imsc
2016
toronto

21st International Mass Spectrometry Conference

August 20–26, 2016
Metro Toronto Convention Centre
255 Front Street, West Toronto, ON, Canada

Conference Program

Hosted by
The Canadian Society for Mass Spectrometry

CSMS SCSM
Canadian Society for Mass Spectrometry
Société Canadienne de Spectrométrie de Masse

Contents

Welcome from the IMSC Executive Committee

On behalf of the Canadian Society for Mass Spectrometry, we welcome you to the 21st International Mass Spectrometry Conference in Toronto, Canada.

Canada has a proud and outstanding tradition in mass spectrometry research. The home of pioneers such as Fred Lossing, Alex Harrison, John Holmes, Paul Kebarle, Ken Standing, Mel Comisarow, Bob Boyd, Ray March, Henry Thode and Ted Litherland, Canadians have contributed to every facet of mass spectrometry development. It is the home of SCIEX, one of the world's premier mass spectrometer companies. Mass spectrometry is represented in every university and analytical government laboratory in Canada, and as is evident from the scientific organizing committee, Canada is host to some of the very finest mass spectrometrists in the world, in every mass spectrometry-related discipline.

Toronto is one of the most culturally-diverse cities in the world, where everyone can safely stroll and enjoy public transportation at all hours of the day. Conference participants can enjoy dining in one of the over 9000 restaurants featuring cuisine from across the globe. Whether you take in the Canadian National Exhibition, Ripley's Aquarium, the Hockey Hall of Fame, a relaxing break on Centre Island Park, or a short get-away to visit one of the natural wonders of the world, Niagara Falls, Toronto has venues that will excite everyone.

We are proud to have assembled an outstanding cast of scientific speakers in 40 oral and poster sessions for the conference, covering a wide variety of mass spectrometry disciplines in five major themes: Integrated Omics, Physical and Biophysical Mass Spectrometry, Environmental Mass Spectrometry, Mass Spectrometry in Drug Discovery and Novel Instrumentation. We know you will find the meeting stimulating and return home full of new ideas. Enjoy the meeting!

Your IMSC 2016 executive committee


Paul M Mayer, Chair


Lekha Sleno


Michael Siu


Terry Cyr


Kerry M Peru

Welcome from the IMSF President

Dear Participants at the 21st IMSC,

I'm delighted to welcome all of you to the vibrant city of Toronto and especially to this first IMSC meeting in the Americas! The Executive Board and the representatives of our associated societies from around the world join our hosts, the Canadian Society for Mass Spectrometry, in wishing that you will have a productive and enjoyable stay in Toronto.

I especially want to thank the Executive Committee, Paul Mayer, Terry Cyr, Kerry Peru, and K.W. Michael Siu, who have organized an excellent meeting and the Scientific Committee, whose 23 members have worked so long and hard to produce the dynamic and exciting program.

This is only the second IMSC to be held outside of Europe. The first, held in Kyoto, Japan, in 2012, brought a new dimension to the IMSC conferences and I am sure that this week's events will also prove memorable. Toronto has one of the world's most diverse populations and there will be many opportunities for attendees to share their expertise and experiences with colleagues from around the world and local citizens. We are especially happy for the participation of a large number of students and early-career scientists. Please also watch for information about the 22nd IMSC, to be held in the beautiful city of Florence in 2018.

The International Mass Spectrometry Foundation continues to expand its range of activities to support the growth of our field. Do visit our newly revised website. The Executive Committee is pleased with the success of our first two International Mass Spectrometry Schools, held in Italy (2013) and Brazil (2015), and looks forward to the vote of our Affiliates to select the next locales. We also sponsor visiting speakers and will now add smaller, focused Workshops. We welcome suggestions for other activities.

We hope you enjoy the 21st IMSC and this wonderful city and return home full of enthusiasm for mass spectrometry, stimulating collaborations, and new friends!

Catherine E Costello

PRIME MINISTER · PREMIER MINISTRE

August 20–26, 2016

Dear Friends:

I am pleased to extend my warmest greetings to everyone attending the 21st International Mass Spectrometry Conference (IMSC), hosted by the Canadian Society for Mass Spectrometry.

This year's conference provides an ideal framework to showcase the latest developments in practice and instrumentation, to discuss issues of concern to the scientific community and to offer a variety of professional development activities. The commercial exhibition also gives delegates a chance to view emerging tools and scientific and industrial applications in mass spectrometry.

I would like to thank the organizers for putting together an informative and stimulating program. I also wish to commend everyone taking part in this week-long gathering for their efforts to advance our understanding of our world by seeking out the technological discoveries of tomorrow.

Please accept my best wishes for a memorable and productive event in Toronto.

Sincerely,

The Rt. Hon. Justin P.J. Trudeau, P.C., M.P.
Prime Minister of Canada

Ontario
Premier of Ontario - Première ministre de l'Ontario

August 20 – 26, 2016

A PERSONAL MESSAGE FROM THE PREMIER

On behalf of the Government of Ontario, I am pleased to extend warm greetings to everyone attending the 21st International Mass Spectrometry Conference (IMSC 2016), hosted by the Canadian Society for Mass Spectrometry and the Canadian scientific community.

Since its inception, the International Mass Spectrometry Foundation (IMSF) has worked diligently to advance the science and application of mass spectrometry worldwide by the promotion and dissemination of knowledge.

This conference provides a forum for students, delegates and leaders in industrial mass spectrometry to come together to enhance and exchange their knowledge and skills. I extend my appreciation to the organizers for efforts to draw enlightening speakers, prepare useful workshops and create innovative sessions.

Please accept my best wishes for a successful and productive conference.

Kathleen Wynne

Kathleen Wynne
Premier

CITY OF
TORONTO

Message from the Mayor

It is my pleasure to extend greetings and a warm welcome to everyone attending the 21st International Mass Spectrometry Conference.

This year's conference will be an opportunity for attendees to discuss matters of mutual interest in a setting designed for professional development.

I wish to welcome everyone to our city and encourage you to enjoy Toronto at this time of year as well as learn about our vibrant neighbourhoods.

On behalf of Toronto City Council, please accept my best wishes for an informative and enjoyable conference.

Yours truly,

Mayor John Tory
City of Toronto

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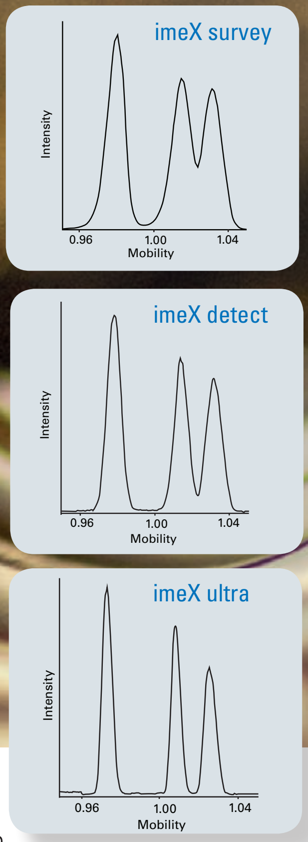

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International Mass Spectrometry Conferences

1st IMSC – London, UK	1958
2nd IMSC – Oxford, UK	1961
3rd IMSC – Paris, FR	1964
4th IMSC – Berlin, GE	1967
5th IMSC – Brussels, BE	1970
6th IMSC – Edinburgh, UK	1973
7th IMSC – Florence, IT	1976
8th IMSC – Oslo, NO	1979

9th IMSC – Vienna, AT	1982
10th IMSC – Swansea, UK	1985
11th IMSC – Bordeaux, FR	1988
12th IMSC – Amsterdam, NL	1991
13th IMSC – Budapest, HU	1994
14th IMSC – Tampere, FI	1997
15th IMSC – Barcelona, SP	2000
16th IMSC – Edinburgh, UK	2003

17th IMSC – Prague, CZ	2006
18th IMSC – Bremen, GE	2009
19th IMSC – Kyoto, JP	2012
20th IMSC – Geneva, CH	2014
21st IMSC – Toronto, CA	2016
22nd IMSC –Florence, IT	2018

IMSF Executive Committee, IMSF National Affiliates, and Scientific Committee

International Mass Spectrometry Foundation (IMSF)

Executive Committee

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- Prof. Dr. Scott A. McLuckey (US) – Region C Representative
- Prof. Marcos N. Eberlin (BR) – Region D Representative

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- Greece – Despina Tsipi
- Hong Kong – April S.Y. Wong
- Hungary – Laszlo Lelik
- India – Suresh Aggarwal
- Ireland – Peter Kenny
- Israel – Michal Sharon
- Italy – Gianluca Giorgi
- Japan – Yosinao Wada
- Korea – Hyun Sik Kim
- Norway – Einar Uggerud
- Peoples Republic of China – Jin-Ying Li
- Poland – Piotr Stefanowicz
- Portugal – Maria Helena Florencio
- Romania – Zaharie Moldovan
- Russia – Albert Lebedev
- Serbia & Montenegro – Mila Lausevic
- Singapore – Manfred Raida
- Slovakia – Vladimir Patoprsty
- Slovenia – Helena Prosen
- South Africa – Egmont Rohwer
- Spain – Encarnación Moyano
- Sweden – Jonas Bergquist
- Switzerland – Bertran Gerrits
- Taiwan – Pao-Chi Liao
- The Netherlands – Rob Vreeken
- Ukraine – Marina Kosevich
- United Kingdom – Christine Eckers
- United States of America – Jennifer Brodbelt

IMSC 2016 Executive Committee

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- Lehka Sleno, Université du Québec à Montréal (CSMS Vice-President)
- Terry Cyr, Health Canada (CSMS Treasurer)
- Kerry Peru, Environment and Climate Change Canada (CSMS Secretary)
- K.W. Michael Siu, University of Windsor (CSMS Past-President)

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- Pierre Chaurand (Départment de chimie, Université de Montréal)
- Travis Fridgen (Chemistry Department, Memorial University)
- Karl Jobst (Ministry of the Environment, Ontario)
- Rebecca Jockusch (Chemistry Department, University of Toronto)
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- Liam Kieser (Department of Physics, University of Ottawa)
- John Klassen (Chemistry Department, University of Alberta)
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- Oleg Krokhin (Manitoba Centre for Proteomics and Systems Biology, University of Manitoba)
- Liang Li (Chemistry Department, University of Alberta)
- Paul Mayer (Chemistry Department, University of Ottawa)
- Terry McMahon (Chemistry Department, University of Waterloo)
- Randy Purves (National Research Council Saskatoon)
- Eric Reiner (Ministry of the Environment, Ontario)
- David Schriemer (Southern Alberta Cancer Research Institute, University of Calgary)
- Lekha Sleno (Départment de chimie, Université de Quebec a Montréal)
- Vince Taguchi (Ministry of the Environment, Province of Ontario)
- Pierre Thibault (Départment de chimie et Institut de Recherche en Immunologie et Cancérologie, Université de Montréal)
- Derek Wilson (Chemistry Department, York University)Thomson Medal Award

Thomson Medal Award

The Thomson Medal Award is named after Sir J. J. Thomson, who was responsible for the first mass spectrograph and its resulting data more than 100 years ago. He also predicted many features of modern mass spectrometry. He discovered the electron using mass spectrometry and won the Nobel Prize in 1906 for his research.

The Thomson Medal Award is sponsored by the International Mass Spectrometry Foundation (IMSF), and the first awards were made in 1985.

2016 Thomson Medal Winners are

Scott McLuckey, Purdue University, USA

Marcos Eberlin, UNICAMP, Brazil

The Thomson Medal Award presentations will take place during the Awards Morning on Wednesday, August 24 in Hall A.

The previous winners are:

2014	C. V. Robinson and R. Zenobi
2012	R. Aebersold, A. Makarov and F. Tureček
2009	C. E. Costello, C. C. Fenselau and P. Roepstorff
2006	J. H. Bowie, M. L. Gross and M. Karas
2003	R. M. Caprioli, F. Hillenkamp and V. L. Talrose
2000	J. B. Fenn, D. F. Hunt and A. G. Marshall
1997	M. T. Bowers, D. E. Games and J. F. J. Todd
1994	C. Brunnée, C. Djerassi and H. Schwarz
1991	K. Biemann, H. Matsuda and N. M. M. Nibbering
1985	J. H. Beynon, R. G. Cooks, K. R. Jennings, F. W. McLafferty and A. O. C. Nier

Curt Brunnée Award

The Curt Brunnée Award will be presented on the occasion of the 21st IMSC in Toronto, August 20-26, 2016. The prize, of $5,000 (USD), is generously sponsored by *Thermo Fisher Scientific* and will be made to an individual for *"outstanding contributions to the development of instrumentation for mass spectrometry by a person under the age of 45 at the time of the award"*.

The 2016 recipient is **Dr. Yury Tsybin** (SpectroSwiss).

The Brunnée Award will be presented during the Awards Morning on Wednesday, August 24 in Hall A.

Previous winners of the award:

2014	Dr. Dimitris Papanastasiou, Fasmatech
2012	Prof. Zheng Ouyang, Purdue University
2009	Dr. Alexander Makarov, Thermo Scientific
2006	Prof. Roman Zubarev, Uppsala University
2003	Dr. Michisato Toyoda, Osaka University
2000	Prof. Scott McLuckey, Purdue University
1997	Prof. Michael Guilhaus, University of New South Wales
1994	Dr. Gareth Brenton, Swansea

CSMS Awards

The Fred P. Lossing Award is awarded by the Canadian Society for Mass Spectrometry to an individual who has made distinguished contributions to mass spectrometry in Canada. Sponsored by **Agilent Technologies Canada Inc.**, the 2016 Lossing Awardee is **Mel Comisarow**, UBC, for his role in the development of FT-ICR.

The Lossing Award will be presented during the Awards Morning on Wednesday, August 24 in Hall A.

