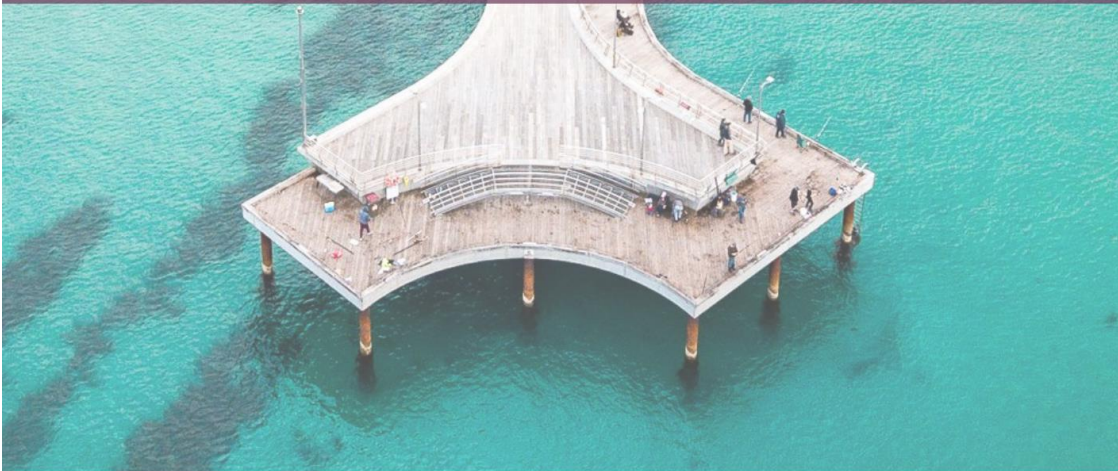


3-6 FEBRUARY 2022 | MANTRA LORNE



Delegate Handbook

27TH ANNUAL LORNE PROTEOMICS SYMPOSIUM



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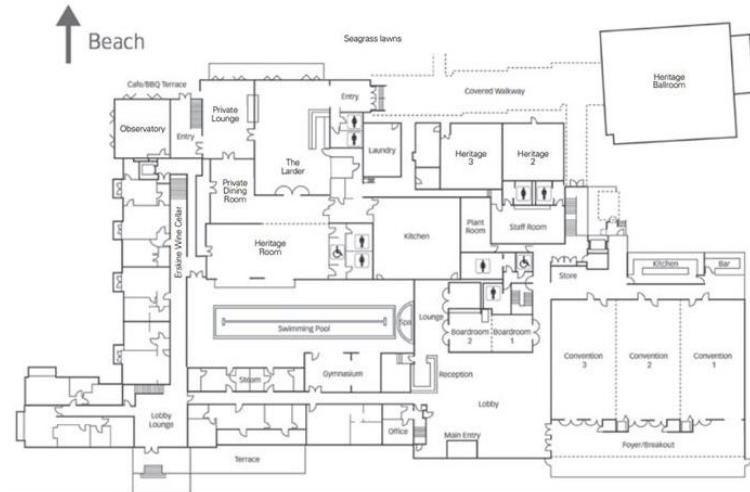
VENUE

Mantra Lorne

Mountjoy Parade, Lorne, VIC 3232, Australia

P: (03) 5228 9777 | F: 03 5289 1185

www.mantralorne.com.au



CONFERENCE SECRETARIAT



ASN Events Pty Ltd

9/397 Smith Street

Fitzroy, VIC 3065, Australia

Contact person on-site:

Jordyn Trolove | M: +61 (0)488 121 355 | E: jordyn.t@asnevents.net.au

EXHIBITOR PRIZE DRAW

You will receive a small card in the back of your name badge which is to be used to enter the prize draw. The prize draw will be completed in the last session on Sunday 6th February. To collect the stickers please visit the exhibitors during Morning Tea, Lunch and Poster Sessions. Once you have received all stars fill out your details on the card and hand into the registration desk.

For every prize draw card completed, Proteomics 2022 are donating \$5 to the Lorne Hospital.

SPEAKER PRESENTATION INSTRUCTIONS

All conference sessions take place in the Heritage Ballroom. Audio-visual equipment will be supplied and there will be a technician on site to assist with any enquiries. Mantra Lorne has a 16:9 screen. **Please make sure your presentation is in 16:9 format** to get the best image. It is the conference preference that ALL presentations be pre-loaded onto the laptop in the session room. Please bring your presentation to the meeting on a USB drive and give this to the technician well in advance of the session you are participating to allow for timely loading and testing. A remote mouse/laser pointer will be provided at the lectern. Please use the pointer to ensure delegates in the overflow rooms are able to follow as you present.

LIGHTNING TALK INSTRUCTIONS

Prior to each poster session there will be a “Lightning Talk” session. Authors of the selected lightning talks are requested to bring their presentation on a USB Flash drive and load in onto the computer within the lecture room by the morning tea prior to their Lightning Talk session, at the latest. **Presentations are limited to 3 minutes** (max 3 slides incl. any title slides).

POSTER PRESENTATION INSTRUCTIONS

Posters should be size A0 portrait orientation and can be attached to the poster boards with Velcro. Additional Velcro supplies can be obtained from the registration desk. The poster boards are located in the Exhibition Hall and numbered according to your poster numbers in the program (please refer to the poster listing on page 26).

There will be 2 dedicated poster sessions:

- **Poster Session One:** Friday, 4 February 2022, from 1:10 pm - 3:10 pm
- **Poster Session Two:** Saturday, 5 February 2022, from 1:20 pm - 2:45 pm

You will be required to stand at your poster during your sessions for discussion.

POSTER SET-UP AND REMOVAL

Poster Session One: Posters will be displayed from the Lunch session on Friday, 4 February and must be removed before the morning tea on Saturday, 5 February.

Poster Session Two: Posters will be displayed from Lunch Session on Saturday, 5 February and must be removed before the morning tea on Sunday, 6 February 2022.

