

6th February 2020

Registration

2:00PM - 7:00PM Auditorium Foyer

Welcome Address

4:00PM - 4:10PM Auditorium

Chair: James Broadbent

The Simpson Lecture

4:10PM - 5:00PM Auditorium

Chair: James Broadbent

4:10 PM **Anne-Claude Gingras**

A proximity map of a human cell *abs# 1*

Ken Mitchelhill Young Investigator Award Lecture

5:00PM - 5:30PM Auditorium

Chair: Sean Humphrey



Session sponsored by

5:00 PM **Rebecca C Poulos**

Strategies to improve reproducibility of large-scale and longitudinal proteomics *abs# 2*

Vendor Talks

5:30PM - 5:45PM Auditorium

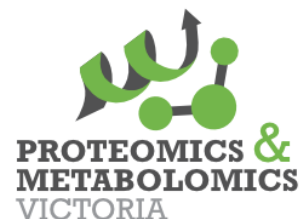
Chair: James Broadbent

Symposium One: Students of the APS (SoAPS)

5:45PM - 7:00PM Auditorium

Chairs: Ashleigh Dale & Shuai Nie

Session sponsored by



5:45 PM **Yi-Hsuan Tu**

The use of natural products in the leather industry: Depilation without damage. *abs# 3*

6:00 PM **Elizabeta Madzharova**

Functional modification of matrix metalloproteinase 9 by substrate glycosylation *abs# 4*

6:15 PM **Louise Uoselis**

The mitochondrial unfolded protein response: a global translational program that repairs local mitochondrial damage *abs# 5*

6:30 PM **Alexander W. Rookyard**

Quantitative proteomics of irreversible cysteine post translational modifications in myocardial ischemia / reperfusion (I/R) injury *abs# 6*

6:45 PM **Chun Zhou**

Glycopeptide variable window SWATH for improved Data Independent Acquisition glycoproteomics *abs# 7*

Welcome Reception

7:00PM - 10:00PM Exhibition Hall

7th February 2020

Registration

7:15AM - 5:00PM Auditorium Foyer

Shimadzu Breakfast Workshop - Benefits of targeted omics workflows and beyond

7:45AM - 8:40AM Auditorium

Confirmed Speakers

Atsuhiko 'Ash' Toyama, Shimadzu Corporation, Singapore/Japan

Chris Bowen, Shimadzu Scientific Instruments, Australia

Program

Two presentations will be given covering the following topics:

“Breaking the sensitivity barrier to unravelling the novel roles of lipid mediators in pathophysiology” by **Ash Toyama, Ph.D.**

1) A brief overview of Shimadzu's targeted omics solution portfolio, each addressing the difficulty of the targeted class of compounds by unique approaches.

2) The recent progress using the LC/MS/MS Lipid Mediators Method Package in a collaborative work with the University of Tokyo, illustrating that method reproducibility is the most critical factor for delivering scientifically meaningful outcome.

3) Tools to assist data processing and interpretation

“The Q-TOF technologies to reproduce the benefits of targeted workflows in high-resolution analyses” by **Chris Bowen**

1) Ultra-fast data acquisition and ion accumulation

2) UFgrating and iRefTOF – simple ideas made possible by meticulous engineering

3) Flight tube thermostability for exceptionally stable mass measurement accuracy

4) DIA capabilities

5) Nexera Mikros, the microflow solution with great ease

This conference acknowledges the sponsorship of



Symposium Two: Disease Proteomics I

8:50AM - 10:20AM Auditorium

Chairs: Patricia Illing & Desmond Li

Session sponsored by



8:50 AM **Philipp E Geyer**

Plasma proteome profiling to assess human health and disease *abs# 8*

9:20 AM **Anthony Purcell**

Precision cancer immunotherapy - can proteomics rise to the challenge? *abs# 9*

9:35 AM **Harley Robinson**

Caveolae formation alters intracellular organelle composition and function *abs# 10*

9:50 AM **Stephanie L Rayner**

Rapid, unbiased identification of protein inclusion components from patient post-mortem brain tissue using Biotinylation by Antibody Recognition (BAR) *abs# 11*