2016 Journal for Mass Spectrometry Student Award Winners

Presentations will be made during the JMS symposium on Wednesday afternoon, Room 206E-F

Mario Francesco Mirabelli and Renato Zenobi. ETH Zurich, Switzerland

Observing proton transfer reactions inside the MALDI plume: experimental and theoretical insight into MALDI gas-phase processes

German Augusto Gómez-Ríos, Nathaly Reyes-Garcés, Ezel Boyacı, Emanuela Gionfriddo, Justen Poole, Barbara Bojko and J Pawliszyn. University of Waterloo, Canada

Fast quantitation of target analytes in complex matrices by solid phase microextraction-mass spectrometry (SPME-MS): recent developments and applications

Gerard Bryan Gonzales, Guy Smagghe, Sofie Coelus, Dieter Adriaenssens, Karel De Winter, Tom Desmet, Katleen Raes and John Van Camp. Ghent University, Belgium

Collision cross section prediction of deprotonated phenolics in a travelling-wave ion mobility spectrometer using molecular descriptors and chemometrics

Toru Takarada. Kobe Pharmaceutical University, Japan

New strategy for analysis of the splicing regulatory factors using high-resolution mass spectrometry

Pedro H. Vendramini, Rosana M. Alberici, Marcos N. Eberlin. University of Campinas, Brazil

EASI-MSI can be used in clinical analysis without loss chemical information?

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Exhibitors of the 21st IMSC

Organization Name	Booth	Hospitality
ACD Labs (Advanced Chemistry Development, Inc.)	1329	
Advion	1119	
Agilent Technologies: AFO Regional Columns & Supplies	1133/1230	716
Analytical Scientist / Texere	1316	
Bioinformtics Solutions Inc.	1333	
Biotage	1312	
Bruker Corporation	1217/1219	714
Hamamatsu	1239	
IM Publications	1123	
Ionbench	1418	
IonSense, Inc.	1218	
ISOSCIENCES	1214	
Jeol USA Inc	1319	
Leco	1223	
Markes International	1315	
MassTech Inc.	1129	
mSPEC group (MSPEC & MS PARTS)	1233/1332	
National Institute of Standards & Technology	1428	
Parker Hannifin Corporation - Filtration and Separation Division	1327	
Peak Scientific	1226	
PerkinElmer	1414	
Pfeiffer Vacuum GmbH	1113	
Photonis	1422	
Phytronix	1412	
Prosolia Inc.	1212	
Rapid Novor Inc.	1416	
Royal Society of Chemistry	1314	
Science Alert	1313	
Scientific Instrument Services	1216	
Sciex	1323/1325	713
Shimadzu Scientific Instruments Inc.	1229	
SpectraWorks Ltd	1318	
Springer	1215	
Themo Fisher Scientific	1322/1324/1326/1328	
VRS	1213	
Waters Coporation	1222/1224	715
Wiley	1115	
Zef Scientific	1317	

Int'l Mass Spectometry Conference 2016

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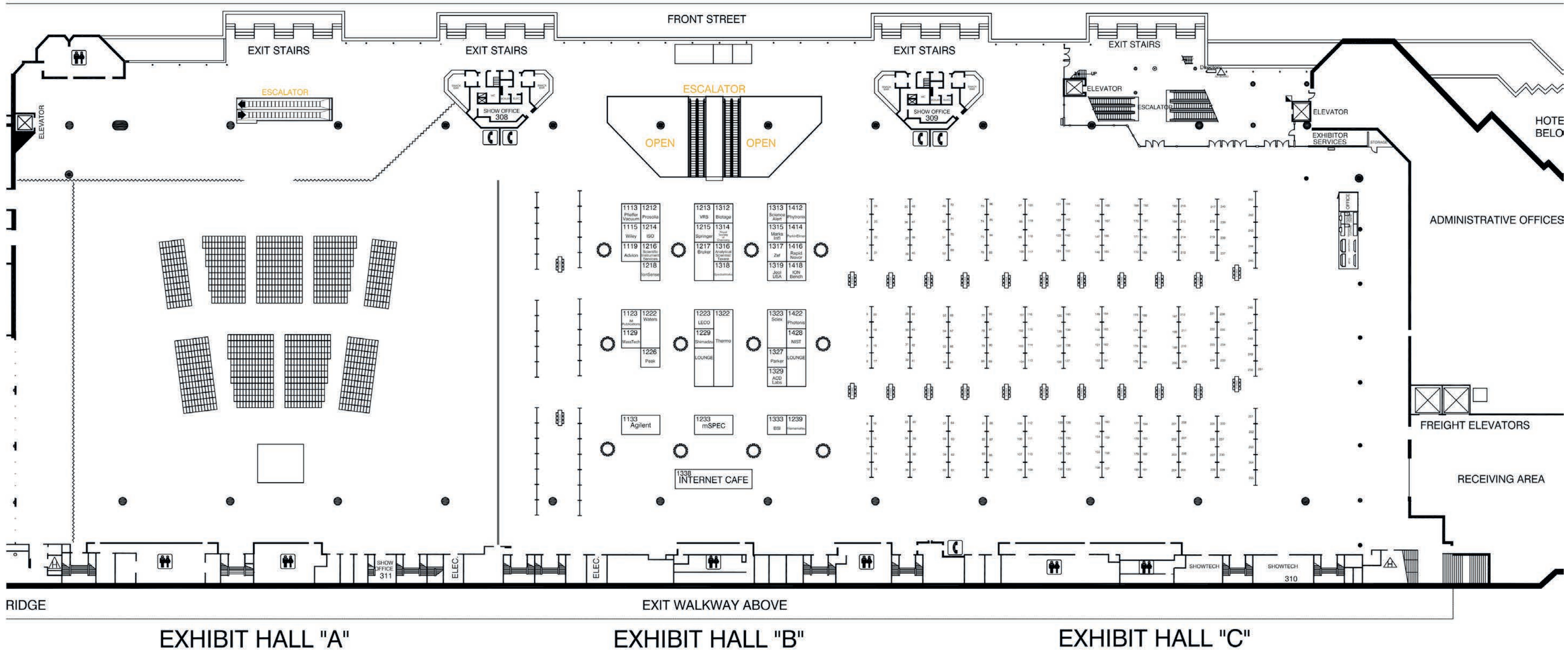
NORTH EXHIBIT LEVEL 300



Int'l Mass Spectometry Conference 2016

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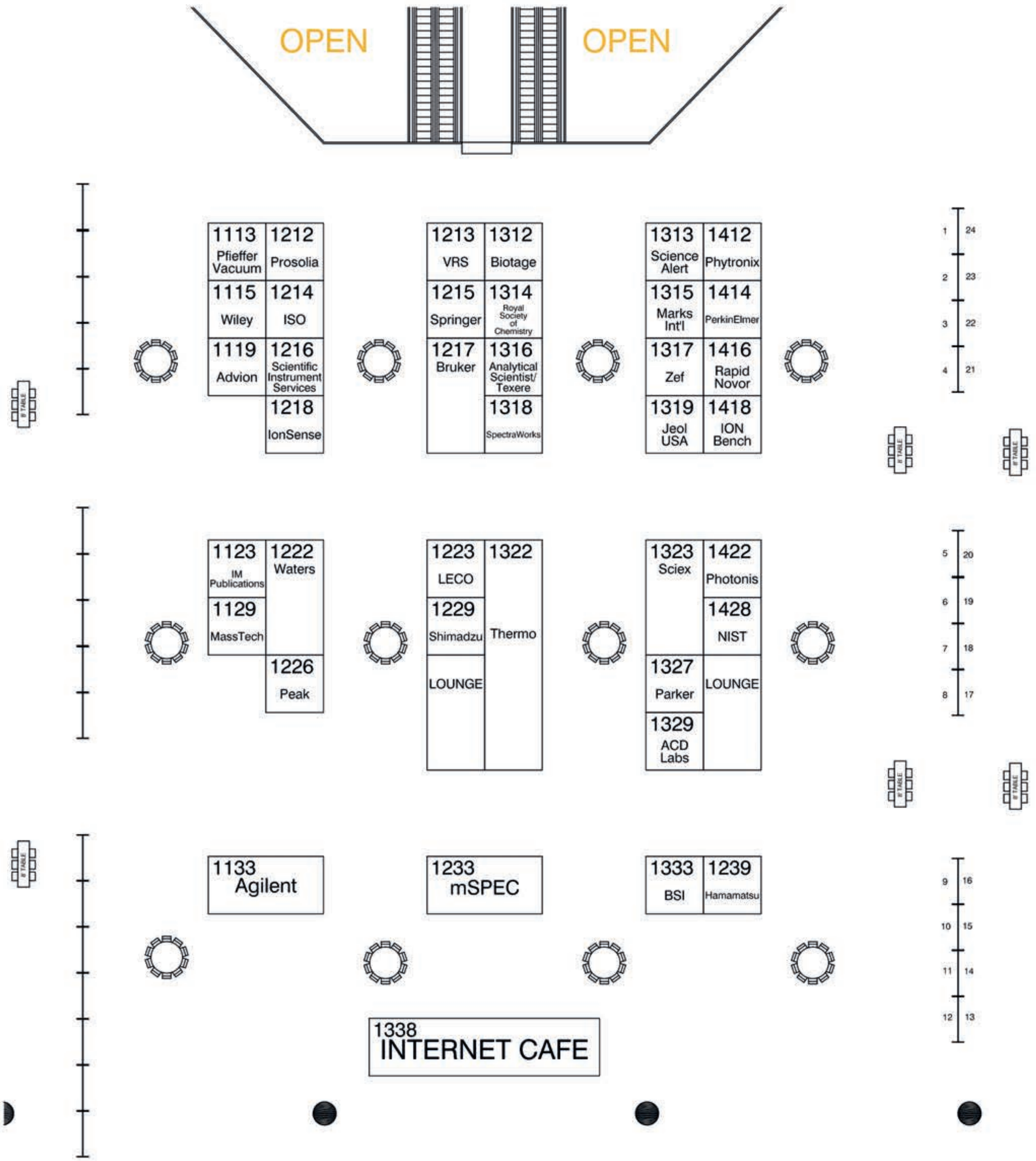

Exhibitors Information

Advanced Chemistry Development, Inc. (ACD/Labs) **Booth 1329**

Advanced Chemistry Development, Inc. (ACD/Labs) is an informatics company that develops and commercializes solutions in support of R&D. We provide integrated knowledge management and a unified platform for chemical structure confirmation, verification, and elucidation using a variety of spectroscopic and spectrometric techniques; and chromatographic method development/optimization. Our solutions also enable scientists to extract and apply knowledge from predicted ADME-Tox and physicochemical property data. Advanced Chemistry Development, Inc. (ACD/Labs) is an informatics company that develops and commercializes solutions in support of R&D. We provide integrated knowledge management and a unified platform for chemical structure confirmation, verification, and elucidation using a variety of spectroscopic and spectrometric techniques; and chromatographic method development/optimization. Our solutions also enable scientists to extract and apply knowledge from predicted ADME-Tox and physicochemical property data.

Advion, Inc. **Booth 1119**

Advion, Inc. was founded in 1993 based on the novel techniques developed within the Cornell University laboratory of Dr. Jack Henion, a leading researcher in the field of Liquid Chromatography/Mass Spectrometry (LC/MS). Pioneers within the industry, Advion offers a variety of fit-for-purpose systems and consumables for life science research. With sales and support offices in North America and Europe and a large network of distributors, Advion is a global company with customers in all of the top pharmaceutical companies, government life science research agencies and universities. Advion continues to expand its diverse portfolio of innovative microfluidic sand mass spec-based products for the life science industry.

Biotage **Booth 1312**

Biotage is a leading provider of Instruments and Consumables for use in Medicinal Chemistry, Organic Chemistry, Peptide Synthesis and Analytical Testing. Check out the Extrahera$^{\text{TM}}$, Simple automation, the Isolera$^{\text{TM}}$ Dalton, Mass Detection for Flash Systems, and the Isolera$^{\text{TM}}$ Spektra with ACITM Accelerated Chromatographic Isolation and Assist which purifies 250 mg in 5 minutes.

Bioinformatics Solutions Inc. (BSI) **Booth 1333**

Bioinformatics Solutions Inc (BSI) is well-known by their complete proteomic analysis software package, PEAKS. PEAKS provides a simple workflow for the identification and quantification of proteins in very complex biological samples with LC-MS. PEAKS includes key features such as de novo sequencing; PEAKS DB; PEAKS PTM; the homology search tool, SPIDER; and PEAKS Q. Through collaborative work, BSI has also been able to further their software by developing new technologies such as the PEAKS AB service, to allow quick and cost effective characterization of mAbs. PEAKS is used by users worldwide, and in numerous labs. Come stop by our booth to find out more.

Hamamatsu Corporation **Booth 1239**

Hamamatsu Corporation is the North American subsidiary of Hamamatsu Photonics K.K. (Japan), a leading manufacturer of devices for the generation and measurement of infrared, visible, and ultraviolet light. These devices include photomultiplier tubes, photodiodes, image sensors, mini-spectrometers, and light sources. Hamamatsu Photonics is dedicated to the advancement of photonics through extensive research. This corporate philosophy results in state-of-the-art products which are used throughout the world in scientific, industrial, and commercial applications.

