## Metabolomics 2017 Detailed Program

\*Agenda subject to change.

Monday 26 June		
Time	Session	Location
8:45 - 10:15	Workshops	
10:15 - 10:30	Break	
10:30 - 12:00	Workshops	
13:15 - 14:00	Opening Ceremony	Great Hall 2
14:00 - 15:00	Plenary Speaker: Krishna Mahadevan	Great Hall 2
	Model-based Engineering of Metabolism	
15:00 - 15:30	Tea and Coffee Break	Foyer
15:30 - 17:10	Systems Biology Methods to Characterise Biological Systems	Meeting Room 1
	Parallel Session 1A	
15:30 - 15:50	Abstract 333	
	A novel systemic approach to patient stratification	
	Maike Aurich, Luxembourg Centre for Systems Biomedicine,	
	University of Luxembourg, Luxembourg	
15:50 - 16:10	Abstract 171	
	Laboratory Evolution Reveals Proximal and Distal Causation to Gene	
	Loss	
	Douglas McCloskey, Center for Biosustainability, Denmark Technical	
16.10 16.20	University, Denmark	
16:10 - 16:30	Abstract 477	
	Comparative metabolomics of xylose-jermenting yeasts by OHPLC-	
	Datricia Abdelnur, Embrana Agroenergy, Brazil	
16.20 - 16.50	Abstract 2/7	
10.30 - 10.30	An Integrative omics approach to disentangling the relationship	
	hetween prenatal vitamin D exposure 17a21 genetic variants	
	sphingolinid metabolism and the development of asthma	
	Jessica Lasky-Su. Brigham and Women's Hospital and Harvard	
	Medical School, United States	
16:50 - 17:10	Abstract 352	
	MicrobiomeAnalyst - a web-based tool for comprehensive	
	statistical, visual and functional analysis of microbiome data	
	JIANGUO XIA, McGill University, Canada	
15:30 - 17:10	Model Organisms	Meeting Room 3
	Parallel Session 1B	
15:30 - 15:50	Abstract 148	
	Actylcholine regulation after single pesticide exposure in	
	relationship to developmental neurotoxicty, benavior and cognitive	
	Siuures III IIIIle Dim Leonards VIII University Netherlands	
	This Leonards, vo oniversity, Netherianus	

15:50 - 16:10	Abstract 420	
	Using Metabolomics to Assess the Early Effects of Zinc and Boscalid	
	On Estuarine Polychaete.	
	Georgia Sinclair, University of Melbourne, Australia	
16:10 - 16:30	Abstract 44	
	MS-based metabolomics reveals BDE47 associated neurometabolic	
	changes	
	JI Fenfen, Hong Kong Baptist University, Hong Kong	
16:30 - 16:50	Abstract 401	
	Metabolomics study of triphenyl phosphate in earthworm Perionyx	
	excavatus: biotransformation products and toxicity	
	Lei Wang, National University of Singapore, Singapore	
16:50 - 17:10	Abstract 150	
	The fate of technical-grade chlordane in mice fed a high-fat diet and	
	its roles as a candidate obesogen	
	wentao zhu, China Agricultural University, China	
15:30 - 17:10	Diabetes and Cardiovascular Disease	Meeting Room 4
	Parallel Session 1C	
15:30 - 15:50	Abstract 350	
	Insufficient Sleep Alters Plasma Metabolites Linked to Insulin	
	Resistance and Diabetes Risk	
	Christopher Depner, University of Colorado Boulder, United States	
15:50 - 16:10	Abstract 279	
	DMGV is a Novel Marker of Liver Fat and Predicts Future	
	Development of Type 2 Diabetes	
	John O'Sullivan, Heart Research Institute, Australia	
16:10 - 16:30	Abstract 341	
	The metabolomic analysis of sequential hair segments reflected the	
	metabolic changes of normal, small-for-gestational-age, and	
	gestational diabetes mellitus affected pregnancies across the	
	trimesters.	
	Ting-Li Han, Liggins Institute, The University of Auckland, Auckland,	
	New Zealand, New Zealand	
16:30 - 16:50	Abstract 237	
	Molecular mechanisms of lung injury during cardiac surgery	
	Raluca Maltesen, Aalborg University Hospital, Dep. of Anaesthesia	
	and Intensive Care, Denmark	
16:50 - 17:10	Abstract 60	
	A non-targetea UHPLC-HRIVIS metabolomics pipeline for metabolite	
	identification; application to cardiac remote ischemic	
	preconditioning	
	NZOUGHEL KOUASSI JUGILI, UNIVERSITE & ANGERS - UFK SANTE - INSTITUT	
17·16 _ 10· <i>1</i> 6	Walcome Recention	Evhibit Hall
17:12 - 18:42	Poster Session 1	ελιιινίι παιί
	L 02/61 26221011 T	