SOCIAL PROGRAM

WELCOME RECEPTION

Date: Thursday, 3 February 2022

Time: 7:00 pm – 10:00 pm

Room: Exhibition Hall

Includes: Drinks & substantial canapes

APS CONFERENCE DINNER

Date: Saturday, 5 February 2022

Time: 7:30 pm – 11:00 pm

Location: Lorne Surf Life Saving Club

Includes: Food, drinks & music

SoAPS DINNER WITH INVITED SPEAKERS

Date: Friday, 4 February 2022

Time: 5:45 pm – 8:30 pm

Location: Croquet Lawn

Includes: BBQ & drinks

All delegates are invited to attend the social functions. The costs are included in the full conference registration. If your name badge does not include a ticket to the social functions and/or you wish to purchase additional tickets for partners, friends and children, please see the ASN staff at the registration desk

FAMILY ROOM

The Walter and Eliza Hall Institute of Medical Research will be supporting parents with young children attending the Lorne Conferences in 2022. The room will have space for activities and play for children while parents will be able to listen to the presentations with the same AV projection. The APS Committee once again applauds this initiative. We are grateful to the Walter and Eliza Hall Institute of Medical Research for their continued support of this initiative to enhance the accessibility of this conference to parents.



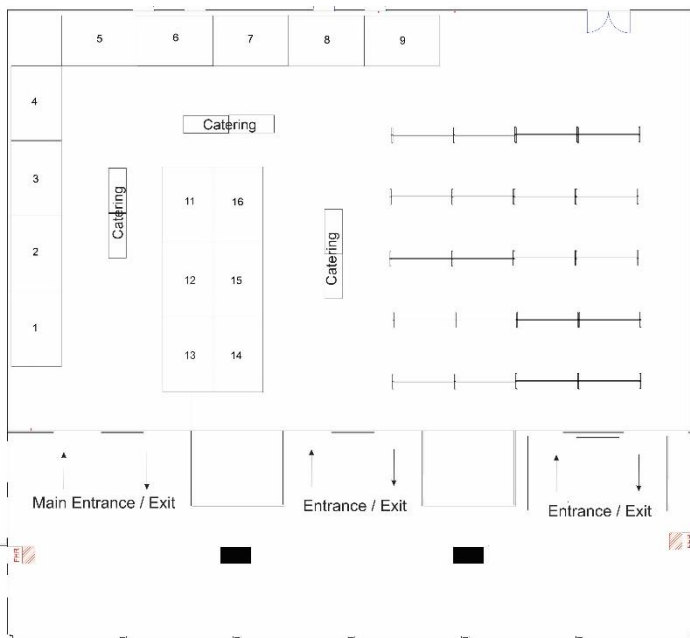
BUS TRANSFER HOME

Bus will depart from the Mantra Lorne on **Sunday 6 February @ 2:45pm sharp** and return to Melbourne Tullamarine Airport (arrival time approx. 5:15pm), and then onto WEHI/University of Melbourne, Royal Parade (arrival time approx. 5:45pm).

IMPORTANT:

- Please ensure you have checked out of your hotel and wait within Mantra Lorne Resort Foyer at least 10 minutes prior to the scheduled departure time.
- Please allow for **2.5 hours to travel from Lorne** for flight bookings.

EXHIBITORS



- Booth 1 – Agilent
- Booth 2 – Pall Laboratory
- Booth 3 – Mimotopes
- Booth 4 – Accurate Mass
- Booths 5 & 6 – Bruker
- Booth 8 -Trajan
- Booths 11 & 16 – SCIEX
- Booth 12 – Mass Dynamics
- Booths 13 & 14 – Thermo Fisher
- Booth 15 - Genesearch

INVITED SPEAKERS

INTERNATIONAL SPEAKERS

VADIM DEMICHEV



Universitätsmedizin Berlin

Vadim Demichev's laboratory at the Institute of Biochemistry, Charité – Universitätsmedizin Berlin, works on making mass spectrometry methods fold change faster and more sensitive, as well as applying them to large-scale proteomic and PTM-omic experiments. While working as a postdoc at the University of Cambridge and the Francis Crick Institute, UK, he focused on computational methods for proteomic data processing, resulting in the development of DIA-NN, a universal automated DIA-MS data analysis suite, which enables comprehensive proteomics using chromatographic methods as fast as several minutes.

REBEKAH GUNDRY



University of Nebraska Medical Center

Dr. Gundry is Professor and Vice Chair of Cellular and Integrative Physiology, Assistant Chief of Basic and Translational Research for the Division of Cardiology and is the Director of the CardiOmics Program at the University of Nebraska Medical Center. The Gundry lab applies mass spectrometry technologies for advancing basic and translational cardiac research and clinical care. Through development and application of innovative approaches and bioinformatic tools to study cell surface glycoproteins and glycans, the Gundry lab aims to answer outstanding questions in stem cell and cardiac biology and disease. Dr. Gundry is a Council Member of HUPO, Co-Chair of the HUPO B/D HPP Cardiovascular Initiative, is on the Board of Directors of US HUPO, and is an Associate Editor of the Journal of Molecular and Cellular Cardiology and a Reviewing Editor for eLife. The Gundry lab is funded by the American Heart Association, Juvenile Diabetes Research Foundation, and National Institutes of Health. In 2021, Dr. Gundry received a prestigious Emerging Investigator Award from NHLBI.

TIANNAN GUO



Westlake University

Tiannan received training of clinical medicine (1999-2006) in Tongji Medical College, Huazhong University of Science and Technology, and learned biology (2001-2005) in Wuhan University, before he moved to Singapore for PhD training in cancer proteomics (2008-2012) in the laboratories of Dr. Newman Sze in Nanyang Technological University and Dr. Oi Lian Kon in National Cancer Centre Singapore. In 2012, Tiannan started his postdoctoral training in the laboratory of Dr. Ruedi Aebersold

in ETH Zurich. Tiannan moved to Sydney as the Scientific Director of ProCan, group leader of Cancer Proteome, Children's Medical Research Institute, conjoint senior lecturer in The University of Sydney Medical School, in March 2017. Tiannan joined the Westlake Institute for Advanced Studies, Westlake University in August 2017 as a Tenure Track Assistant Professor.