IONBENCH **Booth 1418**

IONBENCH - Manufacturer of laboratory furniture for mass spectrometry (LC/GC/MS) & Elevating UHPLC benches. Mass Spec IonBench products integrate MS peripherals, a built-in vacuum pump noise reduction enclosure and protect turbomolecular pumps by reducing vibration by 99%. There is up to 30% savings in laboratory space allocation. Solidly built lockable casters simplify moving the system. Our integrated vacuum pump enclosure reduces noise emissions by 80% down in perception. LC Elevating IonBench, on caster wheels, can be easily lifted up or down by commuting a switch, for a convenient & safe access to the top of your UHPLC

IonSense, Inc. **Booth 1218**

IonSense, Inc. provides open-air ionization products for use with mass spectrometry products from all major vendors. The company offers it automated Total Product Mass Spectrometry technology to the enhance quality control and production efforts in fields of food safety, forensics, drug development, and chemical analysis. IonSense manufactures (DART®) technology and distributes the atmospheric solids analysis probe (ASAP^{TM}) licensed from M&M Mass Spec Consulting. The company endeavors to work with potential DART and ASAP users to provide customized interfaces for use with their existing LC/MS instruments. We invite you to inquire about the potential for using DART or ASAP to investigate your applications.

IsoSciences, LLC **Booth 1214**

IsoSciences, LLC is a leader in the custom synthesis of stable isotope labeled chemicals including vitamins, steroids, drug substances and metabolites. IsoSciences is ISO9001 certified and has an extensive catalog of stable isotope labeled standards available for immediate delivery both as solids and as CertiMass™ exact concentrations solutions. IsoSciences has added over 200 new products over the past year including an extensive range of $^{13}C_3$ labeled steroids, Vitamin D metabolites, $^{13}C_7$-Vitamin B12, $^{13}C_6$-Vitamin K2 MK4,MK7 and MK9. Visit us at www.isosciences.com for more information.

JEOL

Booth 1319

JEOL introduced its first mass spectrometer in 1963 and is a world leader in mass spectrometry, NMR, ESR, and electron microscopy. JEOL MS products include quadrupole, time-of-flight and magnetic sector mass analyzers. JEOL TOF mass spectrometers include the AccuTOF GCx, a versatile high-resolution TOF system offering a variety of ionization methods (EI, CI+/-, FI/FD) that are compatible with GCxGC. The SpiralTOF high-performance MALDI-TOF/TOF system utilizes unique multi-turn ion optics to compress a 17-meter flight path into a compact space. The AccuTOF-DART 4G system is the third generation of the world's first commercial ambient ionization system introduced in 2005.

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Industries around the world continue to trust LECO to deliver technologically advanced products and solutions for analytical science. Today's technologies for separation science resolve complex samples and pioneer high-sample throughput using GCxGC, GCxGC-TOFMS, and GC-TOFMS. High Resolution TOFMS systems offer an unprecedented combination of speed, resolution, mass accuracy, and dynamic range. A unique combination of easy-to-use software and advanced instrumentation provide an innovative solution for today's most demanding applications, including food, flavor/fragrance, petroleum, environmental, and metabolomics. For more information, visit www.leco.com.

Markes International

Booth 1315

Markes International, an industry leader in technology for trace organic analysis, manufactures instrumentation and software that enhances the analytical capability and productivity of gas chromatography. As well as having a long-established reputation for thermal desorption equipment, Markes manufactures BenchTOF™ mass spectrometers (and associated TOF-DS™ software) for single-run GC and GC×GC analysis of target compounds and screening of unknowns. Markes' technological innovation for mass spectrometry also includes ground-breaking Tandem Ionisation® technology, which uses a Select-eV® ion source to generate reference-quality 70 eV EI mass spectra at the same time as repeatable 'soft-ionisation' spectra with an enhanced molecular ion.

MassTech Inc.

Booth 1129

MassTech Inc., located in, Columbia, Maryland USA, is a privately owned analytical instrumentation and technology company incorporated in 2001 for developing AP MALDI, field deployable ion trap mass spectrometer, and conducting on-going research and development. MassTech is the only licensed manufacturer of AP-MALDI ion sources. MassTech's AP MALDI ion source product has been adapted to commercial mass spectrometers from major equipment manufacturers: Agilent, Bruker Daltonics, JEOL, Sciex, Thermo Fisher Scientific, and Waters. MassTech's MT Explorer 50 ion trap mass spectrometer offers desktop performance in a transportable package, has customizable software, and has potential for a variety of applications.

mSPEC Group

Booth 1233/1332

At mSPEC Group we believe that products and relationships should be built to last, that knowledge should be shared and innovation should benefit everyone. Under the umbrella of mSPEC group of companies we have been supporting the mass spectrometry industry since 1996, offering a wide range of ISO certified comprehensive maintenance, application and production support programs designed to meet your needs, however unique they may be. Specialized in: Method development, validation & application support; Full service coverage, preventative maintenance & repairs; Staff proficiency training and production support; Turn-key LCMS laboratory instruments, accessories and consumables.

NIST Mass Spectrometry Data Center (MSDC)

Booth 1428

The NIST Mass Spectrometry Data Center (MSDC) is a part of Biomolecular Measurement Division of the National Institute of Standards and Technology located near Washington, DC. The MSDC is responsible for the development of evaluated reference mass spectral databases for the identification and analysis of chemical compounds by mass spectrometry: It includes the NIST/EPA/NIH Mass Spectral Library (for GC-MS), the NIST Tandem Mass Spectral Library (for LC-MS), the NIST Peptide Mass Spectral Libraries, and the NIST GC Retention Index library. More information can be found at http://chemdata.nist.gov/

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Peak Scientific

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PerkinElmer

Booth 1414

Pfeiffer Vacuum

Booth 1113

Pfeiffer Vacuum is one of the world's leading providers of vacuum solutions. Our portfolio comprises a full range of hybrid and magnetically levitated turbopumps, backing pumps, measurement and analysis devices, components and vacuum chambers. Pfeiffer Vacuum enjoys a reputation for offering innovative, efficient and reliable vacuum solutions. Our products are constantly being optimized through close collaboration with customers from a wide variety of industries and through ongoing development work.

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PHOTONIS is the market leader for mass spectrometer detectors and ion transport solutions. We offer an extensive array of Channeltrons® with Extended Dynamic Range, Custom Microchannel Plates with electro-optic housings, and a wide range of Time of Flight Detectors which reduce time jitter. We also provide patented Resistive Glass technology in capillary tubes, inlet tubes, ion guides, drift tubes, collision cells and monolithic reflectron lenses. Let PHOTONIS design your next instrument detector or ion transport product for reliable results and extended lifetime because better detectors produce better results.

Phytronix

Booth 1412

The leader in quantitative ultra-fast high-throughput analysis solution for mass spectrometry presents the LDTD-96 and LDTD-384 ion sources. These platforms represent a unique shotgun approach that introduces the sample into the mass spectrometer using an ultra-fast Laser Diode Thermal Desorption (LDTD®). The LDTD Ion Source technology is the unique solution to increase your sample analysis throughput for your application needs.

Prosolia, Inc.

Booth 1212

Prosolia, Inc. is a privately-held company engaged in the development, manufacturing and marketing of innovative life science tools that expand the use of mass spectrometers for translational research and molecular analysis. The company's technologies enable a wide variety of basic research, translational science and chemical analysis applications and deliver lower operating costs and faster results by eliminating the need for timeconsuming, costly and error-prone sample preparation steps. The DESI 2D™ and flowprobe™ directly profile hundreds of molecules simultaneously from cells and tissue sections, among other surfaces, while the Velox 360™ PaperSpray® System enables quantitative results on molecules in microliters of biological fluids using a single-use, disposable cartridge.

Rapid Novor Inc.

Booth 1416

Rapid Novor Inc is dedicated to developing unparalleled analytical technologies to drastically change the processes in early stage drug research and development in the bio-pharmaceutical sector. Specializing in the field of mass spectrometry-based proteomics, the Novor team is up for the challenges to solve tough problems such as characterizing antibody proteins. We build bioinformatics software and services that deliver accurate, comprehensive and efficient results and enable the integration for pharmaceutical companies to bring the capabilities in-house.

Science Alert
Booth 1313

Science Alert (www.scialert.net) is a leading ePublishing platform in Asia, committed to provide the services to independent scholarly publishers, societies, associations, and university presses to facilitate the digital dissemination of more than 175 journals. Science Alert also offers a complete manuscript submission, tracking, peer review, and publishing system for journal editors (www.scialert.com).

Shimadzu
Booth 1229

Shimadzu is a leading manufacturer of a wide variety of mass spectrometers, including LCMS, GCMS and MALDI-TOF MS. Ideal for applications in a variety of industries, including foods, pharmaceuticals, toxicology, clinical and environmental, our platforms offer an incomparable fusion of speed and sensitivity to achieve new levels of data quality and throughput. We offer complete analysis platforms, with integrated, enabling software and reliable reagents/consumables. Visit us at IMSC 2016 (or online at Shimadzu.com) to discover why more and more labs are choosing Shimadzu as their most trusted partner for all of their analytical needs.

SpectralWorks Limited
Booth 1318

SpectralWorks Limited is a leading UK based software development company. We provide innovative solutions targeted for markets within the life sciences industry including metabolomics. Coupled with our collaborations in academia and industry, this provides the perfect balance between scientific and software development expertise to provide the best solutions for the end user. As well as providing software consultancy and development services our off the shelf products, such as AnalyzerPro® and RemoteAnalyzer®, provide workflow oriented solutions for mass spectrometry data acquisition and processing. Coupled with our PCA tools we can provide an integrated workflow for your metabolomics projects.

VRS
Booth 1213

VRS are the leading Recruitment Consultancy specialising in jobs within Analytical Chemistry, predominantly Mass Spectrometry & Chromatography (HPLC, GC, LC-MS, GC-MS, ICP-MS). With office locations in the US and Europe we provide unparalleled expertise to jobseekers and employers globally. To jobseekers VRS provide an exciting and diverse range of job opportunities within Analytical Chemistry, both laboratory-based and customer facing (Sales, Engineering, Marketing) roles. We can also provide you with in depth industry knowledge and advice. To employers we identify high calibre professionals at all levels of seniority across a wide spectrum of disciplines, meeting both temporary and permanent staffing needs.

ZefSci
Booth 1317

ZefSci provides maintenance, service contracts, repair and compliance on state of the art Mass Spectrometers, Liquid Chromatographs, Gas Chromatographs (HPLC/UPLC, GC, LC-MS-MS, GC-MS), and other hyphenated analytical techniques used in the Pharmaceutical, Biotechnology, Chemical, Environmental and Food Industries – or anywhere analytical instruments are used. ZefSci started with the vision that a complex LC-MS-MS environment requires a highly technical team with multi-disciplinary knowledge and a strong dedication to customers and their applications. This vision and our strong business ethic have led us to be recognized as a premier independent Engineering and Scientific firm specializing in state of the art chromatography and mass spectrometry.

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Short Courses and Workshops

Short Courses

Fundamentals of Mass Spectrometry

O. David Sparkman, Jürgen H. Gross

Saturday and Sunday, 9am to 5pm, Room 201

A two-day course on the interpretation of mass spectra of organic compounds.

Starting at the introductory level, the course is intended to provide the fundamentals for an understanding of the basic principles and applications of mass spectrometry of organic molecules.

Key topics of the short course are ionization processes, the formation and interpretation of isotopic patterns, uses of high-resolution and accurate mass for molecular formula determination, and an introduction to the fragmentation pathways of odd-electron and even-electron ions.

Information regarding available mass spectral databases will be provided along with how to use them with all types of organic mass spectrometry including MS/MS data. With an emphasis on the analysis of small molecules, you will learn to systematically employ all of the above mass spectral data for compound identification and structure elucidation.

To complete the course, compact lectures on instrumentation and its common modes of operation, as well as on the basics of widespread soft ionization methods such as chemical ionization (CI), field desorption (FD) including LIFIDI, electrospray ionization (ESI), and matrix-assisted laser desorption/ionization (MALDI) and ambient MS (DESI, DART) will be included.

Methodology Lectures (about 80% of the time) plus short simple exercises to assist understanding Language and Presentation English PowerPoint.

Advanced Interpretation of CID Mass Spectra from LC/MS/MS

Robert D. Voyksner

Saturday and Sunday, 9am to 5pm, Room 202

This advanced 2 day course will cover generation and interpretation of Collision Induced Dissociation (CID) mass spectra generated from positive and negative ions formed from the API techniques of electrospray, APCI or APPI.

The course will cover formation of ions, variables in CID mass spectra under tandem MS (triple quadrupole, q-TOF, ion trap) and API transport CID and interpretation of both the molecular ion and common molecular adduct ions and the product ion formed from these species after CID. The interpretation of the product ion mass spectra will be broken down into distinctive fragmentation mechanisms to aid the student to develop a systematic approach towards spectral interpretation. The fragmentation processes covered include single bond cleavage, multiple bond cleavage with charge retention and with charge migration, cyclization, ring opening fragmentation, hydrogen rearrangements, and charge remote fragmentation. The fragmentation mechanisms will be applied to both positive and negative ions. Additionally, CID product ion formation from adducts such as $[M+Na]^+$ $[M+NH_4]^+$ and $[M+F, Cl\ or\ Br]^-$ will be covered. Each of the lectures have imbedded practical problems, which will allow a review of the various fragmentation mechanisms on a variety of compound types. The course will finish with a series of real world LC/MS/MS interpretation problems applicable to pharmaceuticals, clinical, industrial, and forensic and biochemical industry that the students will work on in groups and discuss at the end of the class.

The course is designed for the students who have completed a LC/MS Short Course or who have some working knowledge of LC/MS and want to improve their qualitative interpretation skills for problem solving in LC/MS.

The NSERC CREATE Training program in Mass Spectrometry-enabled Science and Engineering (York University)

Courses are offered at a discount as they are linked to the CREATE program. Discounts are available to all participants.