Tuesday 27 June		
Time	Session	Location
8:45 - 9:45	Plenary Speaker: Hanne Bertram Edibilomics	Great Hall 2
9:45 - 10:30	D Break	Exhibit Hall
10:30 - 12:1	0 The Staple Foods Parallel Session 2A	Meeting Room 1
10:30 - 10:5	0 Abstract 111 A muti-omics approach to understanding flavour-compound production in rice Dara Daygon, The University of Queensland, Australia	
10:50 - 11:1	0 <b>Abstract 461</b> Dietary whole grain modifies microbiota and enhances production of novel compounds associated with energy metabolism Kati Hanhineva, University of Eastern Finland, Finland	
11:10 - 11:3	0 Abstract 303 GC/MS-based metabolomics approach for the discrimination of Indonesian specialty coffee Sastia Putri, Department of Biotechnology, Graduate School of Engineering Japan	
11:30 - 11:5	0 <b>Abstract 272</b> <i>Milk lipidomics: what we know and what we don't</i> Zhiqian Liu, Agriculture Victoria, Australia 0 Round Table Discussion	
10:30 - 12:1	0 Advances is Spatial Metabolomics	Meeting Room 3
10:30 - 10:5	<ul> <li>Parallel Session 2B</li> <li>Abstract 453         Advancing Metabolomics through Imaging Mass Spectrometry and Direct Tissue Analysis         Richard Yost, University of Florida - Southeast Center for Integrated Metabolomics, United States     </li> </ul>	
10:50 - 11:1	0 Abstract 273 Enhanced Negative Mode Ion-less Matrices for Imaging Mass Spectrometry – Assessing MALDI Matrices for Metabolite Annotation and Spatial Metabolomics in Plant and Mammalian Systems Berin Boughton, University of Melbourne, Australia	
11:10 - 11:3	0 Abstract 222 Contaminants removal from tissue samples using DESI Ion Mobility imaging Vincen Wu, Imperial College London, United Kingdom	
11:30 - 11:5	0 Abstract 200	

	MALDI Imaging of lipids and pharmaceuticals in human prostate cancer explants.	
11.50 - 12.10	Abstract 164	
11.50 12.10	NON-UNIFORM DISTRIBUTION OF METABOLITES IN ROOTS AS A	
	RESULT OF A SHORT TERM SALINITY STRESS IN DIFFERING BARLEY	
	CULTIVARS	
	Lenin Sarabia, University of Melbourne, Australia	
10:30 - 12:10	Pregnancy, Infants and Children	Meeting Room 4
	Parallel Session 2C	C C
10:30 - 10:50	Abstract 169	
	Correlation of a plasma metabolite score with duration of hypoxia: a	
	piglet study	
	Julia Kuligowski, Health Research Institute La Fe, Spain	
10:50 - 11:10	Abstract 342	
	Pre-pregnancy maternal obesity can result in metabolic	
	dysregulation and memory impairment in male offspring	
	Xiaobo Zhou, First Affiliated Hospital of Chongqing Medical	
	University, China	
11:10 - 11:30	Abstract 244	
	Rapid characterisation of the vaginal metabolome during pregnancy	
	using desorption electrospray ionization (DESI) MS medical swab	
	analysis	
	Pamela Pruski, Imperial College London, United Kingdom	
11:30 - 11:50	Abstract 314	
	Enrichment of Secondary Bile Acids associated with Food Allergy in	
	Healthy Infant Cohort	
	Yamini Virkud, Massachusetts General Hospital, United States	
11:50 - 12:10	Abstract 83	
	Faecal and serum metabolomics in paediatric inflammatory bowel	
	disease.	
	Vidya Velagapudi, Institute for Molecular Medicine Finland FIMM,	
	University of Helsinki, Finland	
12:10 - 13:30	Lunch	Exhibit Hall
	Platinum Sponsor Presentations	
	Agilent Technologies	Meeting Room 1
	Shimadzu Australasia	Meeting Room 3
	Waters Corporation	Meeting Room 4
13:30 - 15:00	Marine and Microbial Natural Products	Meeting Room 1
	Parallel Session 3A	
13:30 - 14:00	Abstract 143	
	Identifying Marine Natural Products - Pitfalls and Progress	
	Mary Garson, The University of Queensland, Australia	
14:00 - 14:15	Abstract 106	