NEVAN KROGAN

UC San Francisco



Nevan Krogan, PhD, is a molecular biologist, UC San Francisco professor, and director of the intensely interdisciplinary Quantitative Biosciences Institute (QBI) under the UCSF School of Pharmacy. He is also a senior investigator at the Gladstone Institutes. He led the work to create the SARS-CoV-2 interactome and assembled the QBI Coronavirus Research Group (QCRG), which includes hundreds of scientists from around the world. His

research focuses on developing and using unbiased, quantitative systems approaches to study a wide variety of diseases with the ultimate goal of developing new therapeutics. Nevan serves as Director of The HARC Center, an NIH-funded collaborative group that focuses on the structural characterization of HIV-human protein complexes. Dr. Krogan is also the co-Director of three Cell Mapping initiatives, the Cancer Cell Mapping Initiative (CCMI), the Host Pathogen Map Initiative (HPMI) and the Psychiatric Cell Map Initiative (PCMI). These initiatives map the gene and protein networks in healthy and diseased cells with these maps being used to better understand disease and provide novel therapies to fight them. He has authored over 250 papers in the fields of genetics and molecular biology and has given over 350 lectures and seminars around the world. He is a Searle Scholar, a Keck Distinguished Scholar, and was recently awarded the Roddenberry Prize for Biomedical Research.

HO JEONG KWON

Yonsei University



Professor Ho Jeong KWON graduated from Seoul National University (BSc, Korea) and did MS and PhD from University of Tokyo (Japan) and postdoctoral at Harvard (USA). He returned to Korea in 1999 and promoted to full professor in 2008 at the department of biotechnology, Yonsei University. He has been director of chemical genomics Leader/Global Research Laboratory program and serving as an adjunct professor, College

of Medicine, Yonsei University and Lund University (Sweden). He served as the president of AOHUPO (20-present), KHUPO (10-11) and a council member of HUPO (05-08, 15-17, 19-present). He has published over 220 papers in reputed journals and been serving as editor-in-chief of Proteome Science and editor of reputed journals. He has also filed over 50 patents and received many awards including DongHeon Biochemistry Award and Sura Academy Award. His research interests focus on discovery of bioactive small molecules, target identification and validation, integration of omics technologies toward innovations in drug discovery and translational research

AMANDA PAULOVICH

CLIA Targeted Proteomic Laboratory



Dr. Paulovich completed a residency in Internal Medicine at Massachusetts General Hospital and a fellowship in Oncology at Dana-Farber Cancer Institute. She completed her graduate training in genetics with Dr. Lee Hartwell at University of Washington and postdoctoral training in genomics at the Massachusetts Institute of Technology with Dr. Eric Lander. As an oncologist, Dr. Paulovich was struck by the paucity of quantitative assays for measuring clinically relevant phenotypes in her patients, and the limitations that this put on her ability to practice “personalized medicine.” Out of these experiences, she became passionate about developing technologies and strategies for translation of novel diagnostics and therapeutics to enable precision medicine. Over the past 18 years, Dr. Paulovich's interdisciplinary laboratory has focused on proteogenomic approaches to understanding cancer biology and laying the groundwork for the clinical translation of novel diagnostics based on targeted, multiple reaction monitoring (MRM) mass spectrometry.

PAOLA PICOTTI

Institute of Molecular Systems Biology



After her PhD at the University of Padua (Italy), Paola Picotti did postdoctoral research in the group of Ruedi Aebersold at ETH Zurich, where she developed targeted proteomic technologies based on mass spectrometry. In 2011, she was appointed Assistant Professor at the Institute of Biochemistry, ETHZ, and in 2017 tenured Associate Professor at the Institute of Molecular Systems Biology, ETHZ. Major contributions of the Picotti group include the development of structural proteomics technologies to probe in situ protein structural changes, characterization of the determinants of proteome thermostability, large-scale identification of protein-small molecule interactions, and the discovery of regulators of toxic proteins in Parkinson's disease. Dr. Picotti was awarded the Latsis Prize, the Cotter Award of US HUPO, the SGMS award, the EMBO Young Investigator Award, the Friedrich Miescher Award, the Juan- Pablo Albar award of the European Proteome Association, ERC Starting and Consolidator grants, and the EMBO Gold Medal.

NATIONAL SPEAKERS

MICHELLE COLGRAVE



CSIRO

Michelle Colgrave is a Professor of Food and Agricultural Proteomics at CSIRO and holds a joint appointment in the School of Science at Edith Cowan University. Prof Colgrave uses proteomics, the study of proteins using mass spectrometry (MS), to identify, characterise and quantify key proteins and peptides that will benefit Australia's food and agriculture industries and improve human health. Michelle is leading CSIRO's Future Protein Mission and is a Chief Investigator on the Australian Research Council Centre of Excellence in Innovations in Peptide and Protein

Science.

MATT DUN



University of Newcastle

A/Prof Matt Dun received his PhD from the University of Newcastle in 2012. He has been decorated by >25 national and international awards, including the 2019 NSW Premier's Awards for Outstanding Cancer Research Fellow and a Young Tall Poppy Award in 2020. A/Prof Dun has secured successive Cancer Institute NSW Early Career Fellowships (2014-2016 and 2017-2019), an NHMRC Investigator Grant (2020-2025), a Defeat DIPG Chadtough New Investigator Grant (2020-2021) and

successful Cancer Institute NSW and NHMRC Equipment Grants to establish a high-resolution mass spectrometry platform at the University of Newcastle. A/Prof Dun guides the Cancer Signalling Research Group at the University of Newcastle and the Hunter Medical Research Institute, which focuses on paediatric leukaemia, and brain cancer research. His group employs sophisticated pharmaco-phospho-proteo-genomics techniques to characterise the cellular signalling pathways dysregulated by the genetic individualities of a patient's cancer. This profiling strategy attempts to identify novel treatment targets and drug combinations to improve survival.

DAVID GREENING



Baker Heart and Diabetes Institute

A/Prof Greening is Head of Molecular Proteomics group at Baker Heart and Diabetes Institute, and Helen Amelia Hains Fellow, and principal investigator at La Trobe University, Cardiometabolic Health at University of Melbourne, and Monash University. His research integrates mass spectrometry, cell signalling & nanotechnology for the quantitative molecular characterization of different extracellular vesicles (EVs) and function at the cellular and tissue level. His lab studies the definitive

composition and reprogramming of EVs that go beyond their roles as signalling regulators, with important developments in inter-cellular signalling in human health and disease (e.g., cancer,

cardiac disease). He has made important contributions to the field of EVs, defining EVs and their subtypes (incl. exosomes), surface membrane composition, and developments as engineered therapeutics. Awarded Australian Field Leader in proteomics, Ludwig Research Medal, and Royan Stem Cell Biomedicine Award, he is the Chief Investigator in numerous nationally funded projects, and extensive partnerships with commercial and translational networks. He is the President of Aust./NZ Society for Extracellular Vesicles (ANZSEV) and organising committee International Society for Extracellular Vesicles (ISEV) congress (2022).