Career Paths for Mass Spectrometry in Academia

Saturday, 9am to 5pm, Room 203

In this course, international academic leaders in mass spectrometry will share with you the story of the evolution of their careers in academia: How they got into to the buisness, how their research programs evolved over time and their involvement in major conceptual or technical advances in their fields. The course will provide ample time for formal and informal discussion with each speaker, culminating in a panel discussion on "Maximizing success in Academic Careers in Mass Spectrometry"

Career Paths for Mass Spectrometry in Industry

Saturday, 9am to 5pm, Room 203

In this course, leaders in industrial mass spectrometry from a broad range of multinational companies including Sanofi-Pasteur, Sciex, Waters, Maxxam, Fluidigm, Ionics and many others will share stories on: Career paths in industry, historical perspectives on the development of their company / sector, entrepreneurial stories or 'case study' industrial research projects in mass spectrometry. The course will offer ample time for formal an informal discussion with each speaker, culminating in a panel discussion on "Maximizing Success in Industrial Careers in Mass Spectrometry" and "Industry / Academic Collaborations in Industrial Mass Spectrometry"

Workshops

All workshops are included with the price of registration, no extra fees are required. Light refreshments will be served.

You've got an idea; Now what?

Torys LLP

Monday, 5:45 pm to 7:00 pm, Room 201

Topics of discussion will include:

- Anatomy of a start-up
  - Making the most of limited resources; finding and attracting talent; getting to proof-of-concept and prototype
- Incorporating a company
  - Incorporation vs. unincorporation structure; shareholders' agreements; accounting needs
- Partnering with others
  - Confidentiality; cross-licensing; joint ownership of IP
- Finding financing
  - Bootstrapping; friends and family; angel investments; government grants
- How to be friendly (attractive) to further investment
  - Series A through IPO; tax structures

You've got a start-up; Now what's your IP play

Torys LLP

Tuesday, 5:45 pm to 7:00 pm, Room 201

Topics of discussion will include:

- Contributing IP to a start-up (or keeping the IP personally)
  - Control of IP; founder(s') assignments and grant-back licenses; employee and contractor assignments
- Why patent your innovation (and when to stop patenting)
  - Exclusionary rights granted by patents; term of patents; application deadlines and cost of obtaining patents
- What makes an innovation patentable?
  - Novelty, non-obviousness, utility, subject matter
- If you don't patent, will you still have protection? (hint: copyright and trade secrets)
  - Copyright, trade secrets, industrial designs
- To patent or not to patent: the case studies of Twitter vs. Alibaba
  - First movers' advantage; patent valuation in an IPO

About Torys LLP:

Torys LLP is an international business law firm that works with entrepreneurs and innovators who need strategic, nimble and cost-effective advice to launch their products and maximize their market share. Our corporate lawyers advise on founder and shareholder agreements, tax issues, financing and partnership agreements. Torys' dedication to excellence across practice areas and industries has resulted in an enviable record of experience in Canada and globally. Our patent lawyers and agents advise on strategy and are experienced in all stages of protecting your innovation, from securing patents to freedom to operate. Torys' legal team keeps pace with your industry—from our North American base in Toronto, New York, Calgary, Montréal, and Halifax, we represent domestic, multinational, new-economy and traditional enterprises at every stage in development.

Careers in Mass Spectrometry

Tony Bristow (On behalf of the British Mass Spectrometry Society)
Wednesday, 5:45 pm to 7:00 pm, Room 201

For the mass spectrometrist, career pathways are very diverse. These can be in various industrial environments (both within and outside a scientific discipline), academia, with the instrument manufacturers and in many other areas of research. To illustrate the wide variety of career options, and debate the future requirements for the "expert" user, mass spectrometrists from diverse backgrounds will provide short presentations describing their career paths. This has been a very popular and successful workshop at previous IMSC meetings and again promises to deliver high impact and thought provoking discussions at IMSC 2016. We look forward to seeing you there.

Trent Conference on Mass Spectrometry Workshop

Prof. Travis Fridgen
Monday to Wednesday, 5:45 pm to 7:00 pm, Room 202

The Trent Conference on Mass Spectrometry is a graduate student centered event that allows students to present their work to their peers in an informal setting. For 32 years the meeting has provided a rich educational and training experience for students in all areas of Mass Spectrometry. The 33rd installment will take place as a workshop at the IMSC. Graduate students wishing to make a 15 min oral presentation should email Prof. Travis Fridgen to have their name, affiliation (with supervisor) and presentation title logged. While open to all, the preference will be given to those not already presenting at IMSC 2016.

Seminars

Waters Lunch Seminars:

Room 202, North Building, Metro Toronto Convention Centre

Monday, August 22
12:30 pm to 1:30 pm

David Heywood, Waters Corporation
Making large scale Omics workflows routine

The analysis of complex biological samples in support of "Omics" style workflows challenges current analytical systems. In this seminar we will discuss the role of ion mobility and informatics which have been developed to increase coverage and streamline biomarker identification in a robust, reproducible and accessible manner.

Tuesday, August 23
12:30 pm to 1:30 pm

Xavier Ortiz Almirall, Ministry of the Environment and Climate Change
Towards an automated untargeted method for microcystins analysis using two dimensional liquid chromatography and ion mobility/quadrupole time of flight mass spectrometry

Microcystins are cyclic heptatpeptide hepatotoxins produced by certain species of cyanobacteria (blue-green algae) found in freshwater environments. These secondary metabolites are toxic to higher organisms, causing human sickness or even death in some cases. Even though only one particular variant is currently regulated under the Ontario Safe Drinking Water Act (microcystin-LR, 1.5 µg/L) and there is only a handful of microcystin standards available in the market, over 90 different microcystins variants have been reported to date. For this reason, it is important to develop non-targeted methods for the analysis of these compounds. The present study describes an automated method for the analysis of microcystins by two dimensional liquid chromatography/quadrupole time of flight mass spectrometry (2D-LC/QTOF-MS) using a Waters Acquity I-Class and Waters Xevo G2-XS. Moreover, uncompleted chromatographic separation of all microcystins variants was further achieved by ion mobility mass spectrometry'

An automated method for microcystins extraction and clean up from water samples was developed using 2D-LC in the *trap* and *elute* configuration was used: a large volume of water sample (500 µl) was directly injected and trapped in the first column. After that, microcystins were desorbed in reverse flow and injected to the analytical column, prior to mass spectrometry analysis.

When the QTOF-MS was operated in high resolution full scan mode (RP ≈ 25.000), the instrument proved to be very sensitive for microcystin-LR (50 fg on column with S/N > 10). Combined with the 2D-LC, the system could detect 100 pg/L of microcistyn-LR in water with S/N>10. Mass accuracy (< 1 ppm) allowed assigning elemental compositions for unknown compounds with confidence. MS/MS mode monitoring the characteristic microcystin ion at m/z=135.0804 was useful to provide quantitative results of targeted compounds in complex samples.

For a more comprehensive characterization of complex algal bloom samples, ion mobility was used to distinguish the different microcystin variants based on their cross-section. This new dimension of separation allowed the identification of some congeners that could not be separated by means of chromatography or mass spectrometry alone. Advanced acquisition methods such as Data Dependant Acquisition (DDA) and Data Independent Acquisition (DIA) were successfully employed to elucidate new microcystin variants in real samples that have not been reported in literature yet.

Wednesday, August 24
12:30 pm to 1:30 pm

TBD
Molecular visualization - current and future perspectives on Mass Spectrometry Imaging

In this lunchtime session, Waters will discuss the latest developments in Mass Spectrometry imaging. We will present the data from both our internal and collaborative research programs, and look at the utility of Mass spec imaging across both preclinical and clinical research.

Waters Breakfast Seminars

Waters Hospitality Suite

Tuesday, August 23
7:00 am to 8:00 am

Dr. Roger Linington, Simon Fraser University
Integration of High-Content Screening and Untargeted Metabolomics for Comprehensive Functional Annotation of Natural Product Libraries

Traditional natural products discovery using a combination of live/dead screening followed by iterative bioassay-guided fractionation affords no information about compound structure or mode of action until late in the discovery process. This leads to high rates of rediscovery and low probabilities of finding compounds with unique biological and/or chemical properties. By integrating image-based phenotypic screening in HeLa cells with high-resolution untargeted metabolomics analysis, we have developed a new platform, termed Compound Activity Mapping, which is capable of directly predicting the identities and modes of action of bioactive constituents for any complex natural product extract library. This new tool can be used to rapidly identify novel bioactive constituents and provide predictions of compound modes of action directly from primary screening data.

This approach inverts the natural products discovery process from the existing 'grind and find' model to a targeted, hypothesis-driven discovery model where the chemical features and biological function of bioactive metabolites are known early in the screening workflow, and lead compounds can be rationally selected based on biological and/or chemical novelty. Advantages of employing integrated Big Data approaches to natural products discovery will be presented, as well as current challenges and limitations associated with these emerging technologies.

Waters Hospitality Suite

Wednesday, August 24
7:00 am to 8:00 am

Patty Sun, Waters Corporation
ionKey [LC/MS] HT- improvements for LC/MC integration

As microflow LC-MS systems continue to evolve, an increasing number of users are looking into applying microflow technologies to various scientific fields. In order to satisfy the wide-ranged needs and provide flexibility in this growing market, the ionKey/MS HT products are introduced as the expansion of the current ionKey/MS offer by adding a series of new features. During the initial launch of the ionKey/MS HT product family, following iKey separation devices are released: 300 µm ID and 5 cm BEH 130Å PsT C18, 1.7 µm, CSH 130Å PsT C18 CSH, 1.7 µm, and HSS T3 100Å, 1.8 µm.

In this presentation, we will discuss the new features of the ionKey/MS HT product family and the benefits of applying 300 µm ID iKey to certain applications. Sensitivity gain and reduced matrix effects are the well-known benefits of micro-scale LC/MS. However, the throughput of microflow LC/MS systems has been a challenge for laboratories performing routine analyses with large number of samples. The 300 µm ID iKey devices packed with the sub 2.0 µm particles achieve the sensitivity gain, throughput, and UPLC grade separation power by using higher flow rates and shorter cycle times.

Bruker Lunch Seminars

Room 206 ABCD, North Building, Metro Toronto Convention Centre

Monday, August 22
12:30 pm to 1:30 pm

Jeffrey N. Agar, Associate Professor and Barnett Institute Fellow, Depts. of Chemistry and Pharm. Sci., Northeastern University
Tracking the Dark Metabolome with a Novel Isotopic Fine Structure Enabled Metabolic Labeling Strategy

Tuesday, August 23
12:30 pm to 1:30 pm

Mel Park, Bruker Daltonics, Director of Research
Ion Mobility Mass Spectrometry Coming of Age

Dr. Sven Meyer, Senior R&D Scientist OMIC's Solutions
A New Dimension to QTOF Technology in the Analytical Lab

LECO Lunch Seminar

Room 206 EF, North Building, Metro Toronto Convention Centre

Tuesday, August 23
12:30 pm to 1:30 pm

Susan D. Richardson, Arthur Sease Williams Professor of Chemistry University of South Carolina
A Novel GC-TOF-MS: Quantifying Priority Unregulated Disinfection By-Products with the Sensitivity of SIM while acquiring Full Range Mass Spectra for Unknown Identification

Agilent Lunch Seminar

Room 203, North Building, Metro Toronto Convention Centre

Tuesday, August 23
12:30 pm to 1:30 pm

Philip Britz-McKibbin: Associate Professor, Cystic Fibrosis Canada Researcher
Improving Sample Throughput, Costs and Data Comparability in Mass Spectrometry using Multiplexed Separations

Separation science plays a key role in enhancing the selectivity, sensitivity and robustness of mass spectrometry (MS)-based metabolomic studies. However, low sample throughput and complicated data processing remain major bottlenecks to biomarker discovery when performing untargeted metabolite profiling. Herein, we introduce multi segment injection-capillary electrophoresis-mass spectrometry (MSI-CE-MS) as a multiplexed separation platform that takes advantage of customized serial injections to enhance sample throughput and data fidelity with quality assurance. MSI-CE-MS offers a cost effective approach for greatly expanding the productivity of MS-based chemical analyses while offering an accelerating data workflow for biomarker discovery in metabolomics.
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Christine Des Rosiers Ph.D., Director, Metabolomics Platform, Montreal Heart Institute (MHI), Professor, Department of Nutrition & Biochemistry, Université de Montréal
Using metabolomics to translate genetic discoveries in personalized medicine approach: Lessons from the iGenoMed Consortium in inflammatory bowel disease

Metabolomics - the most recent addition to the “omics” disciplines - offer a means to measure thousands of low molecular weight compounds from any cell, tissue or body fluid. This provides a global view of alterations in metabolic pathways induced by a given perturbation, whether resulting from a gene mutation or disease onset. Recent developments in technologies have enabled the application of metabolomics in the clinics in a high-through-put manner together with other omics. There are, however, numerous challenges and issues, which need to be taken into account for the successful application of metabolomics to disease biomarker discovery particularly in the setting of large cohort studies integrating other omics data. This presentation

will illustrate how we are tackling these challenges in the context of a multidisciplinary personalized medicine project on inflammatory bowel diseases (IDB) as part of the iGenoMed Consortium (http://www.medgeni.org/node/1), which exploits known IBD genetic risk factors to develop a tests for response to therapy.
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Thermo Lunch Seminars

Room 205, North Building, Metro Toronto Convention Centre

Monday, August 22
12:30 pm to 1:30 pm

TBA
Protein Structure Analysis with Cross-Linking and Top Down MS

Chemical cross-linking combined with mass spectrometry (CX-MS) and Top Down mass spectrometry are powerful methods to probe the structure of proteins, complexes and interactions. The high resolution and mass accuracy of Orbitrap technology, in combination with enhanced fragmentation modes (e.g., HCD, ETD, EtHCD) and MS^n modalities, allow completely unique and effective methods to probe protein structure. New reagents and software facilitate sample preparation and data interpretation to make these capabilities available to all labs. This seminar will feature the latest work on protein structure elucidation, protein characterization and protein-protein interaction networks.