	Lipidome Remodeling at Sea: Viral Infection of a bloom forming	
	Marine Algae mauces the Production of Highly Saturated	
	Sergey Malitsky Weizmann Institute of Science Israel	
14:15 - 14:30	Abstract 57	
220 200	Metabolite Profilina of Red Sea Corals	
	Aleiandra Ortega. KAUST. Saudi Arabia	
14:30 - 14:45	Abstract 278	
	Turning mould into gold: An exploration of mould metabolism to	
	commercialize useful secondary metabolites	
	Kyle Van de Bittner, University of Canterbury, New Zealand	
14:45 - 15:00	Abstract 157	
	HSQC-TOCSY NMR profiling: making informed microbial strain	
	Selection for natural product discovery	
	School of Environment, Criffith University Criffith University	
13:30 - 15:00	Advances in Statistics & Machine Learning	Meeting Room 3
	Parallel Session 3B	0 0 0
13:30 - 14:00	Keynote Speaker	
	Novel methods for data generation and data integration in	
	metabolomics	
	Johan Trygg, Umeå University, Sweden	
14:00 - 14:15	Abstract 256	
	When the microbiome meets the metabolome: A Framework for	
	integrative longitudinal analysis	
	Takoua Jendoubi, School of public health, Imperial College London,	
	United Kingdom	
14:15 - 14:30	Abstract 309	
	Multivariate modelling with unbiased variable selection	
	Carl Brunius, Chalmers University of Technology, Sweden	
14.20 14.45	Carl Brunius, Chalmers University of Technology, Sweden	
14:30 - 14:45	Carl Brunius, Chalmers University of Technology, Sweden Abstract 217 Conture outputtion from high dimensional metabologies datasets	
14:30 - 14:45	Carl Brunius, Chalmers University of Technology, Sweden Abstract 217 Feature extraction from high-dimensional metabolomics datasets using Kapuladan Discourse by Assurant Maximization (KODAMA)	
14:30 - 14:45	Carl Brunius, Chalmers University of Technology, Sweden Abstract 217 Feature extraction from high-dimensional metabolomics datasets using Knowledge Discovery by Accuracy Maximization (KODAMA) Stafana Cassisters, Imperial College, United Kingdom	
14:30 - 14:45	Carl Brunius, Chalmers University of Technology, Sweden <b>Abstract 217</b> <i>Feature extraction from high-dimensional metabolomics datasets</i> <i>using Knowledge Discovery by Accuracy Maximization (KODAMA)</i> Stefano Cacciatore, Imperial College, United Kingdom	
14:30 - 14:45 14:45 - 15:00	Carl Brunius, Chalmers University of Technology, Sweden Abstract 217 Feature extraction from high-dimensional metabolomics datasets using Knowledge Discovery by Accuracy Maximization (KODAMA) Stefano Cacciatore, Imperial College, United Kingdom Abstract 66	
14:30 - 14:45 14:45 - 15:00	Carl Brunius, Chalmers University of Technology, Sweden Abstract 217 Feature extraction from high-dimensional metabolomics datasets using Knowledge Discovery by Accuracy Maximization (KODAMA) Stefano Cacciatore, Imperial College, United Kingdom Abstract 66 A Graphical Cellular Dashboard for Analysis of Metabolomics Data	
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15:00 - 15:30	Break	Exhibit Hall
14:45 - 15:00	Round Table Discussion	
	United Kingdom	
	Alexander Fleming Building, Imperial College, London SW7 2AZ, UK,	
	Andreas Dannhorn, Department of Surgery and Cancer, Sir	
	injury	
	Spatially resolved profiling of Polymyxin B induced acute kidney	
14:30 - 14:45	Abstract 80	
	Australia	
	Anubhav Srivastava, Monash Institute of Pharmaceutical Sciences,	
	obtained through RhopH2 mediated New Permeability Pathways	
	Malaria parasite metabolism is supported by host derived nutrients	
14:15 - 14:30	Abstract 184	
	Institute of Technology Kharagpur, India	
	Koel Chaudhury, School of Medical Science and Technology, Indian	
	NMR based serum lipidomics approach	
	Exploring dormant genital tuberculosis associated infertility - 1H	
14:00 - 14:15	Abstract 366	
	Darren Creek, Monash University, Australia	
	with artemisinin-resistant malaria parasites	
	Multi-omics analysis reveals the biochemical changes associated	

15:30 - 17:00	Genome-scale Modelling & Flux balance analysis Parallel Session 4A	Meeting Room 1
15:30 - 16:00	Abstract 395 Towards dynamic, genome-scale modeling that captures metabolite levels and regulation Mark Styczynski, Georgia Institute of Technology, United States	
16:00 - 16:15	Abstract 458 Deciphering the metabolic responses to polymyxin killing in Acinetobacter baumannii ATCC 19606 by developing a high-quality genome-scale metabolic model Yan Zhu, Monash Biomedicine Discovery Institute, Department of Microbiology, Faculty of Medicine, Nursing & Health Sciences, Monash University, Australia	
16:15 - 16:30	Abstract 328 Dynamic flux modelling of adipocytes stimulated by insulin using 13C-labelled metabolites Lake-Ee Quek, School of Mathematics and Statistics, The University of Sydney, Australia	
16:30 - 16:45	<b>Abstract 282</b> What is the relationship between intracellular and extracellular metabolites? Silas Villas-Boas, University of Auckland, New Zealand	
16:45 - 17:00	Abstract 387	

