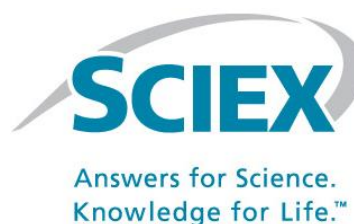


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## THURSDAY, 7th February 2019

**Registration**

2:00pm - 7:00pm Auditorium Foyer

**Welcome Address**

4:00pm - 4:10pm Chair: Stuart Cordwell Auditorium

**The Simpson Lecture**

4:10pm - 5:00pm Chair: Stuart Cordwell Auditorium

4:10PM **Ileana Cristea**

Integrative omics at the core of discoveries in virology

abs# 1

**Ken Mitchelhill Young Investigator Award Lecture**

5:00pm - 5:30pm Chair: Stuart Cordwell Auditorium

5:00PM **Sean J Humphrey**

High-sensitivity phosphoproteomics reveals pathogenic signalling changes in diabetic islets

abs# 2

Proudly supported by

**Symposium One: Students of the APS (SoAPS)**

5:30pm - 7:00pm Chair: Nichollas Scott Auditorium

5:30PM **Tara K Bartolec**

Large scale crosslinking mass spectrometry to map the yeast nuclear interactome

abs# 3

5:45PM **Desmond K Li**

Multi-omic profiling of the liver in a rat model of type 2 diabetes

abs# 4

6:00PM **Kevin Huynh**

In-depth lipidomic profiling of the Australian imaging biomarker and lifestyle flagship study of aging

abs# 5

6:15PM **Harley R Robinson**

Development of integrative Protein and Lipid Organelle Profiling (iPLOP) method for high throughput organelle analysis

abs# 6

6:30PM **Ashleigh L Dale**

Defining the Campylobacter jejuni interactome by cross-linking mass spectrometry (XL-MS)

abs# 7

6:45PM **Kirti Pandey**

In depth definition of the immunopeptidome in haematological malignancies and its potential for immunotherapy

abs# 8

**Welcome Reception**

7:00pm - 10:00pm Exhibition Hall

**Registration**

6:45am - 6:40pm

Auditorium Foyer

**ThermoFisher Workshop**

7:15am - 8:45am

Auditorium

- **Ralf Schittenhelm**

A DIA-based, phosphoproteomic study to decipher pathways involved in MCP-1/ CCR2 chemokine signalling

- **Nichollas Scott**

An atlas of protein-protein interactions across mouse tissues

Proudly Supported by


**Symposium Two: Disease Proteomics I**

9:00am - 10:30am Chair: Mark Molloy

Auditorium

9:00AM **Je-Yoel Cho**

Lung cancer proteome biomarkers and in vitro diagnostics-multivariate index assay

abs# 9

9:30AM **Pouya Faridi**

Spliced HLA peptides, a novel source for immunotherapy

abs# 10

9:50AM **Rebecca C Poulos**

1,566 prostate cancer proteomes generated by PCT-SWATH mass spectrometry reveal insights into patient survival and time to recurrence

abs# 11

10:10AM **Christoph Krisp**

Proteomic profiling of stage I – IV colorectal carcinoma specimen for early onset biomarker detection

abs# 12

**Morning Tea**

10:30am - 11:00am

Exhibition Hall

**Symposium Three: Environmental, microbial, plant proteomics**

11:00am - 12:50pm Chair: Michelle Colgrave

Auditorium

11:00AM **Setsuko Komatsu**

Soybean proteomics: Application to elucidation of flooding-tolerant mechanisms

abs# 13

11:30AM **William Klare**

Proteomics for vaccine discovery: development of two potential whole-protein vaccines with efficacy against *Pseudomonas aeruginosa*

abs# 14

11:50AM **Utpal Bose**

Identification and quantitation of wheat and barley  $\alpha$ -amylase trypsin inhibitors, the triggers of non-coeliac gluten sensitivity

abs# 15

12:10PM **Xinle Tan**

SWATH-MS reveals functional differences between glycogenin 1 and 2 in yeast metabolism

abs# 16

12:30PM **Balu Balan**

RNA binding proteins mediated post transcriptional regulation in protist stage transitions