Tuesday, August 23
12:30 pm to 1:30 pm

TBA
Complete Characterization of Biologics: mAbs and ADCs

Peptide mapping, subunit top/middle down analysis, and intact native and denatured analysis: The new Thermo Scientific™ Q Exactive™ BioPharma solution can do it all. Use the high resolution and mass accuracy of Orbitrap technology to generate exemplary data and Thermo Scientific™ BioPharma Finder™ software to analyze sequence variance, sites of modification, carbohydrate structure, etc. Verify these findings at the subunit level with top/middle down sequence analysis. Get a full picture of biologic heterogeneity, including glycosylation, linkers, drug conjugates, etc., with denatured and native intact analysis. This seminar will introduce the Q Exactive BioPharma solution and showcase examples of comprehensive characterization of biologic drugs.

Wednesday, August 24
12:30 pm to 1:30 pm

TBA
Advances in Accurate, High-Throughput Quantitative Proteomics

The ability to perform accurate protein quantification at low levels lets scientists unravel the complexity of protein interactions and track protein abundance changes in a wide variety of samples. When combined with multiplexing capabilities, quantitative proteomics provides a deep and comprehensive understanding of the molecular mechanisms underlying biological processes and disease states. Thermo Scientific™ TMT™ isobaric mass tag labeling combined with Orbitrap high resolution accurate mass (HRAM) mass spectrometry (MS) enable greater multiplexing capacity, resulting in increased depth of quantitative proteomic analysis across larger numbers of samples. The improved sensitivity and accuracy achieved with Orbitrap HRAM MS and synchronous precursor selection (SPS)-based MS3 technology on the Thermo Scientific™ Orbitrap Tribrid™ MS systems provide a unique, unmatched capability to accurately measure the most subtle changes in low-abundance proteins. In this seminar, we will discuss multiplexed quantitative proteomics and present real-world applications from leading research laboratories.

Oral Program

Saturday, August 20, 2016

9:00 AM – 5:00 PM	***Short course – Fundamentals in MS – Day 1*** David Sparkman & Jürgen Gross	Room 201
9:00 AM – 5:00 PM	***Short course – Advanced interpretation CID mass spectra LC/MS/MS – Day 1*** Robert D. Voyksner	Room 202
9:00 AM – 5:00 PM	**The NSERC CREATE training program in mass spectrometry-enabled science and engineering (York University)** Career Paths for Mass Spectrometry in Academia	Room 203

Sunday, August 21, 2016

9:00 AM – 5:00 PM	***Short course – Fundamentals in MS – Day 2*** David Sparkman & Jürgen Gross	Room 201
9:00 AM – 5:00 PM	***Short course – Advanced interpretation CID mass spectra LC/MS/MS – Day 2*** Robert D. Voyksner	Room 202
9:00 AM – 5:00 PM	**The NSERC CREATE training program in mass spectrometry-enabled science and engineering (York University)** Career Paths for Mass Spectrometry in Industry	Room 203
5:00 PM - 6:00 PM	***Plenary lecture -*** ***Mass spectrometry imaging in the service of human health*** Richard N. Zare, Department of Chemistry, Stanford University	Hall A, Level 300
6:00 PM – 6:30 PM	***Opening ceremony***	Hall A, Level 300
6:30 PM – 8:30 PM	***Opening reception***	Exhibits Hall B Level 300

Monday, August 22, 2016

8:30 AM – 9:15 PM	***Plenary Lecture -*** ***Native MS in structural biology: characterization of non-covalent complexes by SID/IMMS or SID/HRMS*** Vicki Wysocki, Ohio State University	Hall A, Level 300
9:30 AM – 12:00 PM	***Metabolomics I*** Chairs: Matej Orešič & Guowang Xu	Room 201
9:30 AM	**Unexpected characteristics and artificial changes of body fluids: crucial factors in clinical metabolomics** Dr. Rainer Lehmann, University Hospital Tuebingen / Central Laboratory	
10:00 AM	**New advances in high-performance chemical isotope labeling LC-MS for metabolomics** Dr. Liang Li, University of Alberta	
10:30 AM	**Interpreting LC-MS/MS-spectra from primary metabolites for tandem MS-based ^{13}C-fluxomics** Mr. Jannick Kappelmann, Research Center Juelich	
11:00 AM	**Extending a high quality reference tandem mass spectral library for more comprehensive metabolite identification** Dr. Xiaoyu Yang, National Institute of Standards and Technology	
11:20 AM	**On-line breath analysis with secondary electrospray ionization reveals altered metabolic signatures between patients with different severities of COPD** Mr. Martin Thomas Gaugg, ETH Zürich	
11:40 AM	**SRM assays for endogenous biochemical markers of internal exposure** Dr. Zdenek Spacil, Masaryk University	

9:30 AM – 12:00 PM	***Proteomics of the PTMs*** Chair: Pierre Thibault	Room 202
9:30 AM	**Electron transfer dissociation (ETD) mass spectrometry and studies of the nucleocytosolic O-GlcNAc PTM** Dr. Al Burlingame, University of California San Francisco	
10:00 AM	**Deciphering PTM cross-talk by middle-down protein analysis using ETD MS/MS** Ole Jensen, University of Southern Denmark	
10:30 AM	**SUMO system interactome** Brian Raught, University of Toronto	
11:00 AM	**Discovery of novel PTMs mediated by bacterial effectors** Dr. Xiaoyun Liu, Peking University	
11:20 AM	**A mass spectrometry-based novel chemical method to specifically and globally analyze cell surface glycoproteins** Dr. Ronghu Wu, Georgia Institute of Technology	
11:40 AM	**Quantitative analysis of induced reversible cysteine oxidation in an atherosclerotic model via modified biotin switch assays** Dr. Juergen Kast, University of British Columbia	

9:30 AM – 12:00 PM	***Gaseous biomolecules: conformations, energetics and reactions*** Chair Rebecca Jockusch	Room 203
9:30 AM	**The structure of duplex nucleic acids in the gas phase** Dr. Valérie Gabelica, Inserm, France	
10:00 AM	**An infrared spectroscopy approach to follow beta-sheet formation in peptide amyloid assemblies** Mr. Waldemar Hoffmann, Freie Universitaet Berlin	
10:30 AM	**New developments in 2D UV-MS cold ion spectroscopy of biomolecules** Dr. Oleg Boyarkine, EPFL	
11:00 AM	**Mass spectrometry fragmentation methods (BIRD, SORI-CID, IRMPD): powerful techniques to study physical chemistry of guanine quadruplexes** Mr. Mohammad Azargun, Memorial University	
11:20 AM	**Electron photodetachment, an efficient relaxation mechanism for electronically excited nucleic acids anions?** Dr. Alexandre Giuliani, Synchrotron SOLEIL	
11:40 AM	**Probing the gaseous structure of a β-hairpin peptide with hydrogen/deuterium exchange (HDX) and electron capture dissociation (ECD)** Ms. Rita Straus, NSERC CREATE York University and University of Toronto	

9:30 AM – 12:00 PM	***Ultra high resolution MS & Petroleomics*** Chair: Karl Jobst	Room 205
9:30 AM	**Petroleomics and environmental monitoring: a more detailed view using FTICR MS** Dr. Mark Barrow, University of Warwick	
10:00 AM	**Characterization of the Gulf of Mexico Deepwater Horizon oil spill and natural oil seeps by FT-ICR MS** Dr. Vlad Lobodin, National High Magnetic Field Laboratory	
10:30 AM	**Orbitrap GC-MS: one year on** dr Alexander Makarov, Thermo Fisher Scientific	
11:00 AM	**Characterizations of heavy petrochemical fractions: high temperature GCxGC with HR-TOFMS detection and thermal analysis-photo ionization TOFMS** Dr. Ralf Zimmermann, University Rostock and Helmholtz Zentrum München	
11:20 AM	**The use of high resolution SpiralTOF MS and mass defect analysis for the characterization of coals and complex polymeric samples** dr Thierry Fouquet, National Institute of Advanced Industrial Science and Technology (AIST), Japan	
11:40 AM	**Performance limits in ultrahigh resolution FT ICR mass spectrometry and the main limiting factors** Dr. Evgeny Nikolaev, Institute of Energy Problems of Chemical Physics Russian Acad. Sciences	

Monday

9:30 AM – 12:00 PM	***Advances in analytical separations for MS*** Chair: Oleg Krokhin	Room 206A-D
9:30 AM	**Slicing proteomics to unveil the human proteome** Dr. Yasushi Ishihama, Kyoto University	
10:00 AM	**Method and software workflow for integrating paired CE-MS and LC-MS bottom-up proteomics data from SDS-PAGE pre-fractionated samples** Dr. Yassene Mohammed, Center for Proteomics and Metabolomics, Leiden University Medical Center	
10:30 AM	**On-line coupling of field-flow fractionation with mass spectrometry for lipoproteins and metalloproteins** Dr. Myeong Hee Moon, Yonsei University	
11:00 AM	**Supercritical fluid chromatography coupled to high resolution mass spectrometry for dereplication and quantification of lipids** Dr. David Touboul, CNRS ICSN	
11:20 AM	**Analysis of derivatized glycans using differential mobility spectrometry** Dr. J. Larry Campbell, SCIEX	
11:40 AM	**Optimal selection of separation chemistry for 3D-LC-MS/MS in bottom-up proteomics** Dr. Oleg Krokhin, University of Manitoba	
12:00 PM – 3:00 PM	Lunch Seminars, Poster Sessions	
1:00 PM – 3:00 PM	Authors of Odd Number Posters Present *Advanced chromatographic methods in environmental analysis* *Advances in analytical separations for MS* *Ambient ionization methods* *Biomolecular structure: covalent labeling and crosslinking* *Chemical proteomics* *Clinical proteomics* *Emerging and persistent environmental contaminants* *FAIMS/DMS and new developments in IMS instrumentation* *Gas phase ion chemistry and spectroscopy* *Gaseous biomolecules: conformations, energetics and reactions* *IMS developments in MS: computations, collision cross sections & complex mixtures* *Integrated omics* *Lipidomics* *Metabolomics* *Proteomics of PTMs* *Quantitative targeted proteomics* *Ultra high resolution mass spectrometry and petroleomics*	

3:00 PM – 5:30 PM	***Lipidomics I*** Chair: Jeff Smith, Markus Wenk	Room 201
3:00 PM	**New ion-mobility and ion-activation strategies for lipid structure elucidation** Dr. Stephen Blanksby, Queensland University of Technology	
3:30 PM	**Healthy plasma lipidome** Dr. Andrej Shevchenko, MPI of Molecular Cell Biology and Genetics	
4:00 PM	**Natural variation of blood plasma lipids in healthy Asian individuals** Markus Wenk, National University of Singapore	
4:30 PM	**TrEnDi using isotopically-labelled diazomethane to increase sensitivity and selectivity of PE, PC and PS derived from complex biological samples** Mr. Carlos Canez, Carleton University	
4:50 PM	**Accurate quantification of polyunsaturated glycerophospholipids by shotgun lipidomics** Dr. Kai Schuhmann, MPI CBG Dresden, Germany	
5:10 PM	**Broad separation of lipid isomers using high-definition differential ion mobility spectrometry and a range of ionizing species** Mr. Andrew Bowman, Wichita State University	

3:00 PM – 5:30 PM	***Integrated Omics*** Chair: Liang Li	Room 202
3:00 PM	**IR MALDESI: a novel molecular microscopy method** Dr. David Muddiman, North Carolina State University	
3:30 PM	**Integrated omics approach centered on MS-based metabolomics to decipher mechanism implicated in human diseases** Dr. Guowang Xu, Dalian Institute of Chemical Physics, CAS	
4:00 PM	**Integrated proteomic datasets for biomarker discovery and verification of bladder cancer** Dr. Yi-Ting Chen, Chang Gung University	
4:30 PM	**Increasing arginine production in *C. glutamicum* by rational strain design using a combination of metabolomics and proteomics** Dr. Aiko Barsch, Bruker Daltonics	
4:50 PM	**Combined metabolomic and proteomic studies of DOCK8-Hyper IgE syndrome** Dr. Anas Abdel Rahman, King Faisal Specialist Hospital and Research Center	
5:10 PM	**Rapid identification of mechanisms of action through systems biology** Dr. Akos Vertes, George Washington University	
3:00 PM – 5:30 PM	***Biomolecular structure: covalent labeling and crosslinking*** Chairs: Christoph Borchers & David Schreimer	Room 203
3:00 PM	**XL-FASP: a new integrated cross-linking workflow to study extra large membrane protein complexes** dr Julia Chamot-Rooke, Institut Pasteur, CNRS	
3:30 PM	**XPlex: a multi residue cross-linking strategy for protein structure determination** dr Fabio Gozzo, Unicamp	
4:00 PM	**Functional group selective derivatization for comprehensive shotgun lipidome analysis and multiplexed lipid quantitation** Dr. Gavin Reid, University of Melbourne	
4:30 PM	**Structural mass spectrometry: novel tool to study transcription factor/DNA interaction** Dr. Petr Novak, Institute of Microbiology	
4:50 PM	**Probing the time scale of FPOP (fast photochemical oxidation of proteins): radical reactions extend over tens of milliseconds** Mr. Siavash Vahidi, University of Western Ontario	
5:10 PM	**Surface accessibility and dynamics of macromolecular assemblies captured by covalent labelling mass spectrometry and molecular simulations** Dr. Argyris Politis, King's College London	
3:00 PM – 5:30 PM	***Advanced chromatographic methods in environmental analysis*** Chair: Eric Reiner	Room 205
3:00 PM	**Cryogenic zone compression (CZC) and comprehensive two-dimensional gas chromatography (GC×GC) coupled to (HR)MS for measuring hyper-trace compounds** Dr. Jef Focant, University of Liege	
3:30 PM	**Why is firefighting dangerous? characterization of mixed-halogenated dioxins and furans in fire debris using GCxGC-TOFMS and APGC-MS/MS** Dr. Frank Dorman, Penn State Unversity	
4:00 PM	**Fishing halogenated environmental contaminants in biota based on isotopic pattern and mass defect provided by high resolution MS profiling** Dr. Ronan Cariou, LABERCA-Oniris, France	
4:30 PM	**Advantages of comprehensive two-dimensional gas chromatography-high resolution time-of-flight mass spectrometry in petroleomics** Mr. Jonathan Byer, LECO Corporation	
4:50 PM	**Quantitative profiling by SFC and UHPLC-MS/MS reveals metabolic phenotype of internal exposure to phthalates** Dr. Zdenek Spacil, Masaryk University	
5:10 PM	**Applications of ambient ionization mass spectrometry and LC-MS/MS for studying multi-phase chemistry in indoor environments** Dr. Shouming Zhou, University of Toronto	