	Enhancing tetanus toxin production through fermentation maps	
	Esteban Marcellin, The University of Queensland, Australia	
15:30 - 17:00	Frontiers in Lipidomics	Meeting Room 3
	Parallel Session 4B	
15:30 - 16:00	Abstract 425	
	The use of ion mobility coupled with high resolution mass	
	spectrometry to improve separation and identification of lipid	
	biomarkers in metabolic diseases	
	Julian Griffin, University of Cambridge, United Kingdom	
16:00 - 16:15	Abstract 212	
	Exploring the use of ultra-high performance supercritical fluid	
	chromatography mass spectrometry (UHPSFC-MS) for lipidomics	
	applications	
	Joost Brandsma, University of Southampton, United Kingdom	
16:15 - 16:30	Abstract 436	
	Comprehensive High-Throughput Targeted Lipidomics	
	kevin huynh, Baker Heart and Diabetes Institute, Australia	
16:30 - 16:45	Abstract 346	
	Quantitative Lipidomics and Discovery Metabolomics Applied to	
	Human Sebum	
	Elizaveta Freinkman, Metabolon, Inc., United States	
16:45 - 17:00	Round Table Discussion	
	Big fat back-track: mapping desaturase activity using ozone-induced	
	dissociation mass spectrometry	
	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia	
15:30 - 17:00	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary	Meeting Room 4
15:30 - 17:00	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary Parallel Session 4C	Meeting Room 4
<b>15:30 - 17:00</b> 15:30 - 16:00	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary Parallel Session 4C Abstract 228	Meeting Room 4
<b>15:30 - 17:00</b> 15:30 - 16:00	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary Parallel Session 4C Abstract 228 Metabolomics: The solution to assessing herbal medicine safety?	Meeting Room 4
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<b>15:30 - 17:00</b> 15:30 - 16:00 16:00 - 16:15 16:15 - 16:30	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary Parallel Session 4C Abstract 228 Metabolomics: The solution to assessing herbal medicine safety? Garth Maker, Murdoch University, Australia Abstract 156 A multi-platform metabolomics approach to identify unique compounds present in Australian bush food Fe Calingacion, University of Queensland, Australia Abstract 89 Comparative analysis of phytochemicals in the leaf extracts of Pittosporum angustifolium cultivars via LC-MS based plant metabolomics. ANUJA PATIL, SCHOOL OF PHARMACY, UNIVERSITY OF QUEENSLAND, Australia Abstract 263 Deen metabolome appotation and the peressity of a thought	Meeting Room 4
<b>15:30 - 17:00</b> 15:30 - 16:00 16:00 - 16:15 16:15 - 16:30	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary Parallel Session 4C Abstract 228 Metabolomics: The solution to assessing herbal medicine safety? Garth Maker, Murdoch University, Australia Abstract 156 A multi-platform metabolomics approach to identify unique compounds present in Australian bush food Fe Calingacion, University of Queensland, Australia Abstract 89 Comparative analysis of phytochemicals in the leaf extracts of Pittosporum angustifolium cultivars via LC-MS based plant metabolomics. ANUJA PATIL, SCHOOL OF PHARMACY, UNIVERSITY OF QUEENSLAND, Australia Abstract 263 Deep metabolome annotation and the necessity of a thought experiment	Meeting Room 4
<b>15:30 - 17:00</b> 15:30 - 16:00 16:00 - 16:15 16:15 - 16:30 16:30 - 16:45	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary Parallel Session 4C Abstract 228 Metabolomics: The solution to assessing herbal medicine safety? Garth Maker, Murdoch University, Australia Abstract 156 A multi-platform metabolomics approach to identify unique compounds present in Australian bush food Fe Calingacion, University of Queensland, Australia Abstract 89 Comparative analysis of phytochemicals in the leaf extracts of Pittosporum angustifolium cultivars via LC-MS based plant metabolomics. ANUJA PATIL, SCHOOL OF PHARMACY, UNIVERSITY OF QUEENSLAND, Australia Abstract 263 Deep metabolome annotation and the necessity of a thought experiment Gregory Genta-Jouve University Paris Descartes, France	Meeting Room 4
<b>15:30 - 17:00</b> 15:30 - 16:00 16:00 - 16:15 16:15 - 16:30 16:30 - 16:45	dissociation mass spectrometry Stephen Blanksby, Queensland University of Technology, Australia Nature's Apothecary Parallel Session 4C Abstract 228 Metabolomics: The solution to assessing herbal medicine safety? Garth Maker, Murdoch University, Australia Abstract 156 A multi-platform metabolomics approach to identify unique compounds present in Australian bush food Fe Calingacion, University of Queensland, Australia Abstract 89 Comparative analysis of phytochemicals in the leaf extracts of Pittosporum angustifolium cultivars via LC-MS based plant metabolomics. ANUJA PATIL, SCHOOL OF PHARMACY, UNIVERSITY OF QUEENSLAND, Australia Abstract 263 Deep metabolome annotation and the necessity of a thought experiment Gregory Genta-Jouve, University Paris Descartes, France Bound Table Discussion	Meeting Room 4

Exhibit Hall

## 17:15 - 18:45 Poster Session 2

19:00 - 20:30 EMN Reception

Wednesday 28 June			
Time	Session	Location	
8:45 - 9:45	Plenary Speaker: Anthony Carroll	Great Hall 2	
	Natural Products		
9:45 - 10:30	Break	Exhibit Hall	
10:30 - 12:10	Natural Products and Metabolomics - Advancing Two Fields	Meeting Room 1	
	Parallel Session 5A	0 1	
10:30 - 10:50	Abstract 190		
	Comprehensive LC-MS/MS metabolomic profiling of fungal culture		
	collections – insights into the chemical space of fungal secondary		
	metabolites		
	Mark Sumarah, Agriculture and Agri-Food Canada, Canada		
10:50 - 11:10	Abstract 302		
	Defining the dark metabolism of the malaria parasite		
11.10 11.20	Abstract 267		
11:10 - 11:30	ADSITACE 307 Development of Software for Efficient NMR Metabolomics		
	Screening of Natural Products		
	Kimberly Colson, Bruker BioSpin, United States		
11:30 - 11:50	Abstract 62		
11.50 11.50	Differences in the bioloaical architecture between visceral and		
	subcutaneous adipose tissue revealed by transcriptomics and		
	metabolomics		
	Nasim Bararpour, University Center of Legal Medicine, Switzerland		
11:50 - 12:10	Abstract 104		
	Next generation, 'standards-free' metabolite identification pipeline		
	Ryan Renslow, Earth and Biological Sciences Directorate, Pacific		
	Northwest National Laboratory (PNNL), Richland, WA, USA, United		
	States		
10:30 - 12:10	Multi-omics / Systems Biology	Meeting Room 3	
	Parallel Session 5B		
10:30 - 10:50	Abstract 315		
	A Systems Biology Approach to the Understanding of Asthma		
	Severity through the Integration of Metabolomic, Transcriptomic		
	ana Epigenetic networks		
	Kachel Kelly, Brigham and Women's Hospital Harvard Medical		
10.50 11.10	Abstract 178		
10:50 - 11:10	Severity through the Integration of Metabolomic, Transcriptomic and Epigenetic networks Rachel Kelly, Brigham and Women's Hospital Harvard Medical School, United States Abstract 178		