MICHELLE HILL



QIMR Berghofer Medical Research Institute

Michelle Hill obtained a PhD from The University Queensland, and conducted postdocs in Switzerland, Ireland and back at UQ. She established the Cancer Proteomics Group at UQ Diamantina Institute in 2007, then relocated and expanded the research program to the Precision and Systems Biomedicine Laboratory at QIMR Berghofer Medical Research Institute. The lab aims to improve modifiable health outcomes

by addressing better diagnostic tests and non-drug prevention approaches addressing metabolic and microbiome disturbances that lead to diseases. Michelle has research projects on several obesity-associated cancers, including oesophageal adenocarcinoma, advanced prostate cancer, multiple myeloma and ovarian cancer. The laboratory applies a range of techniques including multi-omics, molecular cell biology and clinical trials. Michelle has been a member of the Australasian Proteomics Society since 2007, and has been an advocate for the Queensland proteomics and mass spectrometry community. Michelle is a Council member of the Human Proteome Organisation.

NICOLE MIFSUD



Monash University

Nicole Mifsud obtained her PhD from The University of Melbourne in transplantation immunology and is the Head of the Clinical Immunology Group in the Biomedicine Discovery Institute at Monash University. She completed postdoctoral training at the Ludwig Institute for Cancer Research (Melbourne) and Department of Medicine, Monash University/Alfred Hospital. Her research program explores T cell-mediated immune responses

in transplantation, drug hypersensitivity and cancer in the pursuit of improved clinical outcomes for patients and the development of novel immunotherapeutics. In the transplantation arena, she has made important contributions to understanding the roles of T cell alloreactivity and virus-induced T cell cross-reactivity in graft rejection. More recently she has coupled investigations of cellular immunology with immunopeptidomics to characterise immunogenic peptide epitopes involved in T cell allorecognition, paving the way for development of diagnostic tools for immune monitoring of alloreactive T cells following transplantation. Nicole Mifsud obtained her PhD from The University of Melbourne in transplantation immunology and is the Head of the Clinical Immunology Group in the Biomedicine Discovery Institute at Monash University. She completed postdoctoral training at the Ludwig Institute for Cancer Research (Melbourne) and Department of Medicine, Monash

University/Alfred Hospital. Her research program explores T cell-mediated immune responses in transplantation, drug hypersensitivity and cancer in the pursuit of improved clinical outcomes for patients and the development of novel immunotherapeutics. In the transplantation arena, she has made important contributions to understanding the roles of T cell alloreactivity and virus-induced T cell cross-reactivity in graft rejection. More recently she has coupled investigations of cellular immunology with immunopeptidomics to characterise immunogenic peptide epitopes involved in T cell allorecognition, paving the way for development of diagnostic tools for immune monitoring of alloreactive T cells following transplantation.

NICOLLE PACKER

Macquarie University



Prof Nicki Packer has had an extensive and varied research career in both Chemistry and Biological Sciences. She helped establish the Australian Proteome Analysis Facility (APAF) and co-founded Proteome Systems Ltd, a biotechnology company in which her group developed glycoanalytical technology and informatics tools. She has gained national and international recognition for her research in glycomics, using proteomics and bioinformatics approaches and linking it to biological functional research. Her current research is in the structure, function, informatics and application of glycans and their conjugates as molecular markers, focusing on their role in cancer, therapeutics and microbial infection. Nicki currently holds positions as Distinguished Professor of Glycoproteomics, Deputy Director of the MQ Biomolecular Discovery Research Centre, CI in two ARC Centres of Excellence (NanoScale BioPhotonics and Synthetic Biology), is Interim Academic Lead of APAF at Macquarie University, Sydney, and as Principal Research Leader at the Institute for Glycomics, Griffith University, Queensland.

TARA PUKALA

University of Adelaide



Tara Pukala obtained a PhD from the University of Adelaide in 2006, under the supervision of Prof John Bowie. This was followed by a postdoctoral position at the University of Cambridge, UK, working with Prof Dame Carol Robinson in the field of native mass spectrometry. Tara returned to Australia to her current role as lecturer in the Discipline of Chemistry at the University of Adelaide in 2008. Here she leads a multidisciplinary research group focused on developing new approaches, primarily utilising mass spectrometry and bioconjugation chemistry, to investigate the structure, function and interactions of macromolecules important in biology and human health. Tara is also currently Director of the Adelaide Proteomics Facility and since 2020 has served as President of the Australian and New Zealand society for mass spectrometry. She was awarded the Bowie medal from that society in 2017 for her contributions to the field.

RALF SCHITTENHELM



Monash University

A/Prof Schittenhelm studied Biochemistry at the University of Bayreuth, Germany, and completed his PhD in 2009 from the University of Zurich, Switzerland. He joined the Swiss Federal Institute of Technology (ETH Zurich) – and later Monash University – to study cell cycle progression, signaling transduction networks and various autoimmune diseases using high-resolution mass spectrometry for which he was awarded several Swiss National Foundation (SNF) fellowships. In 2016, he was appointed as

Director of the Monash Proteomics & Metabolomics Facility (MPMF) to provide state-of-the-art mass spectrometric expertise to researchers and the broader community.

BEN SCHULZ



University of Queensland

Ben Schulz studied Chemical Engineering and Science at The University of Queensland, after which he joined Proteome Systems in 2001. In 2004 he moved to the ETH Zurich in Switzerland for doctoral studies in yeast systems biology. He joined the School of Chemistry & Molecular Biosciences at The University of Queensland as a postdoctoral research fellow in microbial glycosylation in 2008 and is now Associate Professor in Biochemistry. He has a research program in molecular systems biology

with a focus on the mechanisms, biological roles, and applications of protein glycosylation in biopharmaceuticals and fermented beverages.

MORTEN THAYSEN-ANDERSEN



Macquarie University

Dr Morten Thaysen-Andersen's research program in Analytical Glycoimmunology at Macquarie University in Sydney aims to advance our understanding of the glycobiology underpinning the human innate immune system and immune-related diseases including microbial infections, inflammation and cancer. His team develops and applies novel mass spectrometry-based glycomics and glycoproteomics technologies while also drawing on tools in protein and carbohydrate chemistry and

methods in immunology, structural biology and molecular biology to unravel fundamental glycobiological processes of the innate immune system.