abs# 17

**Lightning Talks One**

12:50pm - 1:10pm Chair: Ben Crossett

Auditorium

**Stuart Brown**

A search for predictive biomarkers of ovine pre-partum vaginal prolapse

abs#64

**Alexander W. Rookyard**

Multi-omic profiling of metabolic dysfunction caused by myocardial ischemia / reperfusion (I/R) injury

abs#65

**Rohan Shah**

Proteomic heterogeneity of high-grade serous ovarian carcinomas

abs#66

**Dylan J Harney**

High-throughput sample preparation for proteomic analysis using 3d-printing

abs#67

**Syeda Sadia Ameen**

Deep neuroproteomics reveal defective synaptic signalling in excitotoxicity

abs#68

**Inga Boll**

The sweet connections in neurotransmission – investigating sialylated glycosylation in the active zone of nerve terminals

abs#69

### Lunch and Poster Session One

1:10pm - 2:45pm

Exhibition Hall

Proteomics 2019 & Metabolomics Symposium posters are displayed together. Please refer to the poster listing on page 20.

Proudly supported by



### SCIEX Workshop

2:45pm - 3:45pm

Auditorium

• **Katherine Hyland**

Global Technical Marketing - Food and Environmental – SCIEX

Proudly supported by



### Free Afternoon

2:45pm - 5:00pm

### Symposium Four: Post-translational modifications and signalling

5:00pm - 6:40pm Chair: Melanie White

Auditorium

5:00PM **Joshua J Hamey**

Methylation throughout the proteome: The methyltransferases tell the story

abs# 18

5:20PM **Elise J Needham**

Interactions between small molecules recapitulate the exercise phosphoproteome and regulate protein secretion in vitro

abs# 19

5:40PM **Soumya Mukherjee**

Distribution of isomerized and racemized amyloid  $\beta$  isoforms in the Human Brain using ion-mobility mass spectrometry

abs# 20

6:00PM **Samantha J Emery-Corbin**

The reduced protein methylation network in the early-branching protozoan parasite, *Giardia duodenalis*

abs# 21

6:20PM **Heung-Chin Cheng**

Phosphoproteomic analysis incorporating titanium dioxide - and phosphotyrosine superbinder SH2 domain-affinity purification unveils unique signaling mechanism of the tumour suppressor protein kinase CHK in colorectal cancer cells

abs# 22

### Festival of Food

7:30pm - 10:30pm

Unisango, Jashn & Lorne Central

Network with fellow delegates during a relaxed food festival style function. With three restaurants combining there will be something for everyone, including Japanese (Unisango), Indian (Jashn) and Australian (Lorne Central) cuisine.

**Metabolomics Symposium - Welcome**

8:55am - 9:00am Chair: Berin Boughton Horizons Room

**Metabolomics Symposium - Opening Plenary**

9:00am - 9:30am Chair: Berin Boughton Horizons Room

9:00AM **Ron M.A. Heeren** *abs# 23*  
Spatial proteomics with translational imaging mass spectrometry**Metabolomics Symposium - Session One: Imaging and small molecules**

9:30am - 10:30am Chair: Berin Boughton Horizons Room

9:30AM **Darren Creek** *abs# 24*

Combining chemical biology tools with metabolomics to identify small molecule targets of peroxide antimalarials

9:50AM **Simone Rochfort** *abs# 25*

The cannabis metabolome

10:10AM **Alastair B Ross** *abs# 26*

Rapid Evaporative Ionisation Mass Spectrometry: a new tool for rapid screening of detailed composition data in food

**Metabolomics Symposium - Morning Tea**

10:30am - 11:00am Exhibition Hall

**Metabolomics Symposium - Session Two: Lipidomics**

11:00am - 12:50pm Chair: Michelle Hill Horizons Room

11:00AM **Robert Trengove** *abs# 27*

Utilising metabolic profiling and inflammation markers as diagnostic tools

11:30AM **Gavin Reid** *abs# 28*

Uncovering the role of brain-derived lipid exosomes in Alzheimer's disease

11:50AM **Ahmed Mohamed** *abs# 29*

Lipidr: targeted lipidomics analysis workflow in R

12:10PM **Shuai Nie** *abs# 30*The developmental lipidome and proteome of *Haemonchus contortus* reflect unique adaptations in the transition to parasitism12:30PM **Lauren A Thurgood** *abs# 31*

Hooked on fat: nutrient uptake in chronic lymphocytic leukaemia

12:50PM **Rong Xu** *abs# 32*

Surfaceome of exosomes secreted from the colorectal cancer cell line SW480

**Metabolomics Symposium - Lunch & Poster Session**

1:10pm - 2:30pm Exhibition Hall

Metabolomics Symposium &amp; Proteomics 2019 posters are displayed together. Please refer to the poster listing on page 21.