	Intergenerational changes in faecal microbiome and metabolome in	
	a C57BL/6J mouse colony	
	Marten Snel, South Australian Health and Medical Research	
	Institute, Australia	
11:10 - 11:30	Abstract 388	
	Integrative Omics Approach Reveals Coordinate Regulation of	
	Metabolites Glycosylation and Stress Hormones Biosynthesis by TT8	
	in Arabidopsis	
	Shivshankar Umashankar, National University of Singapore,	
	Singapore	
11:30 - 11:50	Abstract 154	
	Multi-omics Analysis of Esophageal Adenocarcinoma: How Lipid	
	Metabolism Affects Cancer Progression	
	Jeffrey Molendijk, The University of Queensland Diamantina	
	Institute, The University of Queensland, Brisbane, QLD, Australia,	
	Australia	
11:50 - 12:10	Abstract 139	
	Differential multi-fluid network sheds light on metabolic processes	
	altered in end-stage renal disease	
	Jonas Zierer, Helmholtz Zentrum München/King's College London,	
	United Kingdom	
10:30 - 12:10	Cancer	Meeting Room 4
	Parallel Session 5C	
40.00 40.50		
10:30 - 10:50	Abstract 48	
10:30 - 10:50	Abstract 48 LC-MS-based metabolomics revealed SLC25A22 as an essential	
10:30 - 10:50	Abstract 48 LC-MS-based metabolomics revealed SLC25A22 as an essential regulator in aspartate-derived amino acids and polyamines in KRAS-	
10:30 - 10:50	Abstract 48 LC-MS-based metabolomics revealed SLC25A22 as an essential regulator in aspartate-derived amino acids and polyamines in KRAS- mutant colorectal cancer	
10:30 - 10:50	Abstract 48 LC-MS-based metabolomics revealed SLC25A22 as an essential regulator in aspartate-derived amino acids and polyamines in KRAS- mutant colorectal cancer Xiaona LI, State Key Laboratory of Environmental and Biological	
10:30 - 10:50	Abstract 48 LC-MS-based metabolomics revealed SLC25A22 as an essential regulator in aspartate-derived amino acids and polyamines in KRAS- mutant colorectal cancer Xiaona LI, State Key Laboratory of Environmental and Biological Analysis, Department of Chemistry, Hong Kong Baptist University,	
10:30 - 10:50	Abstract 48 LC-MS-based metabolomics revealed SLC25A22 as an essential regulator in aspartate-derived amino acids and polyamines in KRAS- mutant colorectal cancer Xiaona LI, State Key Laboratory of Environmental and Biological Analysis, Department of Chemistry, Hong Kong Baptist University, China	
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	Ion mobility–mass spectrometry based high-throughput	
	metabolomics facilitates metabolite biomarker discovery in	
	colorectal cancer	
	Zhiwei Zhou, Chinese Academy of Sciences, China	
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	Platinum Sponsor Presentations	
	Thermo Fisher Scientific	Meeting Room 1
	Bruker Corporation	Meeting Room 3
	SCIEX	Meeting Room 4
13.30 - 15.00	New Tools in Natural Product Annotation	Meeting Room 1
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13.30 - 14.00	Abstract 313	
13.30 11.00	Novel 11HPI C-MS-SPF-NMR and 11HPI C-timsTofMS/MS Tools for	
	Higher-throughout Confident Metabolite Identifications and to	
	Address the Number One Grand Challenge of Metabolomics	
	Llovd Sumner University of Missouri United States	
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11100 11110	Illtrahigh-resolution metabolomics for heterogtom-containing	
	specialized metabolites	
	Rvo Nakabavashi, RIKEN Center for Sustainable Resource Science.	
	Japan	
14:15 - 14:30	Abstract 258	
11110 11100	CANOPUS - Comprehensive categorization of unknowns using	
	tandem mass spectrometry	
	Kai Dührkop, Friedrich-Schiller University, Jena, Germany	
14:30 - 14:45	Abstract 43	
	An automated, auantum-chemical in silico metabolite library engine	
	for multidimensional NMR spectroscopy	
	Ryan Renslow, Farth and Biological Sciences Directorate, Pacific	
	Northwest National Laboratory (PNNL). Richland, WA, USA, United	
	States	
14:45 - 15:00	Abstract 292	
	Substance class annotation for long candidate lists in metabolite	
	identification using structural ontologies	
	Sarah Scharfenberg, Leibniz Institute of Plant Biochemistry,	
	Germany	
13:30 - 15:00	Environment: Dipping into the Water	Meeting Room 3
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13:30 - 14:00	Keynote Speaker	
	Environmental Metabolomics	
	Jun Kikuchi, Riken, Japan	
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	LIPIDOMICS APROACH TO IDENTIFY NOVEL SALINITY RESPONSE	
	MECHANISUMS IN BARELY ROOTS	
	Thusitha Rupasinghe, Metabolomics Australia, Australia	
1/1.15 - 1/1.30	Abstract 271	