10:05 AM **Mark A Baker**

Splicing up your sex life *abs# 12*

Vendor Talks

10:20AM - 10:30AM Auditorium

Chairs: Patricia Illing & Desmond Li

Morning Tea

10:30AM - 11:00AM Exhibition Hall

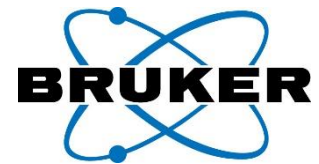
This conference acknowledges the sponsorship of



Symposium Three: Environmental, Microbial, Plant Proteomics

11:00AM - 12:50PM Auditorium

Chairs: Mark Condina & Balu Balan



Session sponsored by

11:00 AM **Matthias Trost**

The role of ubiquitylation on the phagosome: a tale of inflammatory responses and vesicle trafficking *abs# 13*

11:30 AM **Angela Juhasz**

Proteogenomic characterization of einkorn wheat cultivars with low celiac disease response *abs# 14*

11:50 AM **Lok Man**

Multi-omic analysis and functional validation of *Campylobacter jejuni* grown with intestinal bile salts *abs# 15*

12:05 PM **Delphine Vincent**

Proteomics tools for medicinal cannabis *abs# 16*

12:20 PM **Sophia Escobar-Correas**

DIGESTIVE PHYSIOLOGY AND PROTEOMICS FOR CONTROLLING AN INVASIVE PEST *abs# 17*

12:35 PM **Tao Wang**

LC-MS/MS-based multi-omics approach to elucidate developmental adaptations in the parasitic nematode *Haemonchus* *abs# 18*

Lightning Talks One

12:50PM - 1:10PM Auditorium

Chair: Ben Crossett

12:50 PM **Cassandra Pegg**

Cellular glycoproteome and proteome during influenza infection *abs# 19*

12:53 PM **Balu Balan**

“RNA regulons” as potential drivers of *Giardia duodenalis* stage transition *abs# 20*

12:56 PM **Joel Cain**

Identification of novel *N*-glycosylation sites from the bacterium *Campylobacter jejuni* *abs# 21*

12:59 PM **Robert JA Goode**

Understanding glycopeptide antibiotic synthesis by mass spectrometric analysis of polycyclic peptides *abs# 22*

1:02 PM **Hannah McKerchar**

Characterising insult-induced protein-protein crosslinks formed during food processing *abs# 23*

1:05 PM **Gabriel Goncalves**

Multi-omic analysis reveals the pro-inflammatory cytokine IFN γ modulates the immunopeptidome of triple negative breast cancer cells. *abs# 24*

Lunch and Poster Session One

1:10PM - 3:10PM Exhibition Hall

ThermoFisher Workshop

2:10PM - 3:10PM Auditorium

Dissecting the roles of glycosylation on bacterial proteins within the *Burkholderia* genus

Dr Nichollas Scott

Department of Microbiology and Immunology, The University of Melbourne

Bio: Dr Scott completed his PhD at the University of Sydney (2007 to 2012) on the development of MS approaches for the study of bacterial protein modifications. The key focus of his doctorate was the establishment of a protocol for enriching bacterial glycopeptides irrespective of glycan composition. In 2012 with the aid of a NHMRC Early Career Fellowship he moved to the University of British Columbia to undertake a postdoc with Prof Leonard Foster. Within the Foster lab Dr Scott began applying quantitative proteomics approaches to study protein interactions and bacterial glycosylation systems at a systems level. From 2012 to 2015 Dr Scott spearheaded projects to characterise bacterial glycosylation systems across Gram-negative pathogens including, *Acinetobacter baumannii*, *Burkholderia cenocepacia* and *Ralstonia solanacearum*. In 2016 Dr Scott returned to Australia where he completed a second postdoc in the laboratory of Prof Elizabeth Hartland, developing novel enrichment approaches to track Arginine-glycosylation. In 2017, on the back of two national awards from the Australasian Proteomics Society (the

2016 International Early Career Award & the 2017 Ken Mitchelhill Award), NHMRC and ARC funding Dr Scott established his independent research group in the Department of Microbiology and Immunology at the University of Melbourne. Since 2017 Dr Scott's lab has sought to identify and track microbial glycosylation events to understand the role of glycosylation in microbial pathogenesis. In 2019 in recognition of his contribution to the field of glycoconjugate research Dr Scott was awarded the 2019-IGO Young Glycoscientist Award from the International Glycoconjugate Organization.