PROGRAM

THURSDAY, 3 FEBRUARY 2022

Welcome to Country and Welcome Address

Chair: Peter Hoffmann

4:00 PM – 4:10 PM

Heritage Ballroom

The Simpson Lecture

Chair: Marc Wilkins

4:10 PM – 5:00 PM

Heritage Ballroom

4:10PM

Nicolle Packer

#glycotime has arrived!

abs# 1

Ken Mitchell Young Investigator Award Lecture

Chair: Joshua Hamey

5:00 PM – 5:30 PM

Heritage Ballroom

5:00PM

Sri H Ramarathinam

The HLA class II haplodome and the selection of class II ligands for immunosurveillance

abs# 2

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Vendor Talks

Chair: Peter Hoffmann

5:30 PM – 5:45 PM

Heritage Ballroom

Symposium One: Students of the APS (SoAPS)

Chair: Joel Steele & Marc Wilkins

5:45 PM – 7:00 PM

Heritage Ballroom

5:45PM

Dylan J Harney

Sexually dimorphic response to intermittent fasting in the liver proteome leads to altered innate immune signalling

abs# 3

- 6:00PM Anastasia Chernykh**
Unexpected *O*-glycosylation of human corticosteroid-binding globulin protects against neutrophil elastase and impedes cortisol release
abs# 4
- 6:15PM Dilana Staudt**
Global phosphoproteomic characterisation of oncogenic signalling using phospho heavy-labelled-spiketde FAIMS stepped-CV DDA (pHASED)
abs#
- 6:30PM Mahya Bahmani**
Proteomic analysis of environment effect on malting barley near isogenic lines
abs# 6
- 6:45PM Matthew P Challis**
Thermal stability proteomics identifies protein targets for antimalarial compounds
abs# 7

Welcome Reception

7:00 PM – 10:00 PM

Convention Centre

FRIDAY, 4 FEBRUARY 2022

Thermo Fisher Breakfast Workshop

7:15 AM – 8:15 AM

Heritage Ballroom

sponsored by **ThermoFisher**
SCIENTIFIC

Symposium Two: Disease Proteomics I

Chairs: Chairs: Anthony Purcell & Laura Dagley

8:50 AM - 10:20 AM

Heritage Ballroom

- 8:50AM Amanda Paulovich**
Building new clinical solutions for personalized oncology via proteogenomic
abs# 8
- 9:20AM Mark Larance**
Ultra-sensitive platelet proteome profiling charts the response to thrombin dosage and reveals unexpected *O*-glycosylation
abs# 9

- 9:35AM** **Mark P Molloy**
 Unexpected Single-shot LC-MS of microsampled dried whole blood to detect over 1600 proteins improves blood biomarker studies *abs# 10*
- 9:50AM** **Yu Ju Chen**
 Not provided at time of publishing *abs# 11*

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Morning Tea and Networking

10:20 AM – 11:00 AM

Convention Centre

Symposium Three: Environmental, Microbial, Plant Proteomics

Chairs: Samantha Emery-Corbin & James Broadbent

11:00 AM - 12:35 PM

Heritage Ballroom

- 11:00AM** **Michelle Colgrave**
 CSI(RO) food forensics – The case of the dubious falafel. *abs# 12*
- 11:25AM** **Ben L Schulz**
 Systems biology proteomics, metabolomics, and genomics of barley and yeast to investigate beer production *abs# 13*
- 11:50AM** **Gavin E Reid**
 Multi-omic analysis to characterize metabolic adaptation of the *E. coli* lipidome in response to environmental stress *abs# 14*
- 12:05PM** **Paul A Haynes**
 Proteomic analysis of different varieties and species of rice under various stress conditions *abs# 15*
- 12:20PM** **Delphine Vincent**
 Mining the wheat grain proteome. *abs# 16*

sponsored by



HUPO-HPP Grand Project Launch

12:35 PM - 12:50 PM

Heritage Ballroom

Lightning Talks One

Chair: Ben Crossett

12:50 PM - 1:10 PM

Heritage Ballroom

- 12:50PM** **Elise J Needham**
Personalised phosphoproteomics identifies functional signalling
abs# 17
- 12:53PM** **Shouxiang Zhang**
Mapping cysteine exposure of proteins *in situ* with a bi-functional
aggregation-induced emission fluorescent probe *abs# 18*
- 12:56PM** **Peter D Verhaert**
Mass Spectrometry HistoChemistry for single cell peptidomics
in *Homo sapiens* FFPE biobanks *abs# 19*
- 12:59PM** **Angela Juhasz**
Gluten digestion – a more complex story than ever thought *abs# 20*
- 1:02PM** **Molly K Talbot**
Acute treatment with antioxidant *N*-propionylglycine improves
contractile function and minimises the extent of cysteine redox post-
translational modifications in the diabetic heart as identified by
quantitative mass spectrometry *abs# 21*
- 1:05PM** **Harley R Robinson**
Infrared spectroscopy for rapid quality control and quantitation of
lipid samples *abs# 22*

Lunch and Poster Session One

1:10 PM – 3:10 PM

Convention Centre

sponsored by



SCIEX Lunch Workshop

1:30 PM – 2:30 PM

Heritage Ballroom

sponsored by



Symposium Four: Bioinformatics, Data Science and Machine Learning

Chairs: Sri Ramarathinam & Ignatius Pang

3:15 PM - 4:50 PM

Heritage Ballroom

- 3:15PM** **Nicholas Williamson**
Phosphomatics: Web based interactive analysis of phosphoproteomic data *abs# 23*
- 3:40PM** **Katherine E Scull**
Haplodome: a web-based knowledgebase and toolkit for searching, visualising and analysing mass spectrometry immunopeptidomics data *abs# 24*
- 3:55PM** **Dan Andrews**
Proteome-wide estimation of the change in protein stability due to missense mutation *abs# 25*
- 4:10PM** **Manika Singh**
DIA-seq: A novel isoform-level multi-omics data analysis pipeline identifies brain-specific changes in mouse model of behaviour *abs# 26*
- 4:25PM** **Vadim Demichev**
The future of DIA proteomics *abs# 27*