	Can metabolomics approaches be used to determine the impact of	
	pollution in estuarine environments?	
14:30 - 14:45	Abstract 86	
	Mapping carbon fate during coral bleaching: the application of 13C metabolomics	
	Katie Hillver, Victoria University of Wellington, New Zealand, New	
	Zealand	
14:45 - 15:00	Abstract 427	
	Discrimination of natural and in vitro marine biofilms by LC-MS	
	metabolomics	
	Laurie Favre, MAPIEM, France	
13:30 - 15:00	Diet, Weight, and Physical Activity Parallel Session 6C	Meeting Room 4
13:30 - 14:00	Abstract 474	
	Systemic Impact of Roux-en-Y Gastric Bypass Surgery	
	JIA LI, Imperial College London, United Kingdom	
14:00 - 14:15	Abstract 356	
	How Blood Removal Affects Exercise Performance and the Plasma Metabolome	
	Nathan Lawler, Centre for Integrative Metabolomics &	
	Computational Biology, School of Science, Edith Cowan University,	
	Australia	
14:15 - 14:30	Abstract 281	
	Metabolomic analysis of the effects of a ten week high protein diet	
	In older men	
	Amber Milan, Liggins Institute, Oniversity of Auckland, New Zealand	
14:30 - 14:45	Abstract 82	
	Analysis of the metabolomic responses to high protein means in woman at increased matabolic disease rick	
	Brenan Durainavagam Liggins Institute New Zealand	
14:45 - 15:00	Abstract 241	
	The effects of changing the liquid/solid content of an isoenergetic	
	test meal on gastric emptying and the blood lipidome	
	Xuefei Li, Department of Biochemistry, University of Cambridge,	
	United Kingdom	
15:00 - 15:30	Break	Exhibit Hall
15:30 - 17:00	Metabolite Identification, Libraries, & Cheminformatics	Meeting Room 1
	Parallel Session 7A	
15:30 - 16:00	Abstract 264	
	Identifying epimetabolites by mass spectrometry-based	
	cheminformatics	
	Hiroshi Tsugawa, RIKEN, Japan	
16:00 - 16:15	Abstract 268	
	Curated open-access LC-Orbitrap-MS/MS spectral library of	
	endogenous metabolites and lipids	

	Prasad Phapale, EMBL, Germany	
16:15 - 16:30	Abstract 88	
	The whole is easier than the parts: Improving molecular formula	
	identification using Gibbs sampling on fragmentation trees	
	Marcus Ludwig, Friedrich-Schiller-University Jena, Germany	
16:30 - 16:45	Abstract 301	
	Automated metabolite substructure recommendation from	
	unexplained spectra using pattern mining	
	Aida Mrzic, University of Antwerp, Belgium	
16:45 - 17:00	Abstract 445	
	Towards accessible, standard and reproducible Metabolomics	
	Reza Salek. EMBL-EBI. United Kingdom	
15:30 - 17:00	Wine, the Great Gift from Bacchus	Meeting Room 3
	Parallel Session 7B	U U
15:30 - 16:00	Keynote Speaker	
	Metabolomics tools and approaches for characterisina flavours.	
	phenolics and auality markers in arapes and wine	
	Markus Herderich. The Australian Wine Research Institute. Australia	
16:00 - 16:15	Abstract 128	
	A metabolomic approach to determine the influence of arape	
	ripening, cultivar, vinevard site and vintage on wine composition	
	Leigh Schmidtke, Charles Sturt University, National Wine and Grane	
	Industry Centre Australia	
16.15 - 16.30	Abstract 464	
10.15 10.50	Targeted metabolomics to provide insights into the role of trace	
	sulfur compounds in wine groma and quality	
	Vilma Hysenai, Metabolomics Australia, The Australian Wine	
	Research Institute PO BOX 147 Glen Osmond 5064 Australia	
16.20 - 16.45	Abstract 162	
10.30 - 10.45	Licina standardised drift-tube ion mobility to enhance non-targeted	
	assessment of the wine metabolome	
	Tim Causon, University of Natural Resources and Life Sciences	
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10.45 17.00	A metabolomics approach to investigating red wine mouth-feel	
	Emma Sherman. The New Zealand Institute for Plant & Food	
	Research New Zealand	
15.30 - 17.00	Population-based Metabolomics Research	Meeting Room 4
15.50 17.00	Parallel Session 7C	Weeting Nooni 4
15:30 - 16:00	Abstract 166	
13.30 10.00	Irinary metabolic profiles associated with 5-year changes in	
	hiomarkers of alucase homeostasis: an NMP spectroscopy based	
	studu	
	Suuy Maik Diotznor University Medicine Creifsweld, Cormony	
16,00 16:15	Abstract 290	
10:00 - 10:15	ADSTRACT 289	

19:30 - 22:30	Conference Dinner	Plaza Ballroom
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4745 40 55	Seizo Koshiba, Tohoku University, Japan	
	Prospective Cohort Studies	
	Metabolomics Approach in Tohoku Medical Megabank Project	
16:45 - 17:00	Abstract 230	
	Kingdom	
	Computational Systems Medicine. Imperial College London, United	
	Beatriz Jiménez, MRC-NIHR National Phenome Centre.	
	phenotyping of populations	
_	A robust analytical pipeline for high throughput molecular	
16:30 - 16:45	Abstract 239	
	Stacey Reinke, Murdoch University, Australia	
	with asthma	
	omics asthma cohort identified tryptophan dysregulation associated	
10.10 10.50	Urinary metabolomics-based sub-phenotyping of a large-scale multi-	
16:15 - 16:30	Abstract 179	
	Agricultural Sciences Sweden	
	UN SHI Department of Molecular Science, Swedish University of	
	Plasma metabolites associated with type 2 diabetes in a Swedish	
	Placma matchalitas associated with type 2 diabates in a Swedich	