Abstract: Protein glycosylation, the chemical addition of sugars to proteins, is an important but poorly understood aspect of bacterial physiology. Recently we identified that multiple human pathogens of the *Burkholderia* genus possess a conserved O-linked glycosylation system. High-throughput screening studies have shown the inhibition of glycosylation profoundly impacts virulence in *Burkholderia*, yet little is known about the underlying mechanism. Using the Cystic fibrosis pathogen *B. cenocepacia* as a model we have sought to improve our understanding of the role of glycosylation within *Burkholderia* species. Using state of the art proteomics approaches we have now identified >70 proteins are glycosylated at over 110 sites across strains of *B. cenocepacia*. Mutagenesis studies have shown that the loss of glycosylation leads to profound effects on the proteome with quantitative proteomics/degradomics revealing that a subset of glycoproteins require glycosylation for stability. Using thermal proteomics, we have also begun to track the effect of glycosylation on protein stability within the proteome. Our quantitative proteomics, degradomics and thermal proteomics results support that glycosylation plays multiple roles in the biology of *B. cenocepacia*. By understanding how glycosylation contributes to *B. cenocepacia* protein function this work will improve our ability to harness bacterial glycosylation to create bespoke glycoconjugates.

Direct measurement of protein translation and degradation rates In vivo at proteomic scales in the clinic and beyond; new approaches to stable isotope metabolic labelling and analysis

Dr Owen Duncan

School of Molecular Sciences, The University of Western Australia

Bio: Dr Duncan is a Post-doctoral Research Fellow working in Harvey Millar's laboratory at the University of Western Australia. His main area of work is the development of mass spec based data acquisition and processing focusing on metabolic incorporation of stable isotopes for measuring flux at the protein level (protein synthesis and degradation rates). His PhD studies were supervised by Prof. Ryan Lister and Jim Whelan where he used early QTOF instruments combined with an intricate free flow electrophoresis based subcellular fractionation workflow to establish the mitochondrial outer membrane proteome in higher plants. He has since worked with nanoflow proteomics daily and have recently been involved in the establishment and commissioning of the Western Australian Proteomics core facility established with NCRIS funding in December 2019 which is focused on the delivery of flux proteomics to researchers nationally.

Abstract: Protein abundances are established by the combination of synthesis and degradation; the direct measurement of which has been complex and time consuming for individual proteins and simply not possible at scale. Advances at the University of Western Australia using stable isotope labelling combined with mass spectrometry has allowed the parallel measurement of synthesis and degradation rates of hundreds to thousands of protein species in a single sample. In collaboration with researchers at the Fiona Wood Foundation we've refined the use of heavy hydrogen in the form of deuterium oxide ($^2\text{H}_2\text{O}$) coupled to skin biopsies and mass spectrometry to measure the synthesis and degradation

rates of various isoforms of collagen in human burns patients over time in scar vs non scar skin with the aim of both determining when the most effective times are to apply drug based interventions in scar formation and to measure their efficacy. The second part of this talk will cover experimental design and other examples of protein flux measurements.

This conference acknowledges the sponsorship of

Symposium Four: Post-Translational Modifications and Signalling

3:15PM - 4:50PM Auditorium

Chairs: Samantha Emery-Corbin & Benjamin Parker

ThermoFisher
S C I E N T I F I C

3:15 PM **Judit Villen**

To be provided *abs# 25*

3:45 PM **David Komander**

New tools to study protein ubiquitination *abs# 26*

4:05 PM **Stuart Cordwell**

Deciphering irreversible cysteine redox post-translational modifications in myocardial ischemia / reperfusion injury *abs# 27*

4:20 PM **Dylan J Harney**

HNF4A sumoylation is regulated by fasting. *abs# 28*

4:35 PM **Chris Overall**

Protein TAILS tell remarkable tales: Positional proteomics reveals diverse N-Terminomes and proteolytic landscapes in disease *abs# 29*

APS Annual General Meeting

5:00PM - 5:45PM Auditorium

Students of the APS (SoAPS) Event with Invited Speakers

5:30PM - 7:30PM

This conference acknowledges the sponsorship of

ThermoFisher
S C I E N T I F I C

Satellite Symposium - Welcome

8:55AM - 9:00AM Horizons Room

Chair: Melanie White

Satellite Symposium – Opening Plenary

9:00AM - 9:30AM Horizons Room

Chair: Melanie White

9:00 AM **Kylie Bemis**

Challenges in Visualization and Analysis of Mass Spectrometry Imaging Experiments *abs# 30*