APS Annual General Meeting

5:00 PM – 5:45 PM

Heritage Ballroom

Free Evening or Students of the APS (SoAPS) Event

5:45 PM – 8:30 PM

Croquet Lawn

SATURDAY, 5 FEBRUARY 2022

Symposium Five: COVID-19 and Infectious Agents

Chairs: Patricia Illing & Cassandra Pegg

9:00 AM - 10:00 AM

Heritage Ballroom

- 9:00AM** **Chris M Overall**
SARS-CoV-2 3CL^{pro} Host Substrates and Interactors Identify Subversive Pathways in the COVID-19 Cellular coup d'état *abs# 29*
- 9:15AM** **AKM AKMM Muraduzzaman**
Identification of highly pathogenic avian influenza H5N1 T cell epitopes as potential peptide-based vaccine targets using an

immunopeptidomics strategy *abs# 30*

9:30AM

Tiannan Guo

Tensor empowered data analytics for data-independent acquisition
mass spectrometry-based proteomics *abs# 31*

Morning Tea and Networking

10:00 AM – 10:30 AM

Convention Centre

Symposium Six: Disease Proteomics II

Chairs: Elise Needham & Mark Molloy

10:30 AM - 1:00 PM

Heritage Ballroom

10:30AM

Rebekah Gundry

Not provided at time of publishing

abs# 28

11:00AM

Matt Dun

Profiling of the posttranslational architecture of paediatric high-grade gliomas following treatment with central nervous system active therapies to improve response

abs# 32

11:25AM

Nicole Mifsud

Discovery of peptide/MHC epitopes for alloreactive T cells; a major step forward for transplantation immunology

abs# 33

11:50AM

David Greening

Defining extracellular vesicle surfaceome and regulators of intercellular signalling

abs# 34

12:15PM

Kirti Pandey

A combined proteomics and immunopeptidomics approach to identify immunotherapy targets for diffuse intrinsic pontine glioma

abs# 35

12:30PM

David A Skerrett-Byrne

Shifting the paradigm of sperm maturation; global proteomic profiling of epididymal sperm

abs# 36

12:45PM

Louise Uoselis

Temporal landscape of mitochondrial proteostasis governed by the UPR^{mt}

abs# 37

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Lightning Talks Two

Chair: Nathan Croft

1:00 PM - 1:20 PM

Heritage Ballroom

1:00PM Gabriel Goncalves

IFNy Modulates the Immunopeptidome of Triple Negative Breast Cancer Cells by Enhancing and Diversifying Antigen Processing and Presentation *abs# 38*

1:03PM Ashleigh L Dale

An emerging role for protein lysine acetylation during *in vivo*-like growth in *Campylobacter jejuni* *abs# 39*

1:06PM Tara K Bartolec

Exploring the human structural proteome, complexome and interactome with deep, large-scale crosslinking mass spectrometry *abs# 40*

1:09PM Ignatius Pang

Differential abundance analysis of mono- and multi-phosphorylation sites with the ProteomeRiver pipeline *abs# 41*

1:12PM Samantha J Emery - Corbin

DIA-PASEF approaches for rapid and comprehensive plasma proteome analysis *abs# 42*

1:15PM Anup D Shah

Integrative statistical analysis and visualisation of phosphoproteomics and proteomic datasets *abs# 43*

Lunch and Poster Session Two

1:20 PM – 2:45 PM

Convention Centre

Bruker Lunch Workshop

1:30 PM – 2:30 PM

Heritage Ballroom

sponsored by



Free Afternoon

2:45 PM – 4:00 PM

Symposium Seven: Glyscience and Lipids

Chairs: Nichollas Scott & Michelle Colgrave

4:00 PM - 5:20 PM

Heritage Ballroom

4:00PM Morten Thaysen-Andersen

Community Evaluation of Glycoproteomics Software

abs# 44

4:25PM Michelle M Hill

Integrative multiomics unveils pathogenesis mechanisms of altered lipid metabolism in cancer

abs# 45

4:50PM Nathan P Croft

The immune system *does* have a sweet tooth! Characterising the glycosylated immunopeptidome through targeted interrogation of oxonium ion-containing spectra

abs# 46

5:05PM Daniel Kolarich

Leukaemia cell glycoproteomics uncovers the impact of drug resistance on CD38 site-specific glycosylation features and its protein structure

abs# 47

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Symposium Eight: New Technologies

Chairs: Andrew Webb & Mark Condina

5:20 PM - 6:15 PM

Heritage Ballroom

5:20PM Ralf B Schittenhelm

Phospho-Analyst: An interactive web-platform to analyse quantitative phosphoproteomics data 'with one click'

abs# 48

5:45PM Nick Morrice

Post translational modification analysis using Electron Activated Dissociation (EAD) on the ZenoTOF 7600 system

abs# 49

6:00PM Christoph Krisp

Bringing proteomics down to the single cell level

abs# 50

Saturday Keynote Lecture

Chairs: Anthony Purcell & Marc Wilkins

6:15 PM - 6:45 PM

Heritage Ballroom

6:15PM **Paola Picotti**
Bringing 3D proteome snapshots into functional proteomics screens
abs# 51

APS Conference Dinner

7:30 PM – 11:00 PM

Lorne Surf Life Saving Club

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SUNDAY, 6 FEBRUARY 2022

Symposium Nine: Structural Proteomics and Interactomics

Chairs: Mark Larence & Tara Bartolec

9:00 AM - 10:40 AM

Heritage Ballroom

9:00AM **Nevan Krogan**
An International Collaborative Effort to Identify Therapeutics for
COVID-19
abs# 52

9:30AM **Tara L Pukala**
Broadening the molecular view of snake venom proteomes
abs# 53

9:55AM **Subash Adhikari**
Benchmarking thermal proteome profiling techniques for target
interaction studies
abs# 54

10:10AM **Pirjo M Apaja**
Shifting picture of astrocyte responses through targeted spatial
organelle proteomics-based interactions
abs# 55

10:25AM **Thomas Nebl**
Adding native MS and HDX-MS to the protein analytics toolbox
bridging academia and industry
abs# 56

