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Metabolomics GCMS/MS Workshop

Metabolomics 2017 Brisbane Australia
Date: **Tuesday, June 27**
Time: **12:15 pm - 1:15 pm**
Location: **Brisbane Convention Center, Meeting Room 3**

Please join us for an insightful collection of presentations into targeted GCMS/MS metabolomics.

Host:

Chris Bowen - Shimadzu Scientific Instruments, Bio21 Institute, Melbourne, Victoria

Presenters:

1. **David De Souza** - Research & Development Scientist, Metabolomics Australia, Bio21 Institute, Melbourne, Victoria

The Advantages of Moving from Untargeted GCMS Profiling to Comprehensive Targeted GCMS/MS MRM Methodologies
The well-known bottlenecks in metabolomics workflows will be highlighted and addressed. The talk will focus on GCMS/MS MRM targeted analysis and results highlighting the data quality, pathway coverage and data processing advantages of moving away from untargeted mass spectrometry to targeting a large number MRM's (950+) in a single GCMS/MS method covering the primary metabolic pathways.

2. **Sakai Takero** - Shimadzu Global Application Development Centre, Kyoto, Japan

Usefulness of GCMS/MS in Life Science - Analysis of Total Metabolites to Short Chain Fatty Acids
Short chain fatty acids such as acetate, formate and propionate are of great interest. These simple compounds are difficult to analyse quantitatively due in part to their ubiquity. There is no unified methodology and many metabolomics groups are working towards validating a robust method. Here a GCMS/MS methodology and results using derivatization with DMT-MM is presented. In the second part of this talk the usefulness of wide-targeted metabolomics and its application for searching biomarkers in disease will be described.

3. **Prof Eiichiro Fukusaki** - Department of Biotechnology, Graduate School of Engineering, Osaka University, Osaka, Japan

Metabolic Fingerprinting using Automated GCMS/MS Pretreatment and an Introduction into Chiral Metabolomics
Advances in automation coupled to hyphenated mass spectrometric techniques not only improve sample throughput but also data quality. The first part of this talk will show how integrating automation can be implemented in applied metabolomics. Chiral metabolomics is of growing interest. The difficulty of the workflow is often off putting to researchers. Here we present a newly developed simplified methodology for chiral analysis which achieves simultaneous and sensitive analysis of 22 D- and L- amino acids in 10 minutes without derivatization using LCMS/MS.

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