Satellite Symposium - Session One: Software Tools

9:30AM - 10:30AM Horizons Room

Chair: Melanie White

9:30 AM **George GUO**

MassOmics: An R package of a cross-platform data processing pipeline for large-scale GC-MS untargeted metabolomics datasets. *abs# 31*

9:45 AM **Mohammad Shahbazy**

MHCpLogics: a machine learning-based tool for unsupervised data visualisation and cluster analysis of immunopeptidomes *abs# 32*

10:00 AM **Hartmut Schlüter**

OmixLitMiner - Tool for fast evaluation of knowledge and importance of regulated individual proteins derived from differential proteomics *abs# 33*

10:15 AM **Hani Jieun Kim**

CiteFuse enables multi-modal analysis of CITE-seq data *abs# 34*

Satellite Symposium - Session Two: Representing Function

11:00AM - 12:15PM Horizons Room

Chair: Laura Dagley

11:00 AM **Sean J Humphrey**

Stimulomics: large-scale mapping of signalling networks downstream of major cell surface receptors abs# 35

11:30 AM **Elise J. Needham**

Precision phosphoproteomics reveals kinase targets enhancing muscle insulin sensitivity *abs# 36*

11:45 AM **Gene Hart-Smith**

Analytical guidelines for co-fractionation mass spectrometry obtained through global profiling of gold standard *Saccharomyces cerevisiae* protein complexes *abs# 37*

12:00 PM **Anjaneyaswamy Ravipati**
Lipidomic Mapping, Localization and Characterization in Tissues by MALDI-
Imaging Mass Spectrometry *abs# 38*

Satellite Symposium - Session Three: Integrating Multiple Technologies

12:15PM - 1:05PM Horizons Room

Chairs: Anup Shah & Andrew Webb

12:15 PM **Mark Larance**
Multi-Omics Analysis of the Intermittent Fasting Response *abs# 39*

12:35 PM **Stephanie E L Town**
Using genomics and proteomics to understand the antibiotic resistance
capabilities of a bacterial pathogen *abs# 40*

12:50 PM **Hitesh Kore**
Protein coding potential of annotated non-coding RNAs encoded by the human
genome *abs# 41*

Satellite Symposium - Lunch and Poster Session One

1:05PM - 3:15PM Exhibition Hall

Satellite Symposium - Session Four: Interpreting Multiple Technologies

3:15PM - 4:30PM Horizons Room

Chair: Nicholas Williamson

3:15 PM **Ignatius Pang**
The Hitchhiker's Guide to the Yeast Interactome *abs# 42*

3:40 PM **Thomas Kislinger**
Identification of aggressive prostate cancer through in-depth proteomics of tissues
and urines *abs# 43*

4:00 PM **Ralf Schittenhelm**
LFQ-Analyst, an interactive web-platform to analyse quantitative proteomics
data *abs# 44*

4:15 PM **Rebeca Kawahara Sakuma**
Deciphering the stage-specific glycoprotein signatures of colorectal cancer using
integrated mass spectrometry-based omics *abs# 45*

Satellite Symposium - Closing Plenary

4:30PM - 5:00PM Horizons Room

Chair: Ralf Schittenhelm

4:30 PM **David Powell**

Interactive visualisation, and reproducibility in bioinformatics *abs# 46*

Satellite Symposium – Closing Ceremony and Award Presentation

5:00PM - 5:10PM Horizons Room

Chair: Melanie White

8th February 2020

SCIEX Breakfast Workshop

7:00AM - 8:30AM Horizons Room

Steve Tate, PhD – Manager Software Applications Research Group – “Enabling ultra-fast proteomics with deep sample coverage”

Jérémy Potriquet, PhD – Field Application Scientist & OMICS Market Development – “Evaluation of the use of in silico libraries in DIA experiments”

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Registration

8:00AM - 5:30PM Auditorium Foyer

Symposium Five: Statistics, Data Science and Machine Learning

9:00AM - 10:35AM Auditorium

Chairs: Melanie White & Robert Goode

9:00 AM **Martin Krzywinski**

Fitting big science on a small page *abs# 47*

9:30 AM **Pengyi Yang**

Trans-omic characterisation of stem cell networks *abs# 48*

9:50 AM **Cecilia Lindskog**

The Human Protein Atlas - Implications for Human Biology and Precision Medicine *abs# 49*