Thursday 29 June		
Time	Session	Location
8:45 - 9:45	Plenary Speaker: Roy Goodacre	Great Hall 2
	Lighting up the World of Metabolomics	
9:45 - 10:45	Poster Session 4	Exhibit Hall
10:45 - 12:15	Data Mining & Computational Workflows	Meeting Room 1
	Parallel Session 8A	
10:45 - 11:05	Abstract 304	
	Combining text mining and metabolic network algorithms to	
	complement and interpret metabolic profiles	
	Fabien Jourdan, INRA-MetaboHub, France	
11:05 - 11:25	Abstract 77	
	MAIMS: a GAIMS alternative for the deconvolution of UDP-N-acetyl-	
	D-glucosamine 13C mass isotopologue profiles	
	Dries Verdegem, Metabolomics Expertise Center - VIB / KU Leuven,	
	Belgium	
11:25 - 11:45	Abstract 444	
	Identification and discrimination of sparse networks in metabolic systems	
	Lindy Rae, The University of New South Wales, Australia	

11:45 - 12:05	Abstract 414	
	Metabolomics on the cloud using workflows: the PhenoMeNal	
	approach	
	Pablo Andres Moreno Cortez, EMBL-EBI The European	
	Bioinformatics Institute, United Kingdom	
12:05 - 12:15	Abstract 147	
	Automated Real-Time Quality Control of LC-MS Metabolomics Data	
	Jan Stanstrup, Steno Diabetes Center Copenhagen, Denmark	
10:45 - 12:15	Edibilomics	Meeting Room 3
	Parallel Session 8B	
10:45 - 11:05	Abstract 377	
	Estimation of dietary intake; comparison of a dietary biomarker and	
	a 4-day food diary	
	Lorraine Brennan, UCD Institute of Food and Health, Ireland	
11:05 - 11:25	Abstract 108	
	Demonstration of the utility of biomarkers for dietary intake	
	assessment; proline betaine as an example	
	Helena Gibbons, University College Dublin, Ireland	
11:25 - 11:45	Abstract 93	
	MS-based Flavor Profiling of Okinawan Subtropical Plant Resources	
	Yonathan Asikin, Division of Biosphere Resource Science and	
	Technology, Graduate School of Life and Environmental Sciences,	
	University of Tsukuba, Japan	
11:45 - 12:05	Abstract 229	
	Inhibiting lipid oxidation using hydrophobic and hydrophilic natural	
	antioxidants in an oil in water emulsion food system	
	Sara Ghorbani Gorji, University of Queensland, Australia	
12:05 - 12:15	Abstract 220	
	Tomato juice consumption alters the human plasma metabolome	
	Jessica Cooperstone, The Ohio State University, United States	
10:45 - 12:15	Metabolomics in Health and Disease I	Meeting Room 4
	Parallel Session 8C	
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	A combined metabolomics and lipidomics approach enables the	
	stratification of acute-on-chronic liver failure patients according to	
	their severity	
	Francois Fenaille, CEA-INRA UMR 0496, Laboratoire d'Etude du	
	Métabolisme des Médicaments, DRF/Institut Joliot/SPI, Université	
	Paris Saclay, MetaboHUB, France	
11:05 - 11:25	Abstract 319	
	An integrated approach combining metabolomics, lipidomics and	
	alycomics on plasma to highlight metabolism dysregulation in	
	gryconnes on plasma to mynight metabolism dysregulation m	
	hepatic encephalopathy	

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	Pierre BARBIER SAINT HILAIRE, CEA, SPI, Laboratoire d'Etude du Métabolisme des Médicaments, MetaboHUB-IdF, Université Paris		
	Saclay, 91191 Gif-sur-Yvette cedex, France, France		
11:25 - 11:45	Abstract 197		
	BIOMARKER DISCOVERY FOR HEPATITIS C PROGRESSION USING METABOLOMICS		
	Heidi Spratt, University of Texas Medical Branch, United States		
11:45 - 12:05	Abstract 63		
	Investigation of drug-induced steatosis in HepaRG cells using untargeted LC-MS metabolomics		
	Matthias Cuykx, Universiteit Antwerpen - Toxicological Centre, Belgium		
12:05 - 12:15	Abstract 381		
	Integrated omics profiling of NGLY1 deficiency disease		
	Songjie Chen, Stanford University, United States		
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	NMR Quantitates Whole Blood, Tissue and Even MS-Detected Metabolites		
	Daniel Raftery, University of Washington, United States		
14:15 - 14:30	Abstract 198		
	High Throughput Lipid Identification and Quantification Using a		
	Directed HRAM LC-MS-MS approach on a Modified Quadrupole-		
	Orbitrap Mass Spectrometer		
	Reiko Kiyonami, Thermo Fisher Scientific, United States		
14:30 - 14:45			
	METABOLOMICS ANALYSIS DISTINGUISHES BETWEEN STAGES OF		
	REINAL CELL CARCINONIA. A VALIDATION STODT.		
14.45 15.00	Abstract 472		
14.45 - 15.00	Australia 475		
	of human blood. Interlaboratory ring test validation of a rigorously		
	Bekzod Khakimov, Postdoc, Denmark		
15:00 - 15:15	Abstract 72		
19.00 19.19	Assessing Proficiency in Mass Spectrometric Lipid Measurement and		
	Annotation using a NIST International Lipidomics Interlaboratory		
	Comparison Exercise		
	Candice Ulmer, National Institute of Standards and Technology		
	(NIST), United States		
13:45 - 15:15	Plants	Meeting Room 3	
	Parallel Session 9B		
13:45 - 14:15	Keynote Speaker		