**Metabolomics Symposium - Session Three: Disease metabolomics**

5:00pm - 6:10pm Chair: Gavin Reid Horizons Room

5:00PM **Kristin K Brown** *abs# 33*

Metabolic reprogramming in cancer

5:30 PM **Jeffrey Molendijk** *abs# 34*

Multi-omics analysis of esophageal adenocarcinoma reveals impaired lipid antioxidant mechanisms during disease progression

5:50PM **Anubhav Srivastava** *abs# 35*

From phenotypic screens to mode of action: A metabolomics approach to guide the development of novel anti-trypanosomal Drugs

**Metabolomics Symposium - Closing Plenary**

6:10pm - 6:40pm Chair: Gavin Reid Horizons Room

6:10PM **Jessica A Lasky-Su** *abs# 36*

A meta-analysis of metabolites associated with BMI in &gt; 30,000 individuals from the COMETs consortium

**SATURDAY, 9th FEBRUARY 2019**

**Registration**

8:30am - 6:40pm Auditorium Foyer

**Symposium Five: Statistics**

9:00am - 10:30am Chair: Ralf Schittenhelm Auditorium

9:00AM **Olga Vitek** *abs# 37*

Components of reproducible quantitative mass spectrometry-based research: a statistician's perspective

9:30AM **Brett Tully** *abs# 38*

Toffee: A highly compressed file format for time of flight and orbitrap DIA-MS

9:50AM **Anup D. Shah** *abs# 39*

LFQ-Analyst: An interactive web-platform to analyse quantitative proteomics data

10:10AM **Hannah Huckstep** *abs# 40*

Signalling networks in the analysis of proteomic data

**Morning Tea**

10:30am - 11:00am Exhibition Hall

**Symposium Six: Disease Proteomics II**

11:00am - 1:10pm Chair: Anthony Purcell Auditorium

11:00AM **Leonard Foster** *abs# 41*

An atlas of protein-protein interactions across mammalian tissues

11:30AM **Albert Lee** *abs# 42*

Pathogenic mutation in the ALS/FTD gene, CCFN, causes elevated Lys48-linked ubiquitylation and defective autophagy

11:50PM **Mark Larance** *abs# 43*

Systems proteomics of the intermittent fasting response highlights the importance of HNF4A

12:10PM **Nathan P Croft** *abs# 44*

Systems immunology reveals the importance of direct and cross-presentation in driving cytotoxic T lymphocyte responses to distinct epitopes

12:30PM **Ahmed Mohamed** *abs# 45*

Integrated time-series analysis of proteomic and transcriptomic profiles for activated human T-cell function

12:50PM **Terry C.C Lim Kam Sian** *abs# 46*

New insights into HLA-B27 peptide repertoire: Elucidating the connection between *Salmonella* infection and ankylosing spondylitis

**Lightning Talks Two**

1:10pm - 1:30pm Chair: Nicholas Williamson Auditorium

**Shawn Goh** *abs# 102*

Peptides and Penicillins: Identifying the immunogenic  $\beta$ -lactam ligand(s)

**Stephanie E L Town** *abs# 103*

Using genomics and proteomics to understand the antibiotic resistance capabilities of an isolate

**Md Arifur Rahman** *abs# 104*

Extractomes profiling reveals potential role of key proteins in *Staphylococcus aureus* biofilm using TMT-based quantitative mass spectrometry

**Sayantani Chatterjee** *abs# 105*

Accessing the mannose-6-phosphate glycoproteome using titanium dioxide (TiO<sub>2</sub>) enrichment

**Ryan J Separovich** *abs# 106*

The role of upstream phosphorylation in the regulation of histone methylation

**Naomi Koh Belic** *abs# 107*

Characterisation of human adipose stem cells

**Lunch and Poster Session Two**

1:30pm - 2:45 pm Exhibition Hall

Please refer to the poster listing on page 22.

