

8th June 2012
Fluidigm BioMark HD & AccessArray System
Fluidigm presented the different applications of the BioMark HD & AccessArray system including single cell gene expression analysis, target enrichment and amplicon tagging for NGS and SNP genotyping.

18th June 2012
The QuantStudio 12K Flex
Life technologies presented the different applications of the QuanStudio high throughput qPCR system.
Next-Generation Sequencing – Special Interest Group

The Ramaciotti Centre in association with Bioplatforms Australia, the Victor Chang Cardiac Research Centre and the Australian Genome Research Facility organise the ‘NSW Next-Generation Sequencing Special Interest Group meeting’. This special interest group was established to encourage discussion and interactions around Next-Generation Sequencing. To encourage attendance, seminars are held at different locations across Sydney.

22nd March 2012
Westmead Millennium Institute
Dr Russell Diefenbach
Senior Research Fellow, Head Molecular Viral Transport and Assembly Group, Centre for Virus Research, Westmead Millennium Institute.

Dr Monica Miranda Saksena
Research Fellow, Centre for Virus Research, Westmead Millennium Institute
“Correlation of Herpes Simplex Virus type 1 strain variations with defects in transport and assembly in neurones”

Dr David Midgley
Research Scientist, CSIRO Energy Transformed Flagship

21st June 2012
University of New South Wales
Dr Stuart Gilchrist
School of Biological Earth and Environmental Science, UNSW
“Australian pest fruit flies: a genomic ménage à trois.”

Dr Mark Cowley
Garvan Institute for Medical Research.
“Exploring the functional landscape of pancreatic cancer.”

4th October 2012
Victor Chang Cardiac Research Institute
Dr Warren Kaplan, Bioinformatics Specialist, Garvan Institute of Medical Research
“Garvan Galaxy: Next-gen sequence analysis for all.”

Prof Joel Mackay
School of Molecular Bioscience, University of Sydney
“First steps in next gen space for analysis of the function of human ZRANB2 – a putative RNA processing factor.”

29th November 2012
Westmead Millennium Institute
Joel Barratt
University of Technology, Sydney
“The use of Next-Gen sequencing technologies to study Dientamoeba fragilis.”

Claire Deakin
Children’s Medical Research Institute
“Investigating the feasibility of next generation sequencing for analysing the complexity of molecular barcode libraries.”

Conferences

The Centre exhibited at:
Lorne Cancer
February 2012
Lorne Genome
February 2012
Combio
Adelaide - September 2012
The Australian Network of Cardiac and Vascular Developmental Biologists (ANCVDB) Conference
Sydney – November 2012

Education and Training

Microarray and sequencing data generated by the Centre features in the work of many Honours and PhD students. Many students from the Centre nodes and other educational organisations benefit from its resources. In a typical year approximately 35 PhD students and 25 Honours/Diploma/MPhil students will benefit from the Centre’s resources and expertise.

The Ramaciotti Centre also enjoys showing, groups of university and school students round the Centre. This year we hosted visits from third year cell biology students from UNSW Faculty of Medicine, and third year molecular genomic students from UNSW Faculty of Science.
The Ramaciotti Centre supports research across a broad range of areas. Opposite are selected publications from 2012 by researchers who used the Centre’s services:


The Ramaciotti Centre gratefully acknowledges the support it receives from funding bodies.

### Awards in 2012

**Australian Research Council Linkage Infrastructure, Equipment and Facilities**


$650,000

**Other**

**UNSW Major Research Equipment and Infrastructure Initiative Scheme (MREII)**

Fluidigm Biomark C1 system

$248,420

### Continuing

**Bioplatforms Australia Super Science Project for the Education Investment Fund**

2010-2013: $2,650,000

**NSW State Government Science Leveraging Fund**

2011–2013: $300,000
Acknowledgments

The Ramaciotti Centre would like to thank Bioplatforms Australia for their continued support. The Centre staff would like to thank Dr Warren Kaplan from the Peter Wills Bioinformatic Centre for his support throughout 2012. We would also like to thank Tom Sedgwick, Adrian Plummer, Martin Thompson, Brad Jones, Chris Cannon and Robin Herron from Science Faculty IT for their invaluable support.

Photographs


Page 7  The sequencing laboratory.

Page 9  Affymetrix GeneTitan (B Robertson)

Page 11  Illumina HiSeq (T Russell & H Mangs)

Page 15  Pippin prep, library preparation for NGS.

Page 16  Illumina MiSeq (J Chan)

Page 19  Exhibitor stand at Combio Adelaide (T Russell)

Design dd(too)

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The Ramaciotti Centre for Gene Function Analysis

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