3:00 PM – 5:30 PM	***Ambient ionization methods*** Chair: Graham Cooks	Room 206 A-D
3:00 PM	**C–H bond silylation of aromatic heterocycles catalyzed by potassium t-butoxide in microdroplets** Dr. Richard Zare, Department of Chemistry, Stanford University	
3:30 PM	**Intrasurgical brain tumor diagnosis and surgical margin definition by desorption electrospray ionization-mass spectrometry** Dr. R. Graham Cooks, Purdue University	
4:00 PM	**Ambient MS based analytical platform for rapid identification of brain cancer tumor tissues** Dr. Evgeny Nikolaev, Institute of Energy Problems of Chemical Physics Russian Acad. Sciences	
4:30 PM	**Nanospray desorption electrospray ionization (nano-DESI) imaging of biological systems** Dr. Julia Laskin, Pacific Northwest National Laboratory	
4:50 PM	**DESI-MS imaging of AMMOENG 130 in zebrafish** Mr. Demian Ifa, York University	
5:10 PM	**Development and characterization of an airborne laser-spark ion source for ambient desorption/ionization mass spectrometry** Mr. Andreas Bierstedt, Federal Institute for Materials Research and Testing	
5:45 PM – 7:00 PM	**Workshops**	
	You've got an idea; Now what? Torys, LLP	Room 201
	Trent Conference	Room 202
7:00 PM – 8:00 PM	**Dinner Break**	
8:00 PM – 11:00 PM	**Corporate Hospitality Suites**	700 Level, South Building MTCC

Tuesday, August 23, 2016

8:30 AM – 9:15 PM	***Plenary lecture -*** ***Expanding the number of chemicals measured in environmental media: challenges for analytical mass spectrometry*** Derek Muir, Environment and Climate Change Canada	Hall A, Level 300
9:30 AM – 12:00 PM	***Chemical proteomics*** Chairs: Juergen Kast, Gavin Reid	Room 201
9:30 AM	**Charting the cellular interactome by proteome-wide cross-linking mass spectrometry** Dr. Albert Heck, Utrecht University	
10:00 AM	**Tracking drug action in living cells by thermal profiling of the proteome** Dr. Mikhail Savitski, EMBL	
10:30 AM	**Activity-based probes for selective penicillin-binding protein visualization** Dr. Erin Carlson, University of Minnesota	
11:00 AM	**Metal labelling as a detection functionality for tri-functional capture compounds (CCs) to detect protein targets of small molecules** Ms. Oleksandra Kuzmich, Humboldt Universität zu Berlin	
11:20 AM	**High-throughput identification of the protein targets of bioactive natural products** Mr. Hongbo Guo, University of Toronto	
11:40 AM	**Identification of the molecular target of a growth inhibiting compound in *Staphylococcus aureus* using a chemical proteomics strategy** Ms. Elena Kunold, TU Munich	
9:30 AM – 12:00 PM	***Quantitative targeted proteomics*** Chair: Xiaohong Qian	Room 202
9:30 AM	**Extending the limits of deep DIA in human cell line and mouse brain tissue samples** Dr. Lukas Reiter, Biognosys AG	

10:00 AM	**Mass spec western: target absolute quantification of proteins and post-translational modifications** Mr. Mukesh Kumar, MPI-CBG, Dresden, Germany	
10:30 AM	**Comprehensive relative quantification of the cytochromes P450 by micro-LC and SWATH® acquisition and data processing using cloud computing** Dr. Sibylle Heidelberger, Sciex	
11:00 AM	**A simplified approach to fast and accurate, high throughput targeted MS2 quantitation using internal standards** Dr. Romain Huguet, Thermo Fisher Scientific	
11:20 AM	**Quantitation of residual proteins in an HSV-2 vaccine candidate using LC-MRM** Dr. Andrew James, Sanofi Pasteur	
11:40 AM	**Fundamental aspects and diagnostic potential of immunocapture in bottom-up LC-MS/MS** Dr. Leon Reubsaet, Department of Pharmaceutical Chemistry, School of Pharmacy	
9:30 AM – 12:00 PM	***Gas phase ion chemistry and spectroscopy*** Chairs: Travis Fridgen & Philippe Maitre	Room 203
9:30 AM	Photoisomerization of molecular ions in a tandem ion mobility spectrometer Dr. Evan Bieske, evanjb@unimelb.edu.au	
10:00 AM	**IRMPD spectroscopy of fragments from proline-analog-containing peptides** Dr. John Poutsma, College of William and Mary	
10:30 AM	**Infrared-driven chemistry on isolated transition metal clusters: catalytic reaction barriers from IR-MPD and BIRD** Dr. Stuart Mackenzie, University of Oxford	
11:00 AM	**Reactivity and spectroscopic features of key intermediates in Cisplatin drug chemistry** Dr. Simonetta Fornarini, Università degli Studi di Roma La Sapienza	
11:20 AM	**Evaluation of the Sharpless epoxidation by ESI-MS and IRMPD spectroscopy** Dr. Thiago C. Correra, IQ-USP - Brazil	
11:40 AM	**Observing proton transfer reactions inside the MALDI plume: experimental and theoretical insight into MALDI gas-phase processes** Mr. Mario Francesco Mirabelli, ETH Zurich	
9:30 AM – 12:00 PM	***Emerging and persistent environmental contaminants*** Chair: Sue Richardson	Room 205
9:30 AM	**Exploring environmental chemical space through HR/AM mass spectrometry and cheminformatics: The example of wastewater-derived organic micropollutants** Dr. Lee Ferguson, Duke University	
10:00 AM	**Orbitrap™ based gas chromatography-mass spectrometry to characterize semi-volatile and volatile disinfection by-products in water** Dr. Cristina Postigo, Institute for Environmental Assessment and Water Research (IDAEA-CSIC)	
10:30 AM	**New approaches for characterization of unknown precursors of disinfection byproducts in water** Dr. Xing-Fang Li, University of Alberta	
11:00 AM	**What's in a cloud? A semi-volatile GC/MS study** Dr. Albert Lebedev, Lomonosov Moscow State University	
11:20 AM	**Aqueous film forming foam (AFFF) components and related perfluoroalkyl and polyfluoroalkyl substances (PFASs) in Canadian surface waters** Ms. Lisa D'Agostino, University of Toronto	
11:40 AM	**General strategies to increase the repeatability in environmental non-target screening by liquid chromatography-high resolution mass spectrometry** Mr. Tobias Bader, Zweckverband Landeswasserversorgung (and Leuphana University Lüneburg)	
9:30 AM – 12:00 PM	***FAIMS/DMS and new developments in IMS instrumentation*** Chair: Randy Purves	Room 206A-D
9:30 AM	**Differential ion mobility separations at the extremes of resolution and field strength** Dr. Alexandre Shvartsburg, Dept. of Chemistry, Wichita State University	

Tuesday

10:00 AM	**Improved isotopic labelling quantitation for large scale proteomic analyses using high field asymmetric waveform ion mobility spectrometry (FAIMS)** Mr. Eric Bonneil, IRIC-Université de Montréal	
10:30 AM	**Differential ion mobility and tandem mass spectrometric analysis of a series of chlorogenic acid isomers in fruit juice** Dr. Anas El-Aneed, College of Pharmacy and Nutrition, University of Saskatchewan	
11:00 AM	**Characterization of sphingolipids from plasma by LC-differential mobility spectrometry-MS/MS** Dr. Sibylle Heidelberger, Sciex	
11:20 AM	**Protein structural studies using ion mobility MS and in-source ion activation techniques** Dr. Ruwan Kurulugama, Agilent Technologies	
11:40 AM	**Ion mobility mass spectrometry coming of age** Dr. Melvin Park, Bruker Daltonics, Inc	
12:00 PM - 3:00 PM	Lunch Seminars, Poster Sessions	
1:00 PM – 3:00 PM	Authors of Even Number Posters Present *Advanced chromatographic methods in environmental analysis* *Advances in analytical separations for MS* *Ambient ionization methods* *Biomolecular structure: covalent labeling and crosslinking* *Chemical proteomics* *Clinical proteomics* *Emerging and persistent environmental contaminants* *FAIMS/DMS and new developments in IMS instrumentation* *Gas phase ion chemistry and spectroscopy* *Gaseous biomolecules: conformations, energetics and reactions* *IMS developments in MS: computations, collision cross sections & complex mixtures* *Integrated omics* *Lipidomics* *Metabolomics* *Proteomics of PTMs* *Quantitative targeted proteomics* *Ultra high resolution mass spectrometry and petroleomics*	
3:00 PM – 5:30 PM	***Lipidomics II*** Chair: Jeff Smith & Markus Wenk	Room 201
3:00 PM	**Lipidomics in biomedical research: weighing the pros and cons of a targeted vs. untargeted mass-spectrometry-based approach for biomarker discovery** Christine Des Rosiers, Montreal Heart Institute	
3:30 PM	**SIMPLEX: a combinatorial multimolecular omics approach for systems biology** Dr. Robert Ahrends, ISAS	
4:00 PM	**Conformational atlas of lipid structure for directed characterization in lipidomics and molecular phenomics** Dr. John McLean, Vanderbilt University	
4:30 PM	**Discriminating isomeric (O-acyl)-hydroxy fatty acids (OAHFAs) by tandem mass spectrometry** Dr. David Marshall, Queensland University of Technology	
4:50 PM	**Investigating the lipidomic dynamics of torpor through examination of hibernating squirrel liver tissue and dehydrated frog leg tissue** Ms. Katrin Blank, Carleton University	
5:10 PM	**High-throughput measurement of lipid turnover rate in HeLa cell based on metabolic heavy water labeling** Ms. Byoungsook Goh, Gwangju Institute of Science and Technology	
3:00 PM – 5:30 PM	***Clinical proteomics*** Chair: Thomas Kislinger	Room 202
3:00 PM	**Decoding ligand receptor interactions** Dr. Bernd Wollscheid, ETH Zurich	

3:30 PM	**TBA** Hanno Steen, Boston Children's Hospital	
4:00 PM	**Identifying key stem cell-associated proteins in normal blood development and leukemia** Dr. Erwin Schoof, Princess Margaret Cancer Centre, University Health Network	
4:30 PM	**From systems biology towards a diagnostic tool for platelet function** Dr. Albert Sickmann, ISAS	
4:50 PM	**A novel mass spectrometry based assay for the diagnosis and typing of systemic amyloidosis** Dr. Paul Boersema, ETH Zurich	
5:10 PM	**Novel biomarkers for detecting recurrence of ovarian cancer by combining patient derived xenografts with N-glycosylation enrichment strategies** Mr. Ankit Sinha, Princess Margaret Cancer Centre	
3:00 PM – 5:30 PM	***Noncovalent interactions: proteins, nucleic acids, and small molecules I*** Chairs: John Klasen & Valerie Gabelica	Room 203
3:00 PM	**Native mass spectrometry of protein-protein and protein-drug complexes** Dr. Joseph Loo, University of California, Los Angeles	
3:30 PM	**Probing very high mass noncovalent assemblies with mass spectrometry** Dr. Renato Zenobi, ETH Zurich	
4:00 PM	**Understanding the stability of non-covalent complexes of macromolecules in charged droplets by molecular simulations** Dr. Styliani (Stella) Consta, Department of Chemistry	
4:30 PM	**The gas phase structures of self-assembled cyclotricatechylene cation-pi and anion-pi complexes** Dr. Nicole Rijs, Karlsruhe Institute of Technology	
4:50 PM	**A native MS study of RNA kissing complexes and their interaction with magnesium cations** Ms. Clémence RABIN, INSERM U1212 - ARNA Lab	
5:10 PM	**Mass spectrometry of non-covalent bound membrane proteins in nanodiscs with LILBID-MS** Mr. Oliver Peetz, Goethe-University of Frankfurt	
3:00 PM – 5:30 PM	***Novel applications in sampling real time sample analysis by MS I-direct analysis*** Chair: Chris Gill	Room 205
3:00 PM	**Microfabricated technologies for addressing molecular measurements: microchip CE-nESI and highly pressure mass spectrometry** Dr. J. Michael Ramsey, University of North Carolina at Chapel Hill	
3:30 PM	**Solid phase microextraction-transmission mode and direct analysis in real time: an efficient tool for fast analysis of contaminants in complex samples** Dr. Emanuela Gionfriddo, University Of Waterloo	
4:00 PM	**Using MS with molecular imprinting to develop new environmental monitoring tools** Dr. Stefana Egli, Memorial University of Newfoundland	
4:30 PM	**Direct SPME-ambient MS couplings: towards the non-chromatographic era** Mr. Mario Francesco Mirabelli, ETH Zurich	
4:50 PM	**Snap-shot monitoring of acoustically levitated containerless microreactions via ambient ionization mass spectrometry** Ms. Elizabeth Crawford, Universität des Saarlandes	
5:10 PM	**Photoionization-generated dibromomethane cation chemical ionization TOFMS for rapid and sensitive detection of volatile sulfur compounds** Dr. Jichun Jiang, Dalian Institute of Chemical Physics, Chinese Academy of Sciences	