### Thermo Fisher Workshop

2:45pm - 3:45pm

Auditorium

- **Mark Larance**  
Bloody plasma proteomics
- **Steve Binos**  
Plasma proteome profiling using the FAIMS pro interface on the fusion lumos tribrid mass spectrometer

Proudly supported by 

### Bruker Workshop

2:45pm - 3:45pm

Horizons Room

- **Leonard Foster**  
Maximizing proteoform coverage with the timsTOF Pro and Julienne
- **Ron Heeren**  
Translational imaging mass spectrometry: Combined throughput and resolution
- **Rune Larsen**  
Realising the potential of ultrasensitive phosphoproteomics on the timsTOF Pro

Proudly supported by



### Free Afternoon

2:45pm - 4:00pm

### Symposium Seven: Glycomics

4:00pm - 5:20pm Chair: Morten Thaysen-Andersen

Auditorium

- 4:00PM **Benjamin L Schulz** *abs# 47*  
Glycosylation in sparkling wines
- 4:20PM **Joel A Cain** *abs# 48*  
Proteomics reveals multiple phenotypes associated with *N*-linked glycosylation in *Campylobacter jejuni*
- 4:40PM **Hannes Hinneburg** *abs# 49*  
Post-Column Make-up Flow (PCMF) of organic modifiers enhances the sensitivity of capillary-flow PGC-LC-MS/MS-based glycomics
- 5:00PM **Cassandra L Pegg** *abs# 50*  
Dynamic cellular glycoproteome and proteome during influenza infection

### Symposium Eight: New Technologies I

5:20pm - 6:40pm Chair: Peter Hoffmann

Auditorium

- 5:20PM **Blaine R Roberts** *abs# 51*  
Application of ion mobility and electron capture dissociation (ECD) mass spectrometry to top-down and bottom-up proteoform characterization
- 5:40PM **Hartmut Schlüter** *abs# 52*  
Laser ablation for tissue sampling for proteomics and metabolomics
- 6:00PM **Nicolai Bache** *abs# 53*  
Evaluation of a novel LC system that embeds analytes in pre-formed gradients for rapid, ultra-robust proteomics
- 6:20PM **Kevin Schug** *abs# 54*  
Reversed phase x reversed phase on-line comprehensive two-dimensional liquid chromatography of intact proteins with triple quadrupole mass spectrometric detection

### APS Annual General Meeting

6:40pm - 7:30pm

Auditorium

### Students of APS (SoAPS) Dinner with Invited Speakers

7:30pm - 8:30pm

Lorne Central

Attendees are welcomed to join the APS Conference Dinner from 8:30pm.

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### APS Dinner

7:30pm - 10:30pm

Horizons Room

**Registration**

8:30am - 1:30pm Auditorium Foyer

**Symposium Nine: New Technologies II**

9:00am - 10:40am Chair: Andrew Webb Auditorium

9:00AM **Radoslaw Sobota** abs# 55

Mass spectrometry based, proteome-wide strategy for discovery and characterization of cellular nucleotide-protein interactions

9:20AM **Steven G Williams** abs# 56

High-throughput proteomic analysis of FFPE tissue using PCT-SWATH MS

9:40AM **Laura F Dagley** abs# 57

Universal Solid-Phase Protein Preparation (USP<sup>3</sup>) for high-throughput clinical proteomics

10:00AM **Alice Ly** abs# 58

Developments in the sample preparation of formalin-fixed paraffin-embedded tissues for MALDI imaging

10:20AM **Purushothaman Kathiresan** abs# 59

A new procedure of de yolking improves the proteome analysis in zebrafish early embryos

**Morning Tea (Winners of Vendors Prizes and Passport Prize)**

10:40am - 11:10am Exhibition Hall

**Symposium Ten: Interactomics**

11:10am - 12:20pm Chair: Marc Wilkins Auditorium

11:10AM **James E Bruce** abs# 60

Interactome dynamics; our initial observations with *in vivo* cross-linking

11:40AM **Daniela-Lee Smith** abs# 61

Large-scale detection of protein-protein interactions via size-exclusion chromatography, protein correlation profiling and crosslinking mass spectrometry

12:00PM **Dhana Gorasia** abs# 62

A comprehensive protein interactome of the type IX secretion system components in *Pophyromonas gingivalis* revealed using complementary proteomics approach