10:05 AM **Michael G Leeming**

Phosphomatics: A knowledge-based approach to investigating high-throughput phosphoproteomics data *abs# 50*

10:20 AM **Daryl Wilding-McBride**

Delving deeper into the proteome with an improved and highly parallelised feature detection pipeline for the Bruker timsTOF Pro *abs# 51*

Morning Tea

10:35AM - 11:00AM Exhibition Hall



This conference acknowledges the sponsorship of

Symposium Six: Disease Proteomics II + KHUPO

11:00AM - 1:05PM Auditorium

Chairs: Rommel Mathias & Harley Robinson

11:00 AM **Aleksandra Filipovska**

Fidelity of protein synthesis is required for energy production *abs# 52*

11:30 AM **Michelle M Hill**

Addressing unmet clinical diagnostic needs with proteomics *abs# 53*

11:50 AM **Keshava K. Datta**

Global proteomic and phosphoproteomic profiling to identify proteins and pathways that regulate cell survival in hypoxic conditions *abs# 54*

12:05 PM **Lauren A Thurgood**

Analysis of FFPE tissues to investigate lymph node protein expression in patients with leukemia *abs# 55*

12:20 PM **Per E. Andren**

Simultaneous mass spectrometry imaging of multiple neuropeptides in the brain and alterations induced by experimental Parkinsonism and L-DOPA therapy *abs# 56*

12:35 PM **J. Eugene Lee**

Reference proteome-based subtyping of liver cancer *abs# 57*

12:50 PM **Taejoon Kwon**

Ciliary proteome from motility-defective multiciliated cells *abs# 58*

Lightning Talks Two

1:05PM - 1:30PM Auditorium

Chair: Nathan Croft

1:05 PM **Christopher H Caboche**

Mini-malting and mini-mashing methods for early stage validation of new barley varieties and malt accreditation and quality control of beer brewing *abs# 59*

1:09 PM **Ryan Separovich**

The role of upstream phosphorylation in the regulation of histone methylation *abs# 60*

1:13 PM **Natasha Vassileff**

Revealing the proteome of brain derived exosomes isolated from human amyotrophic lateral sclerosis post-mortem tissues *abs# 61*

1:17 PM **Rune H Larsen**

Development of a primary cell proficient phosphoproteomic workflow *abs# 62*

1:21 PM **Elena Smertina**

Studying uncharacterised non-structural proteins of Rabbit haemorrhagic disease virus *abs# 63*

1:25 PM **Amy BP Ribet**

Mapping the lysosomal transporter proteome of osteoclasts uncovers new regulators of bone homeostasis *abs# 64*

Lunch and Poster Session Two

1:30PM - 2:45PM Exhibition Hall



Session sponsored by

Bruker Workshop

2:30PM - 3:30PM Auditorium

Mass spectrometry (MS)-based proteomics has become a powerful technology for the identification and quantification of thousands of proteins. However, the coverage of complete proteomes is still very challenging due to the limited speed, sensitivity and resolution of current mass spectrometers.

The timsTOF Pro uses the Parallel Accumulation Serial Fragmentation (PASEF) acquisition method to provide extremely high speed and sensitivity to reach new depths in shotgun proteomics and phosphoproteomics, using low sample amounts.

We are privileged to have two international speakers who will present some of their cutting edge results from the latest ion mobility enabled platform

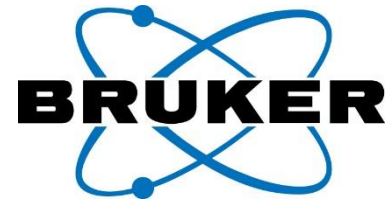
Prof. Matthias Trost - Professor of Proteomics Institute for Cell and Molecular Biosciences, Faculty of Medical Sciences, Newcastle University, UK

Using the timsTOF Pro to study ubiquitylation in innate immunity

Dr. Ben Collins - School of Biological Sciences, Queens University, Belfast, UK

Data-independent acquisition combined with parallel accumulation – serial fragmentation combined (diaPASEF): Bottom-up proteomics with increased ion usage