Morning Tea and Networking

10:40 AM – 11:10 AM

Convention Centre

Symposium Ten: Post-translational Modifications and Signalling

Chairs: Melanie White & Dylan Harney

11:10 AM - 12:30 PM

Heritage Ballroom

- 11:10AM** **Melissa Davis**
Not provided at time of publishing *abs# 57*
- 11:35AM** **Sean Humphrey**
Not provided at time of publishing *abs# 58*
- 12:00PM** **Ghizal Siddiqui**
Plasmodium falciparum's redox homeostasis is perturbed by
peroxide antimalarials *abs# 59*
- 12:15PM** **Edward SX Moh**
Establishing a multi-glycomics workflow to enable analysis of the
total glycome *abs# 60*

Closing Keynote Lecture

Chair: Stuart Cordwell

12:30 PM - 1:00 PM

Heritage Ballroom

- 12:30PM** **Ho Jeong Kwon**
Exploring drug-target-phenotype interaction using label-free small
molecules with LC-MS/MS and its translational impact *abs# 61*

Closing Ceremony and Award Presentation

Chair: Peter Hoffmann

1:00 PM - 1:30 PM

Heritage Ballroom

Bus Transfer to Melbourne Airport & City

2:45 PM Departing from the Mantra Lorne

The bus will travel first to Tullamarine (Melbourne) Airport (arrival time approx. 5:15pm), then into Melbourne city, dropping passengers at WEHI/University of Melbourne, Royal Parade (arrival time approx. 5:45pm).

POSTER LISTING

LIGHTNING POSTER PRESENTATIONS

Elise J Needham

Personalised phosphoproteomics identifies functional signalling

abs# 17

Shouxiang Zhang

Mapping cysteine exposure of proteins *in situ* with a bi-functional aggregation-induced emission fluorescent probe

abs# 18

Peter D Verhaert

Mass Spectrometry HistoChemistry for single cell peptidomics in *Homo sapiens* FFPE biobanks

abs# 19

Angela Juhasz

Gluten digestion – a more complex story than ever thought

abs# 20

Molly K Talbot

Acute treatment with antioxidant *N*-propionylglycine improves contractile function and minimises the extent of cysteine redox post-translational modifications in the diabetic heart as identified by quantitative mass spectrometry

abs# 21

Harley R Robinson

Infrared spectroscopy for rapid quality control and quantitation of lipid samples

abs# 22

Gabriel Goncalves

IFN γ Modulates the Immunopeptidome of Triple Negative Breast Cancer Cells by Enhancing and Diversifying Antigen Processing and Presentation

abs# 38

Ashleigh L Dale

An emerging role for protein lysine acetylation during *in vivo*-like growth in *Campylobacter jejuni*

abs# 39

Tara K. Bartolec

Exploring the human structural proteome, complexome and interactome with deep, large-scale crosslinking mass spectrometry

abs# 40

Ignatius Pang

Differential abundance analysis of mono- and multi-phosphorylation sites with the ProteomeRiver pipeline

abs# 41

Samantha J Emery-Corbin

DIA-PASEF approaches for rapid and comprehensive plasma proteome analysis

abs# 42

Anup D Shah

Integrative statistical analysis and visualisation of phosphoproteomics and proteomic datasets *abs# 43*

POSTER SESSION ONE - FRIDAY, 4 FEBRUARY 2022**Matthew J Fitzhenry**

Gas-phase fractionation of intact *E. coli* proteins by FAIMS *abs# 101*

Aziz AA Alnakli

A bioinformatic approach to Characterize the microbial proteome of the human plasma of SARS-CoV-2 patients *abs# 102*

Ching-Seng Ang

Getting more out of FLAG-Tag co-immunoprecipitation mass spectrometry experiments using FAIMS *abs# 103*

Ritchlynn Mr Aranha

The role of modifiers of the antigen presentation pathway on spliced peptide presentation in melanoma *abs# 104*

Utpal Bose

Identification and quantitation of alpha-amylase trypsin inhibitors in selectively bred ultra-low gluten barley lines *abs# 106*

Liesl M Bramberger

Investigating the effect of different HDACi on the antigen processing and presentation pathway in DIPG *abs# 107*

Daniel Bucio Noble

Optimising DIA Library Production *abs# 108*

Joel Cain

Detection of novel protein coding regions in *Campylobacter jejuni* using N-TAILS *abs# 109*

The Huong Chau

Mapping the Dynamic Glycome of Resting and Thrombin-Activated Platelets *abs# 110*

Sagar Dalal

Cell-type-specific identification by different glycan features in mammalian brain cells. *abs# 111*

Chris Desire

The importance of denaturing conditions for protein and peptide quantification by tryptophan fluorescence: a proteomic case study *abs# 112*

| | | |
|----------------------------------|--|-----------------|
| Toby A Dite | Multiplexing dimethyl labelled samples to enhance MS1 quantitation in single-cell proteomics | <i>abs# 113</i> |
| William A Donald | Multiplexed screening of thousands of natural products for protein-ligand binding in native mass spectrometry | <i>abs# 114</i> |
| Marisa N. Duong | Translational Proteomics: Establishing a Mass Spectrometry Assay for Biomarkers of Oesophageal Cancer | <i>abs# 115</i> |
| Izac Findlay | Phosphoproteomic profiling to complement genomics approaches to guide treatment selection for paediatric high-grade gliomas. | <i>abs# 116</i> |
| Zacary P Germon | Assessment of redox post-translational modifications (OxPTMs) reveals the mechanisms underpinning oncogenic signaling in FLT3-mutant Acute Myeloid Leukaemia | <i>abs# 117</i> |
| Shawn Goh | Use of functional T-cell assays and immunopeptidomics to decipher the molecular mechanism underpinning penicillin allergy | <i>abs# 118</i> |
| Joel P.A. Gummer | Confirmatory analysis of snake venoms by LC-HRMS for application to coronal toxicology | <i>abs# 119</i> |
| Fatemeh Habibpourmehraban | Distinct proteomic responses to multiple abiotic stresses in two rice genotypes | <i>abs# 121</i> |
| Joshua J Hamey | Crosstalk between phosphorylation and methylation on an essential protein translation factor | <i>abs# 122</i> |
| Sara Hamzelou | Mass spectrometry-based proteome analysis of seed dormancy in <i>Xanthium strumarium</i> L. (common cocklebur) | <i>abs# 123</i> |
| Daniel Hermanson | Proteome Discoverer 3.0 software with the CHIMERYS intelligent search algorithm: an AI-driven leap forward in peptide identification | <i>abs# 124</i> |
| Enzo Huang | Benchmark of Micro-flow Chromatograph for Robust Proteomics Analysis | <i>abs# 125</i> |