**Closing Keynote Lecture**

12:20pm - 12:50pm Chair: Peter Hoffman Auditorium

12:20PM **Mikhail Savitski** abs# 63

Protein stability in drug discovery and molecular biology

**Closing Ceremony and Award Presentation**

12:50pm - 1:30pm Chair: Stuart Cordwell Auditorium

Awards supported by



and



**Bus transfer to Melbourne Airport & City**

2:25pm – 5:45pm Cumberland Lorne

2:25pm sharp **Departing from the Cumberland 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 SESSION ONE – PROTEOMICS 2019

Friday, 8<sup>th</sup> February

|                              |  |         |
|------------------------------|--|---------|
| <b>Stuart Brown</b>          | A search for predictive biomarkers of ovine pre-partum vaginal prolapse  | abs# 64 |
| <b>Alexander W. Rookyard</b> | Multi-omic profiling of metabolic dysfunction caused by myocardial ischemia / reperfusion (I/R) injury                                   | abs# 65 |
| <b>Rohan Shah</b>            | Proteomic heterogeneity of high-grade serous ovarian carcinomas  | abs# 66 |
| <b>Dylan J Harney</b>        | High-throughput sample preparation for proteomic analysis using 3d-printing  | abs# 67 |
| <b>Syeda Sadia Ameen</b>     | Deep neuroproteomics reveal defective synaptic signalling in excitotoxicity  | abs# 68 |
| <b>Inga Boll</b>             | The sweet connections in neurotransmission – investigating sialylated glycosylation in the active zone of nerve terminals                | abs# 69 |
| <b>Lee A Gethings</b>        | Rapid qualitative and absolute quantification of plasma based proteins using a novel scanning quadrupole DIA acquisition method          | abs# 70 |
| <b>Lee A Gethings</b>        | Glycopeptide fragmentation optimization and quantitation by multi collision energy ramp scanning quadrupole data independent acquisition | abs# 71 |
| <b>Heather Patsiouras</b>    | Multi-omic characterisation of bladder and lung carcinomas using a novel scanning quadrupole DIA acquisition method                      | abs# 72 |
| <b>Nasim Shah Mohammadi</b>  | Proteomic profiling analysis of Australian seagrass, <i>Zostera muelleri</i> under copper stress   | abs# 73 |
| <b>Guangxu Ma</b>            | Larval development of the barber’s pole worm is under tight post-transcriptional control   | abs# 74 |
| <b>Akila Seneviratne</b>     | Chemical and random additive noise elimination (crane)   | abs# 75 |
| <b>Boris Reljic</b>          | Multi-omic approaches for elucidating the assembly and function of mitochondrial respiratory chain complexes                             | abs# 76 |
| <b>Merridee A Wouters</b>    | Sexual dimorphism and epileptogenesis in developing and adult rat brains   | abs# 77 |
| <b>Pawel Sadowski</b>        | Fully automated all-in-one sample preparation for high-throughput spectral library generation and SWATH-based quantitation               | abs# 78 |
| <b>Johanna E E Tuomisto</b>  | Tissue-specific immunopeptidome of HLA-B*57:01 in drug hypersensitivity reactions  | abs# 79 |