This conference acknowledges the sponsorship of



Symposium Seven: Glycoscience

4:00PM - 5:20PM Auditorium

Chairs: Nichollas Scott & Matthew Briggs

4:00 PM **Stacy Malaker**

Defining the "mucinome": enzyme toolkit for enrichment and analysis of mucin-domain glycoproteins *abs# 65*

4:30 PM **Ethan Goddard-Borger**

Tools and methods for probing the biology of tryptophan C-mannosylation *abs# 66*

4:50 PM **Morten Thaysen-Andersen**

Granule-Specific *N*-Glycosylation and Chlorination Activity of Neutrophil Myeloperoxidase *abs# 67*

5:05 PM **Shutao Mei**

Immunopeptidomic analysis reveals that deamidated HLA-bound peptides arise predominantly from deglycosylated precursors *abs# 68*

5:20 PM **Kathirvel Alagesan**

Synthetic Glycopeptides assisted large scale glycoproteomics from sample preparation to data analysis *abs# 69*

Symposium Eight: New Technologies I

5:20PM - 6:40PM Auditorium

Chair: Jarrod Sandow

5:20 PM **James Hudson**

Proteomics Combined with Human Cardiac Organoids to Find New Mechanisms Driving Maturation and Regeneration *abs# 70*

5:40 PM **Mark Larance**

Characterisation of a putative new metabolic hormone in human plasma *abs# 71*

5:55 PM **Parthiban Periasamy**

Strategies to enrich low-molecular weight proteins for proteomic analysis *abs# 72*

6:10 PM **Brooke A Dilmetz**

Rapid separation and identification of beer spoilage bacteria by inertial microfluidics and MALDI-TOF mass spectrometry *abs# 73*

6:25 PM **Paul D Veith**

Deglycosylation of glycoproteins with trifluoromethanesulfonic acid (TFMS): unravelling the chemistry allows extension of the protocol to the analysis of released glycan chains using standard proteomics methods *abs# 74*

APS Conference Dinner/Festival of Food

7:30PM - 11:00PM Umisango, Jashn & Lorne Central

9th February 2020

Registration

8:30AM - 1:30PM Auditorium Foyer

Symposium Nine: New Technologies II

9:00AM - 10:40AM Auditorium

Chair: Ralf Schittenhelm

9:00 AM **Tara L Pukala**

An integrated mass spectrometry approach towards characterisation of snake venom proteins *abs# 75*

9:20 AM **Nicola Beckett**

Detection of intact insulin analogues in post-mortem vitreous humour using forensic toxicology and proteomic tools – application to overdose casework *abs# 76*

9:35 AM **Brett Hamilton**

functional-Mass Spectrometry Imaging - mapping the location of enzymes by their function *abs# 77*

9:50 AM **Scott Bringans**

PromarkerD as an immunoaffinity mass spectrometry assay for diabetic kidney disease *abs# 78*

10:05 AM **Emmanuelle Claude**
Metabolomic/lipidomic DESI imaging of different cell cultures. *abs# 79*

10:20 AM **Stephan Klatt**
Quantitative, targeted and high-throughput metabolomics workflow of small-volume plasma samples via blood cards. *abs# 80*

Morning Tea (Winners of Vendors Prizes and Passport Prize)

10:40AM - 11:10AM Exhibition Hall

Symposium Ten: Interactomics

11:10AM - 12:20PM Auditorium

Chairs: Mark Larance & Naomi Koh Belic

11:10 AM **Ben Collins**
Complex-centric proteome profiling in one day with SEC-SWATH-MS *abs# 81*

11:40 AM **Melissa Davis**
What are we missing? The hidden impact of missing values in proteomics analysis and results *abs# 82*

12:00 PM **Jeffrey Smith**
Global and sequence-targeted purification of intact RBP-RNA complexes *abs# 83*

12:15 PM **Ashleigh L Dale**
Defining the *Campylobacter jejuni* interactome by cross-linking mass spectrometry (XL-MS) *abs# 84*

Closing Keynote Lecture

12:30PM - 1:00PM Auditorium

Chair: Nichollas Scott

Robert L Moritz
Comprehensive Quantitative Stability Assay (CQSA) system for defining the molecular resolution of protein-compound interactions in *Mycobacterium tuberculosis*. *abs# 85*

Closing Ceremony and Award Presentation

1:00PM - 1:30PM Auditorium

Chair: James Broadbent