3:00 PM – 5:30 PM	***IMS developments in mass spectrometry: computations, collision cross sections, and complex mixtures*** Chair: Brandon Ruotolo	Room 206 A-D
3:00 PM	**New ambient MS and ion mobility MS approaches for multidimensional complex mixture analysis** Dr. Facundo Fernandez, School of Chemistry and Biochemistry	
3:30 PM	**Recent developments in gas molecule scattering approaches for collision cross section/mobility calculations in polyatomic gases** Dr. Chris Hogan, University of Minnesota	
4:00 PM	**Applications of ion mobility separation with electron-based dissociation tandem mass spectrometry** Dr. Catherine Costello, Boston University School of Medicine	
4:30 PM	**Native mass spectrometry and in-source collision-induced unfolding on a commercial helium drift tube ion mobility spectrometer** Dr. Valérie Gabelica, Inserm, France	
4:50 PM	**Ion mobility mass spectrometry uncovers the conformational states of a supercomplex** Dr. Argyris Politis, King's College London	
5:10 PM	**Quantitative IM-MS for structural biology** Justin LP Benesch, University of Oxford	
5:45 PM – 7:00 PM	**Workshops**	
	You've got a start-up; what is your IP play? Torys, LLP	Room 201
	Trent Conference	Room 202
7:00 PM – 8:00 PM	**Dinner Break**	
8:00 PM – 11:00 PM	**Corporate Hospitality Suites**	700 Level, South Building MTCC

Wednesday, August 24, 2016

8:30 AM – 9:15 PM	***Plenary lecture - Curt Brunnée Award:*** Dr. Yury Tsybin, Spectroswiss	Hall A, Level 300
9:30 AM – 12:00 PM	Award lectures	Hall A, Level 300
9:45 AM	**Thomson Medal Award Presentations & Lecture:** Scott McLuckey, Purdue University	
10:30 AM	**Thomson Medal Award Presentations & Lecture:** Marcus Eberlin, University of Campinas	
11:15 AM	**Rapid Communication in Mass Spectrometry Beynon Award Presentation** (no lecture)	
11:30 AM	**CSMS Lossing Award Presentation & Lecture:** Mel Comisarow, University of British Columbia	
12:00 PM – 3:00 PM	Lunch Seminars, Poster Sessions	

1:00 PM – 3:00 PM	**Authors of Odd Number Posters Present** *AstroChemistry* *Atomic MS in environmental applications* *Biomolecular structure: H,D-exchange* *Challenges in biopharmaceutical analysis* *Environomics* *Glycomics* *Imaging - applications* *Imaging - instrumentation* *Innovations in mass spectrometry instrumentation* *Mass spectrometric insights into catalysis* *New trends in mass spectrometry and medicine* *Noncovalent interactions: proteins, nucleic acids, and small molecules* *Novel applications in sampling and real time sample analysis by mass spectrometry* *Novel high throughput techniques* *Phosphoproteomics* *Protein-protein complexes* *Quantitation and Structural elucidation of metabolites and covalent adducts* *Radical peptides* *Top-down proteomics*	
3:00 PM – 5:30 PM	***Metabolomics II*** Chairs: Matej Orešič & Guowang Xu	Room 201
3:00 PM	**Metabolomic Investigation of inflammatory bowel disease phenotypes using GC×GC-HRTOFMS** Dr. Jef Focant, University of Liege	
3:30 PM	**Mass spectrometric analyses in the identification of blood-based biomarkers of traumatic brain injury** Dr. Tuulia Hyötyläinen, University of Örebro	
4:00 PM	**Inter-comparison of modern methods for isotopologue ratio analysis in metabolomics: trueness and uncertainty** Dr. Stephan Hann, University of Natural Resources and Life Sciences - BOKU Vienna	
4:30 PM	**Characterization of the muscle metabolome: does oral bicarbonate function as an ergogenic aide in strenuous interval exercise?** Mr. Philip Britz-McKibbin, McMaster University	
4:50 PM	**A metabolomics approach for the authentication of herbal supplements using UPLC/QTof-MS** Dr. Jimmy Yuk, Waters Corporation	
5:10 PM	**Metabolomic analysis of mouse embryonic fibroblast cells in response to acute starvation with and without Atg7** Dr. Yu Bai, Peking University	
3:00 PM – 5:30 PM	***Phosphoroproteomics*** Chair: Anne-Claude Gingras & Yasushi Ishihama	Room 202
3:00 PM	**Phosphotyrosine interaction proteomics decodes signaling network architecture by functional annotation of *in-vivo* phosphorylation sites** Dr. Jesper Olsen, University of Copenhagen	
3:30 PM	**TBA** Dr. Pedro Beltrao, EMBL-EBI	
4:00 PM	**An expanded toolkit to interrogate the human phosphoproteome** Dr. Judit Villen, University of Washington	
4:30 PM	**Advanced (phospho)proteomics to uncover dynamics and pathway dependence in melanoma drug resistance uncovers novel companion targets** Dr. Maarten Altelaar, Utrecht University	
4:50 PM	**Deconvolution of drug-specific phenotypes associated with nutrient transport using dynamic phosphoproteomics** Dr. Pierre Thibault, Universite de Montreal/IRIC	
5:10 PM	**TBA** Dr. Michael Moran, University of Toronto	

3:00 PM – 5:30 PM	***Biomolecular structure: H,D-exchange*** Chairs: Lars Konnerman & Eric Forest	Room 203
3:00 PM	**Differential HDX to probe ligand mediated receptor signaling** Dr. Patrick Griffin, The Scripps Research Institute	
3:30 PM	**Chaperonin-assisted protein folding** Dr. John R. Engen, Northeastern University	
4:00 PM	**Probing the conformation and ligand binding of neurotransmitter symporter (NSS) proteins by HDX-MS** Dr. Kasper Rand, University of Copenhagen	
4:30 PM	**Time-resolved hydrogen deuterium exchange (HDX) reveals the structural basis of amyloidogenesis inhibition by Alzheimer's drug candidates** Mr. Shaolong Zhu, MS-ESE York University - NSERC CREATE	
4:50 PM	**HDX-MS studies of human SIRT1 activation by STACs** Dr. Han Dai, GlaxoSmithKline	
5:10 PM	**Innovator and biosimilar infliximab: comparability assessment of the host cell proteins and protein higher order structure** Dr. Henry Shion, Waters Corporation	
3:00 PM – 5:30 PM	***Environomics*** Chair: Eric Reiner	Room 205
3:00 PM	***In vivo* metabolomic approach to study developmental neurotoxicity of pesticides: explaining cognitive and motor function effects with metabolomics** Dr. Pim Leonards, VU University	
3:30 PM	**The use of plasma and integrated OMICs approaches for environmental toxicology** Dr. Denina Simmons, University of Waterloo	
4:00 PM	**Environmental metabolomics in marine ecosystems: impact of viral lysis and predation on marine organic matter** Dr. Krista Longnecker, Woods Hole Oceanographic Institution	
4:30 PM	**Measurements of biomarkers of oxidative DNA damage in zebra mussels by GC-MS/MS to evaluate the impact of environmental contaminants on aquatic life** Dr. Pawel Jaruga, National Institute of Standards and Technology	
4:50 PM	**Comprehensive chemistry and mutagenicity of disinfection by-products in swimming pools and spas** Dr. Susan Richardson, University of South Carolina	
5:10 PM	**Development of a highly-sensitive multi-mycotoxin LC-MS method in human plasma for exposure studies** Dr. Dajana Vuckovic, Concordia University	
3:00 PM – 5:30 PM	***Quantitation & structural elucidation of metabolites & covalent adducts*** Chair: Lekha Sleno	Room 206 A-D
3:00 PM	**Use of mass spectrometry to study drug covalent binding and idiosyncratic drug reactions** Dr. Jack Uetrecht, University of Toronto	
3:30 PM	**Sensitive quantification of drug metabolites with and without authentic standards** Dr. Filip Cuyckens, Janssen Pharmaceutical Companies	
4:00 PM	**Structural mass spectrometry for molecular phenomics in systems, synthetic, and chemical biology** Dr. John McLean, Vanderbilt University	
4:30 PM	**Investigation of triapine metabolism by application of electrochemistry and liquid chromatography coupled to mass spectrometry (EC/LC/ESI-MS)** Ms. Karla Pelivan, Institute of Inorganic Chemistry, University of Vienna	
4:50 PM	**ESI-MS/MS study of drug-conjugated dendrimers** Dr. Aura Tintaru, Aix-Marseille Université, CNRS, Institut de Chimie Radicalaire-UMR7273	
5:10 PM	**A novel approach for identification of biologically active phenolic compounds in hops matrices using hybrid quadrupole-orbitrap mass spectrometer** Dr. Martin Dusek, Research Institute of Brewing and Malting	

3:00 PM – 5:30 PM	***JMS Student Awards***	Room 206 E-F
3:00 PM	**Observing proton transfer reactions inside the MALDI plume: experimental and theoretical insight into MALDI gas-phase processes** Mario Francesco Mirabelli, ETH Zurich	
3:30 PM	**Fast quantitation of target analytes in complex matrices by solid phase microextraction-mass spectrometry (SPME-MS): recent developments and applications** German Augusto Gómez-Ríos	
4:00 PM	**Collision cross section prediction of deprotonated phenolics in a travelling-wave ion mobility spectrometer using molecular descriptors and chemometrics** Gerard Bryan Gonzales, Ghent University	
4:30 PM	**New strategy for analysis of the splicing regulatory factors using high-resolution mass spectrometry** Toru Takarada	
5:00 PM	**EASI-MSI can be used in clinical analysis without loss chemical information?** Pedro H. Vendramini, University of Campinas	
5:45 PM – 7:00 PM	**Workshops**	
	Careers in Mass Spectrometry	Room 201
	Trent Conference	Room 202
7:00 PM – 8:00 PM	**Dinner Break**	
8:00 PM – 11:00 PM	**Corporate Hospitality Suites**	700 Level, South Building MTCC

Thursday, August 25, 2016

8:30 AM – 9:15 PM	***Plenary lecture –*** **The composition of comet 67P/Churyumov-Gerasimenko revealed by the mass spectrometers of the Rosetta mission** Hervé Cottin, Université Paris-Est Cretail (Rosetta Mission)	Hall A, Level 300
9:30 AM – 12:00 PM	***Top-down proteomics*** Chair: Neil Kelleher	Room 201
9:30 AM	**High throughput top down proteomics utilizing ultra violet photo dissociation** Dr. Philip Compton, Northwestern University	
10:00 AM	**Top-down mass spectrometry of proteins and protein complexes as a tool for structural biology** Dr. Joseph Loo, University of California, Los Angeles	
10:30 AM	**21 Tesla Fourier transform ion cyclotron resonance mass spectrometer for top-down proteomics** Dr. Christopher Hendrickson, National High Magnetic Field Laboratory	
11:00 AM	**An optimized high-throughput top-down proteomics platform for improving diagnostics in clinical microbiology** Dr. Mathieu Dupré, Institut Pasteur	
11:20 AM	**Top-down sequencing by electron photodetachment dissociation (EPD) to locate ligand and cation binding sites on G-quadruplexes** Dr. Frederic Rosu, Univ. Bordeaux, CNRS ums3033	
11:40 AM	**A quantum chemical tool for the prediction of mass spectra and the identification of fragmentation pathways: inter-side-chain interactions in peptides** Dr. Frank Blockhuys, University of Antwerp	
9:30 AM – 12:00 PM	***Challenges in biopharmaceutical analysis*** Chair: Kevin Bateman	Room 202
9:30 AM	**State-of-the art orthogonal chromatographic, electrophoretic and MS methods for mAbs and ADCs structural assessment at multiple levels** Dr. Alain Beck, Centre d’Immunologie Pierre Fabre (CIPF)	

10:00 AM	**LC/MS-based approaches to therapeutic protein quantitation to support discovery stage pharmacokinetic studies** Dr. Daniel Spellman, Merck Research Laboratories	
10:30 AM	**Rapid characterization of biotherapeutic proteins by size-exclusion chromatography coupled to native mass spectrometry** Mr. Markus Haberger, Roche Diagnostics GmbH	
11:00 AM	**Investigating the differential photosensitivity of tryptophan in a model trp-cage peptide** Ms. Leslie Welch, Genentech a Member of the Roche Group	
11:20 AM	**Towards an automated approach to characterizing the metabolism of biotherapeutic drugs** Dr. Jayne Kirk, Waters	
11:40 AM	**Analytical approaches for quantification of surrogate mAbs in rodent biological matrices using LC-MS** Dr. John Mehl, Bristol-Myers Squibb	
9:30 AM – 12:00 PM	***AstroChemistry*** Chairs: Paul Mayer & Christine Joblin	Room 203
9:30 AM	**Characterization of PAH content and distribution in cosmic dust analogues** Dr. Hassan Sabbah, University Paul Sabatier - IRAP/CNRS	
10:00 AM	**Mass spectrometry in space: highlights of the Rosetta mission** Dr. Andre Bieler, University of Bern	
10:30 AM	**Experimental and theoretical studies of ionic reactions of astrochemical relevance** Dr. Zhechen Wang, University of Colorado at Boulder	
11:00 AM	**H/H_2 loss of dibenzopyrene isomer cations: combining linear ion trap measurements and density functional theory calculations** Mrs Sarah Rodriguez, Institut de Recherche en Astrophysique et Planétologie (IRAP)	
11:20 AM	**Probing surface-induced dissociation of exospheric neutrals using an ultra-fast rotor reactor and GC-MS analysis** Dr. Daniel Austin, Brigham Young University	
11:40 AM	**Reaction dynamics of ionized PAHs** Dr. Paul M Mayer, University of Ottawa	
9:30 AM – 12:00 PM	***Novel applications in sampling & real time sample analysis by MS II-Continuous on-line monitoring*** Chair: Erik Krogh	Room 205
9:30 AM	**Real-time analysis with a transportable high-resolution PTR-FTICR-MS** Dr. Essyllt Louarn, Paris Sud University	
10:00 AM	**Rapid evaporative ionization mass spectrometry – the ultimate tool for real-time analysis?** Dr. Zsolt Bodai, Imperial College London	
10:30 AM	**New mass spectrometric tools to study the flavor formation during the roasting process of coffee beans and nuts in real time** Dr. Ralf Zimmermann, University Rostock and Helmholtz Zentrum München	
11:00 AM	**Kinetic analysis of chemical reactions using electrospray ionization mass spectrometry** Dr. Scott McIndoe, University of Victoria	
11:20 AM	**Multi-sample monitoring on the Mini 12 mass spectrometer** Mr. Christopher Pulliam, Purdue University	
11:40 AM	**Condensed phase membrane introduction mass spectrometry (CP-MIMS): direct, online, measurements of non-volatile analytes in complex aqueous samples** Dr. Chris Gill, Applied Environmental Research Laboratories - Vancouver Island University	
9:30 AM – 12:00 PM	***Imaging – instrumentation*** Chair: Damian Ifa	Room 206A-D
9:30 AM	**Laser ablation atmospheric pressure photoionization mass spectrometry imaging. Instrumentation and applications** Dr. Tiina Kauppila, University of Helsinki	