|   |         |
|---|---------|
| <b>Nichollas E Scott</b>  | abs# 80 |
| Protein O-fucosyltransferase 2 -mediated O-glycosylation of MIC2 is dispensable for <i>Toxoplasma gondii</i> tachyzoite infection   |         |
| <b>Nikeisha J Caruana</b>   | abs# 81 |
| A slimy situation: using integrated label-free quantitative proteomics to uncover potential neuropeptides within the defensive slime secretion of the striped pyjama squid ( <i>Sepioloidea lineolata</i> ) |         |
| <b>Stephan Klatt</b>  | abs# 82 |
| Optimizing red blood cell protein extraction for biomarker discovery  |         |
| <b>Tony J Parker</b>  | abs# 83 |
| How bad is my child's burn. Differences in blister fluid biochemistry to assess paediatric burn wounds  |         |
| <b>Zeynep Sumer-Bayraktar</b>   | abs# 84 |
| Loss of protein N-glycosylation influences peptidoglycan structure in <i>Campylobacter jejuni</i>   |         |
| <b>Nicola Beckett</b>   | abs# 85 |
| Insulin-related deaths: analysis of insulin and synthetic analogues in coronial exhibits by QE Plus Orbitrap  |         |
| <b>Clifford Young</b>   | abs# 86 |
| Identification of isoaspartylated peptides by electron-transfer/higher-energy collision dissociation  |         |
| <b>Andreas Huhmer</b>   | abs# 87 |
| Advancing mass spectrometry-based large-cohort proteomics for precision medicine – An international Cancer Moonshot multiple site study   |         |
| <b>Rajesh Gupta</b>   | abs# 88 |
| SWATH-MS proteomics enabled studying the semen quality in Brahman bulls   |         |
| <b>Simon Foster</b>   | abs# 89 |
| Delineation of the monocyte chemoattractant protein-dependent CCR2 signalling network using phosphoproteomics   |         |
| <b>Dilys TH Leung</b>   | abs# 90 |
| Profiling of ascites proteome in ovarian cancer patients  |         |
| <b>Matthew O'Rourke</b>   | abs# 91 |
| A multidisciplinary approach to the analysis of complex MSI data  |         |
| <b>POSTER SESSION – Metabolomics Symposium</b>  |         |
| <b>Friday, 8<sup>th</sup> February</b>  |         |
| <b>Christine Miller</b>   | abs# 92 |
| Improved lipid profiling workflow using novel iterative MS/MS mode and <i>in silico</i> annotation  |         |
| <b>Christine Miller</b>   | abs# 93 |
| Developing an automated plasma sample preparation method for LC/MS analysis of metabolites  |         |
| <b>Aaron Elkins</b>   | abs# 94 |
| Chemotyping of medicinal cannabis phytocannabinoids   |         |
| <b>Lok Man</b>  | abs# 95 |
| Multi-omics analysis of a nutrient transport protein required for full virulence in <i>Campylobacter jejuni</i>   |         |
| <b>Clara Castaños Sánchez de la Barquera</b>  | abs# 96 |
| Early detection of honey bee malnutrition and colony collapse   |         |
| <b>Amanda Souza</b>   | abs# 97 |
| Improved metabolome coverage and increased confidence in unknown identification through novel automated acquisition strategy combining sequential injections and MS <sup>n</sup>                            |         |

|  |          |
|--|----------|
| <b>Amanda Souza</b><br>Flavonoid annotation using a product ion-dependent MS <sup>n</sup> data acquisition method on a Tribid Orbitrap mass spectrometer                                       | abs# 98  |
| <b>Karyn L Wilde</b><br>Bespoke deuterated lipid molecules for structure function applications from the National Deuteration Facility  | abs# 99  |
| <b>Robert Plumb</b><br>A high throughput single platform for <i>quantitative multiOmics</i>  | abs# 100 |
| <b>Robert Plumb</b><br>High throughput lipidomics using ion mobility enabled rapid LC-MS profiling shows promise for the analysis of human plasma samples obtained from breast cancer patients | abs# 101 |
| <b>Katherine Hyland</b><br>An "OMICS" approach to food profiling, authenticity, and classification   | abs# 138 |

## POSTER SESSION TWO – PROTEOMICS 2018

Saturday, 9th February

|  |          |
|--|----------|
| <b>Shawn Goh</b><br>Peptides and Penicillins: Identifying the immunogenic $\beta$ -lactam ligand(s)  | abs# 102 |
| <b>Stephanie E L Town</b><br>Using genomics and proteomics to understand the antibiotic resistance capabilities of an isolate  | abs# 103 |
| <b>Md Arifur Rahman</b><br>Extractomes profiling reveals potential role of key proteins in <i>Staphylococcus aureus</i> biofilm using TMT-based quantitative mass spectrometry | abs# 104 |
| <b>Sayantani Chatterjee</b><br>Accessing the mannose-6-phosphate glycoproteome using titanium dioxide (TiO <sub>2</sub> ) enrichment   | abs# 105 |
| <b>Ryan J Separovich</b><br>The role of upstream phosphorylation in the regulation of histone methylation  | abs# 106 |
| <b>Naomi Koh Belic</b><br>Characterisation of human adipose stem cells   | abs# 107 |
| <b>Michael MM Mariani</b><br>EasyPep - A new simplified and optimized workflow for MS sample preparation   | abs# 108 |
| <b>Larissa Lago</b><br>Dietary selenium significantly effects rat liver protein expression   | abs# 109 |
| <b>Shannon Holt</b><br>Development of an immune response assay for honey bees  | abs# 110 |
| <b>Chris Desire</b><br>Potential protein biomarkers for the diagnosis of early stage gastric cancer  | abs# 111 |
| <b>Katherine E Scull</b><br>A mass spectrometry quality control website: monitoring SCIEX instruments to maximise productivity   | abs# 112 |
| <b>David Heywood</b><br>Desorption electrospray ionization and data independent analysis profiling of the lipid complement of lysosomal storage disorders                      | abs# 113 |