Enzo Huang

Multi-site assessment of precision and reproducibility of high-throughput capillary-flow LC-MS proteome profiling with novel ultra-high-pressure LC coupled to HRAM MS *abs# 126*

Ziyi Huang

Understanding the immunogenicity of human pluripotent stem cells via an immunopeptidomics approach *abs# 127*

Erin M Humphries

Performance of different trypsin sources on the preparation of formalin-fixed paraffin-embedded tissues for mass spectrometry *abs# 128*

Jason Ito

Protein Biomarkers of Obstructive Airway Diseases *abs# 129*

Peter Jackson

High-throughput multi-capillary SDS gel electrophoresis of proteins *abs# 130*

Edward Kerr

Fermenting yeasts and where to find them *abs# 132*

Tawfeek Khedr

Development and validation of an LC-MS/MS method for the analysis of quinolizidine alkaloid in lupin *abs# 133*

Jiwon Kim

Proteomic analysis of muscle cell organoid identifies proteins and pathways associated with aging *abs# 134*

Catherine Lawn

Barley variety controls the proteomic response to short periods of heat stress *abs# 135*

Yea Rin Olivia Lee

Gelatin-coated indium tin oxide slides improve human cartilage-bone tissue adherence and N-glycan signal intensity for mass spectrometry imaging *abs# 136*

Michael Leeming

Web-based phosphoproteomics data analysis with *Phosphomatics* *abs# 137*

Bruno Madio

Combining the data-driven and hypothesis-driven approaches in one go via a novel intelligent data acquisition Hybrid-DIA mass spectrometry strategy *abs# 138*

Bruno Madio

Routine single-shot identification of >9K proteins and >100K peptides with the next-generation low-flow UHPLC coupled to HRAM MS *abs# 139*

POSTER SESSION TWO - SATURDAY, 5 FEBRUARY 2022**Hartmut Schlüter**

No Title *abs# 151*

Farhad Masoomi-Aladizgeh

SWATH-MS analysis reveals global responses to heat in reproductive tissues of cotton (*Gossypium hirsutum*) *abs# 152*

John McManus

SARM1 in neuronal degeneration: Protein and phosphopeptide changes in a knockout mouse model following intraocular excitotoxic injury *abs# 153*

Parul Mittal

Cancer Tissue Classification Using Supervised Machine Learning Applied to MALDI Mass Spectrometry Imaging *abs# 154*

Kerry A Mullan

Using ggVolcanoR to visualize differential expression datasets *abs# 156*

Dylan H Multari

Assessment of deamidation ratios in modern and ancient bone collagen samples prepared using different extraction methods *abs# 157*

Joost LD Nelis

Towards rapid and robust food allergen quantification *abs# 158*

Ashley Nolan

Synthetic insulin overdose and quantitative analysis in post-mortem vitreous humour – forensic toxicology casework *abs# 159*

Tannith Noye

Mass Dynamics Analysis reveals S100A10 as a candidate protein for therapeutic targeting in Data Independent Acquisition Ovarian cancer cohort. *abs# 160*

Clare E O'Lone

Quantitative proteomics of the malt barley proteome: Understanding the impact of genetic variation on water uptake *abs# 161*

Selvam Paramasivan

Automated Proteomics Workflows for High-Throughput Library Generation and Label-Free Quantitation

abs# 162

Selvam Paramasivan

VPBrowse: An online repository for genome-based representation and quantification of 10,000 bovine proteins

abs# 163

Heather Patsiouras

Cyclic Ion Mobility-Enabled Mass Spectrometer and Application to High Throughput Plasma Proteomics

abs# 164

Heather Patsiouras

LipidQuan -Targeted Lipid Profiling solution

abs# 165

Mika Persson

Quantitative proteomic profiling of diffuse midline glioma cell lines treated with ONC201 identifies increased expression and surface localisation of members of the antigen presentation pathway

abs# 167

Michelle Q Phan

Native mass spectrometry interrogation of protein-ligand interactions and target identification

abs# 168

Rina Pokhrel

Characterisation of chemokine GPCRs signalling in monocytes using state-of-the-art phosphoproteomics approach

abs# 169

Jeremy Potriquet

Zeno MS/MS for Proteomics: IDA and MRMHR Workflows with the ZenoTOF 7600 system

abs# 170

Adam Rainczuk

Automated workflows for DIA data using DIA-NN on the PaSER platform

abs# 171

Umut Mr Rende

Identification and quantification of matrisome proteins in mouse kidneys

abs# 172

David Rudd

Safer next-generation polymyxins targeting priority Gram-negative pathogens

abs# 173

Thusi Rupasinghe

Using EIEIO as a novel fragmentation technique for complete lipid characterization in a complex matrix

abs# 174

Ryan J Separovich

Histone methylation enzymes are post-translationally regulated by upstream signalling pathways in budding yeast *abs# 175*

Chloe Shepherd

Defining the landscape of influenza antigen presentation in lung epithelial cells *abs# 176*

Joel R Steele

Azetidine-2-carboxylic acid incorporation into neuronal cell proteins: An agent for proteinopathies? *abs# 177*

Arineh Tahmasian

Relative quantification of allergens across 46 narrow-leafed lupin (NLL) genotypes for selective breeding applications *abs# 178*

Stephanie E L Town

An investigation into how proteomic informatics can currently address the needs of the clinic in characterising the antimicrobial resistance capabilities of a bacterial infection *abs# 179*

Julian Ugonotti

Immuno-active and antimicrobial paucimannosidic proteins form via a non-canonical truncation pathway in neutrophils *abs# 181*

Swati Varshney

Determination of lithium in various biological samples by ICP-MS. *abs# 182*

Steve Wilson

Ultra-sensitive proteome quantification on the timsTOF SCP mass spectrometer *abs# 183*

Jingran Ye

Novel cancer-specific antigenic epitopes for colorectal cancer immunotherapy *abs# 184*

Jumana M Yousef

Evaluation of RUVIIC normalization method in quantitative label-free DIA proteomics *abs# 185*

Muhammad A Zenaidee

Internal fragment assignments enhance top-down protein sequencing experiments which is beneficial for interrogating protein structure and localising protein-ligand binding *abs# 186*

Chun Zhou

The use of tetracycline-off system to study yeast with deficiency in both Ost3p and Ost6p *abs# 187*

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