	Challenging in Plant Metabolomics: How can we observe and interpret metabolomic data?	
	Miyako Kusano, University of Tsukuba, Japan	
14:15 - 14:30	Abstract 71 An inducible system for anthocyanin accumulation in plants for	
	application in green systems biology	
	Robert Hall, Wageningen Plant Research, Netherlands	
14:30 - 14:45	Abstract 135 Geographic Mosaic of Metabolites in Purple Passionflower	
	(Passiflora incarnata): Testing the Coevolutionary Hypothesis Using	
	Nick Batora, University of Georgia, United States	
14:45 - 15:00	Abstract 69	
	Rice metabolomics: unravelling brown planthopper (BPH) resistance mechanism on BPH-resistant traits	
	umaporn uawisetwathana. National Center for Genetic Engineering	
	and Biotechnology, Thailand	
15:00 - 15:15	Abstract 447	
	A systems analysis of source-to-sink and metabolic regulatory	
	treatments	
	Atsushi Fukushima, RIKEN Center for Sustainable Resource Science,	
	Japan	
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13.43 13.13	Parallel Session 9C	
13:45 - 14:15	Parallel Session 9C Abstract 245	
13:45 - 14:15	Parallel Session 9C Abstract 245 Aiding diagnosis of rare disease: applications of mass spectrometry-	
13:45 - 14:15	Parallel Session 9C Abstract 245 Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases Network	
13:45 - 14:15	Parallel Session 9CAbstract 245Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases NetworkTom Metz, Pacific Northwest National Laboratory, United States	
13:45 - 14:15 14:15 - 14:30	Parallel Session 9C Abstract 245 Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases Network Tom Metz, Pacific Northwest National Laboratory, United States Abstract 449	
13:45 - 14:15 14:15 - 14:30	Parallel Session 9C         Abstract 245         Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases Network         Tom Metz, Pacific Northwest National Laboratory, United States         Abstract 449         Using U-13C glucose to determine the impairments in glucose         metabolism in both acute and chronic anilansy mouse models	
13:45 - 14:15 14:15 - 14:30	Parallel Session 9CAbstract 245Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases NetworkTom Metz, Pacific Northwest National Laboratory, United StatesAbstract 449Using U-13C glucose to determine the impairments in glucose metabolism in both acute and chronic epilepsy mouse models Tanya McDonald. School of Biomedical Science. University of	
13:45 - 14:15 14:15 - 14:30	<ul> <li>Parallel Session 9C</li> <li>Abstract 245</li> <li>Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases Network</li> <li>Tom Metz, Pacific Northwest National Laboratory, United States</li> <li>Abstract 449</li> <li>Using U-13C glucose to determine the impairments in glucose metabolism in both acute and chronic epilepsy mouse models</li> <li>Tanya McDonald, School of Biomedical Science, University of Queensland, Australia</li> </ul>	
13:45 - 14:15 14:15 - 14:30	<ul> <li>Parallel Session 9C</li> <li>Abstract 245</li> <li>Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases Network</li> <li>Tom Metz, Pacific Northwest National Laboratory, United States</li> <li>Abstract 449</li> <li>Using U-13C glucose to determine the impairments in glucose metabolism in both acute and chronic epilepsy mouse models</li> <li>Tanya McDonald, School of Biomedical Science, University of Queensland, Australia</li> <li>Abstract 134</li> </ul>	
13:45 - 14:15 14:15 - 14:30 14:30 - 14:45	<ul> <li>Parallel Session 9C</li> <li>Abstract 245</li> <li>Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases Network</li> <li>Tom Metz, Pacific Northwest National Laboratory, United States</li> <li>Abstract 449</li> <li>Using U-13C glucose to determine the impairments in glucose metabolism in both acute and chronic epilepsy mouse models</li> <li>Tanya McDonald, School of Biomedical Science, University of Queensland, Australia</li> <li>Abstract 134</li> <li>Metabonomic Study of Schizophrenia Using High-Resolution NMR</li> </ul>	
13:45 - 14:15 14:15 - 14:30 14:30 - 14:45	<ul> <li>Parallel Session 9C</li> <li>Abstract 245</li> <li>Aiding diagnosis of rare disease: applications of mass spectrometry- based metabolomics in the Undiagnosed Diseases Network</li> <li>Tom Metz, Pacific Northwest National Laboratory, United States</li> <li>Abstract 449</li> <li>Using U-13C glucose to determine the impairments in glucose metabolism in both acute and chronic epilepsy mouse models</li> <li>Tanya McDonald, School of Biomedical Science, University of Queensland, Australia</li> <li>Abstract 134</li> <li>Metabonomic Study of Schizophrenia Using High-Resolution NMR Spectroscopy</li> <li>Ute Marx, Hochschule Pforzheim, Germany</li> </ul>	
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15:30 - 16:30	– Plenary Speaker: Huiru Tang	Great Hall 2
	Simultaneous Quantification of 124 Amino Metabolites in 22	
	Metabolic Pathways Using UHPLC-MS/MS	
16:30 - 17:00	Closing Plenary Session	Great Hall 2