|  |          |
|--|----------|
| <b>David Heywood</b><br>Optimised Desorption Electrospray Ionisation Mass Spectrometry Imaging (DESI-MSI) method for the analysis of proteins/peptides directly from tissue sections | abs# 114 |
| <b>Delphine Vincent</b><br>Top-down, middle-down and bottom-up proteomics analysis of medicinal cannabis   | abs# 115 |
| <b>Jemma Wu</b><br>Identifying PTM changes from DIA data – a computational workflow  | abs# 116 |
| <b>Srikanth S Manda</b><br>From raw data to biological insights: A computational pipeline for SWATH-MS-based proteomics  | abs# 117 |
| <b>Paul D Veith</b><br>Transpeptidation is a major mechanism of haemoglobin proteolysis by the gingipain cysteine proteinases  | abs# 118 |
| <b>Daniella H Hock</b><br>Using quantitative proteomics to resolve genomic diagnosis of mitochondrial disease  | abs# 119 |
| <b>Jessica van Haeften</b><br>An integrated -omics approach to overtraining biomarker discovery  | abs# 120 |
| <b>Patricia Illing</b><br>Defining the contribution of linear and spliced peptides to the anti-influenza T cell response   | abs# 121 |
| <b>Rune H Larsen</b><br>Development of an optimized end to end phosphoproteomic workflow on the timsTOF PRO  | abs# 122 |
| <b>Yangxiu Wu</b><br>Development of proteomic tools to identify telomere maintenance mechanisms in human cancer  | abs# 123 |
| <b>Shutao Mei</b><br>Recognising the role of post-translational modification in immunopeptidomic peptides by using mass spectrometry and bioinformatics                              | abs# 124 |
| <b>Mehdi Mirzaei</b><br>Proteomics unravel novel molecular mechanisms of Alzheimer's disease in retina   | abs# 125 |
| <b>Shivanjali J Lingam</b><br>Analysis of cysteine redox post-translational modifications in a rat model of type II diabetes mellitus  | abs# 126 |
| <b>Matthew J Fitzhenry</b><br>Detection of collagen proteins of bovine and porcine origin in food products using targeted LC-MS  | abs# 127 |
| <b>Joanna Sacharz</b><br>Understanding the roles of subunits and assembly factors implicated in the biogenesis of human Complex II   | abs# 128 |
| <b>Amanda Souza</b><br>Improved lipid annotation utilizing positive and negative ion MS <sup>2</sup> / MS <sup>3</sup> HCD and CID spectra   | abs# 129 |
| <b>Steve Binos</b><br>A multiplexed enrichment and targeted PRM platform for absolute quantitation of AKT/mTOR, Ras, and p53 signaling pathways targets                              | abs# 130 |

|                         |   |          |
|-------------------------|---|----------|
| <b>Joel A Cain</b>      | Degradomic analysis of a putative C-terminal processing peptidase from <i>Campylobacter jejuni</i>                                      | abs# 131 |
| <b>Mark P Molloy</b>    | Detect more proteins with decreased false positives using filtered SWATH peptide libraries to improve plasma biomarker studies          | abs# 132 |
| <b>Bradley W Wright</b> | Exploring the bacteriophage $\phi$ X174 infection response  | abs# 133 |
| <b>Birgit Schilling</b> | Proteomic profiling of the cell surface of senescent cells  | abs# 134 |
| <b>Melodi G Sen</b>     | The role and regulation of Atg1 in autophagy and DIF-1 induced autophagic cell death of <i>Dictyostelium discoideum</i>                 | abs# 135 |
| <b>William Klare</b>    | Using integrative multi-omics to explore <i>Pseudomonas aeruginosa</i> cellular physiology after adaptation to the Cystic Fibrosis lung | abs# 136 |
| <b>Samah Issa</b>       | Development of a quantitative proteomic standard for Tandem Mass Tags (TMT)   | abs# 137 |
| <b>Paul Shan</b>        | AI-based solutions for MS-based immunopeptidomics with high sensitivity and accuracy  | abs# 139 |