10:00 AM	**An ion funnel based MALDI-MSI interface for Orbitrap mass spectrometers** Dr. Shane Ellis, M4I Institute	
10:30 AM	**Infrared laser ablation microdissection for imaging mass spectrometry** Dr. Kermit Murray, Louisiana State University	
11:00 AM	**Improvements in AP-SMALDI Orbitrap mass spectrometry imaging of biological tissue** Dr. Bernhard Spengler, Justus Liebig University Giessen	
11:20 AM	**Molecular imaging of tissue sections by matrix-free nanophotonic laser desorption ionization mass spectrometry with ion mobility separation** Dr. Bindesh Shrestha, Waters Corp	
11:40 AM	**Liquid extraction surface analysis (LESA) combined with nano-liquid chromatography (nLC) for analyte determination from biological surfaces** Dr. Daniel Eikel, Advion Inc.	
12:00 PM – 3:00 PM	Lunch Seminars, Poster Sessions	
1:00 PM – 3:00 PM	**Authors of Even Number Posters Present** *AstroChemistry* *Atomic MS in environmental applications* *Biomolecular structure: H,D-exchange* *Challenges in biopharmaceutical analysis* *Environomics* *Glycomics* *Imaging - applications* *Imaging - instrumentation* *Innovations in mass spectrometry instrumentation* *Mass spectrometric insights into catalysis* *New trends in mass spectrometry and medicine* *Noncovalent interactions: proteins, nucleic acids, and small molecules* *Novel applications in sampling and real time sample analysis by mass spectrometry* *Novel High throughput techniques* *Phosphoproteomics* *Protein-protein complexes* *Quantitation and structural elucidation of metabolites and covalent adducts* *Radical peptides* *Top-down proteomics*	
3:00 PM – 5:30 PM	***Glycomics*** Chair: Pauline Rudd	Room 201
3:00 PM	**New MS tools for the discovery and characterization of protein-glycan interactions** Dr. John Klassen, University of Alberta	
3:30 PM	**Glycomics in a wind tunnel - ion mobility-mass spectrometry of isomeric glycans and glycopeptides** Dr. Kevin Pagel, Freie Universitaet Berlin	
4:00 PM	**Glycomics, proteomics and glycoproteomics of glioblastoma** Dr. Joseph Zaia, Boston University School of Medicine	
4:30 PM	**Synthetic glycopeptides are unique tools for functional glycoproteomics** Mr. Kathirvel Alagesan, Max Planck Institute of Colloids and Interfaces	
4:50 PM	**Development of N-and O- glycan workflows utilising a novel UPLC-mass detection system for biotherapeutic drug products.** Dr. Mark Hilliard, NIBRT	
5:10 PM	**One sample, one pot and the whole glycome: towards a system to study disorders of protein glycosylation** Ms. Kirsty Skeene, University of York, UK	

Thursday

3:00 PM – 5:30 PM	***Novel high throughput techniques*** Chair: John Janiszewski	Room 202
3:00 PM	**Combining rapid isomer separations and physicochemical property measurements with differential mobility spectrometry** Dr. Scott Hopkins, University of Waterloo	
3:30 PM	**Direct liquid extraction approaches to sample analysis** Dr. Gary Van Berkel, Oak Ridge National Laboratory	
4:00 PM	**The perils, principles, and practice of high-throughput mitochondrial metabolic flux measurements** Dr. Richard Kibbey, Yale University School of Medicine	
4:30 PM	**A novel high-throughput lipidomics platform and its applications to study drug polypharmacology** Dr. Jiejun Wu, Janssen R&D US LLC	
4:50 PM	**Bidimensional FT-ICR MS: unravelling structural information from a complex sample without separation** Dr. Christian Rolando, Université Lille 1, Sciences et Technologie	
5:10 PM	**Picodroplet mass spectrometry for miniaturized high throughput analysis of synthetic biology microbial clones** Dr. Xin Li, Sphere Fluidics Limited	
3:00 PM – 5:30 PM	***Noncovalent interactions: proteins, nucleic acids, and small molecules II*** Chairs: John Klassen & Valerie Gabelica	Room 203
3:00 PM	**Behavior of intrinsically disordered regions in protein complexes** Dr. Satoko Akashi, Yokohama City University	
3:30 PM	**Simultaneous analysis of enzyme structure and activity by kinetic capillary electrophoresis and mass spectrometry** Dr. Maxim Berezovski, University of Ottawa	
4:00 PM	**Construction of accurate supramolecular DNA structures based on mass spectrometric analysis** Dr. Xinhua Guo, College of chemistry, Jilin University	
4:30 PM	**Native state mass spectrometry in natural product and fragment-based drug discovery against malaria protein targets** Ms. Liliana Pedro, Eskitis Institute for Drug Discovery, Griffith University	
4:50 PM	**Structure and dynamics of RNA binding to the non-canonical RNA recognition motif (RRM2) in the human La protein** Ms. Kerene Brown, NSERC CREATE York University and University of Toronto	
5:10 PM	**Exploring the dynamics and function of the flexible domain of Human Histone Deacetylase 2 using mass spectrometry** Ms. Zoja Nagurnaja, University College London	
3:00 PM – 5:30 PM	***Radical peptides*** Chairs: K.W. Michael Siu & Ivan K. Chu	Room 205
3:00 PM	**Ground and excited-state dissociations of biomolecular cation-radicals** Dr. Frantisek Turecek, University of Washington	
3:30 PM	**Photo-electron transfer dissociation of peptides for zwitterion identification** Dr. Ryan Julian, UC Riverside	
4:00 PM	**Structure and reactivity of metal ion adducts of cysteine-containing peptide radicals** Dr. Victor Ryzhov, Northern Illinois University	
4:30 PM	**Reactions of hydroxyl radical and cysteine disulfide derivatives reveal mechanistic detail in radical induced disulfide cleavage** Dr. Yu Xia, Purdue University	
4:50 PM	**TEMPO-assisted free radical initiated peptide sequencing (FRIPS) mass spectrometry** Dr. Han-bin Oh, Sogang University	
5:10 PM	**Radical-mediated peptide tyrosine nitration** Dr. Ivan CHU, University of Hong Kong	

3:00 PM – 5:30 PM	***Imaging – applications*** Chair: Pierre Chaurand & Peter Hoffmann	Room 206 A-D
3:00 PM	**High resolution mapping of N-glycans in FFPE prostate cancer tissues using MALDI-FTICR and rapid MALDI-TOF mass spectrometry imaging** Dr. Richard Drake, Medical University of South Carolina	
3:30 PM	**Bringing mass spectrometry imaging from pathologist bench to patient bedside: from diagnosis to guided surgery** Dr. Isabelle Fournier, University of Lille - France	
4:00 PM	**Mass spectrometry imaging of proteins, lipids and metals in human and mouse chronic traumatic encephalopathy tissues** Dr. Catherine Costello, Boston University School of Medicine	
4:30 PM	**Laser mass spectrometry imaging of cuticular lipids from insects using etched silver substrates** Mr. Andreas Schnapp, University of Münster	
4:50 PM	**Lipid profiling using integrative mass spectrometry imaging (MSI) for nonalcoholic fatty liver disease (NAFLD) in human liver biopsies** Ms. Klara Scupakova, M4I Institute, University of Maastricht	
5:10 PM	**Drug delivery quantitation in single cells with sub micrometric spatial resolution TOF-SIMS** Mr. Anthony Castellanos, Florida International University	
7:30 PM to 11:30 PM	**Banquet** Constitution Hall, Metro Toronto Convention Centre, North Building	Room 105-106 Level 100
Friday, August 26, 2016		
8:30 AM – 9:15 PM	***Plenary lecture -*** **Single cell analysis with electrospray mass spectrometry** Xinrong Zhang, Tsinghua University	Hall A, Level 300
9:30 AM – 12:00 PM	***Mass spectrometric insights into catalysis*** Chairs: Scott McIndoe & Maria Schlengen	Room 201
9:30 AM	**Structure and reactivity of phenyl-hydroxycarbene studied in the gas phase: hydrogen tunneling at room temperature** Dr. Mathias Schäfer, University Cologne, Department of Chemistry	
10:00 AM	**Listening in on reaction intermediates in solution** Dr. Jana Roithova, Charles University in Prague	
10:30 AM	**Threshold CID measurements probe organic and organometallic reaction mechanisms** Dr. Peter Chen, ETH Zürich	
11:00 AM	**A New approach for revealing superatomic cores in transition metal complexes by ESI-MS/MS** Mr. Dmitry Eremin, Zelinsky Institute of Organic Chemistry	
11:20 AM	**Investigating the peroxidase reaction mechanism of human cytochrome c (cyt c)** Ms. Rinky Parakra, University of Otago	
11:40 AM	**Catalytic reaction mechanism elucidation via real time mass spectrometric analysis** Dr. Scott McIndoe, University of Victoria	
9:30 AM – 12:00 PM	***New trends in mass spectrometry and medicine*** Chair: Natalie Agar	Room 202
9:30 AM	**Illuminating the chemistry of human skin surface** Amina Bouslimani	
10:00 AM	**Mass spectrometry in systems medicine: towards the molecular operating theatre** Dr. Ron Heeren, M4I, Maastricht University	
10:30 AM	**Gas chromatography-differential mobility spectrometry for bedside diagnosis and surveillance of fungal pneumonia** Sophia Koo, Harvard University	
11:00 AM	**Mass spectrometric profiling of biomarkers in exhaled breath for medical diagnosis and personalized medicine** Dr. Renato Zenobi, ETH Zurich	

Friday

11:20 AM	**Direct detection of endogenous microRNAs and their post-transcriptional modifications in cancer serum by capillary electrophoresis-mass spectrometry** Dr. Maxim Berezovski, University of Ottawa	
11:40 AM	**High throughput quantification of Tenofovir and Emtricitabine in human plasma using LDTD-MS/MS** Mr. Jean Lacoursiere, Phytronix Technologies Inc.	
9:30 AM – 12:00 PM	***Protein-protein complexes*** Chair: Albert Heck	Room 203
9:30 AM	**Charge detection mass spectrometry: instrumentation and application to virus structure and assembly** Dr. Martin Jarrold, Indiana University	
10:00 AM	**Biophysics of clathrin adaptors and new opportunities for native MS in single particle imaging at XFELs** Dr. Charlotte Uetrecht, Heinrich Pette Institute/ European XFEL	
10:30 AM	**Chemical modification as a path to improved sequencing and structural analysis of proteins and protein complexes** Mr. Daniel Polasky, University of Michigan - Ann Arbor	
11:00 AM	**Uncovering the complexity of protein complexes: A modified Q Exactive Plus Orbitrap instrument for multi-level analysis of protein complexes** Dr. Michal Sharon, Weizmann Institute of Science	
11:20 AM	**A platform to discovery protein complexes in biology samples** Mr. Zhongming Hu, NSERC CREATE, York University, University of Toronto	
11:40 AM	**Molecular simulation study of the dissociation rate and mechanisms of protein complexes in droplets** Dr. Styliani (Stella) Consta, Department of Chemistry	
9:30 AM – 12:00 PM	***Atomic MS in environmental applications*** Chair: Jack Cornett	Room 205
9:30 AM	**Complementary mass spectrometry and chromatography techniques enabling the characterization of arsenic metabolites in chicken meat and liver** Dr. X. Chris Le, University of Alberta	
10:00 AM	**Novel method for determination of ^{90}Sr using thermal ionization mass spectrometry** Dr. Sarata Sahoo, National Institute of Radiological Sciences	
10:30 AM	**Determination of Cd and Te in metal materials and geochemical samples by dynamic reaction cell-inductively coupled plasma mass spectrometry** Dr. Jingyu Hu, NCS Testing Technology Co., Ltd.	
11:00 AM	**Laser-assisted sample introduction for nanoparticle characterization using ICP MS** Dr. Jan Preisler, Masaryk University	
11:20 AM	**Isotopic signature of selected rare earth elements for nuclear activities profiling using cloud point extraction and ICP-MS/MS** Dr. Dominic Lariviere, Laval University	
11:40 AM	**Proper quantification of scandium by ICP-MS/MS: the challenge** Ms. Laurence Whitty-Léveillé, Université Laval	
9:30 AM – 12:00 PM	***Innovations in mass spectrometry instrumentation*** Chair: Scott Tanner	Room 206A-D
9:30 AM	**Ion boosters, superchargers, chemical modifiers – ion chemistry at work. But how?** Prof. Dr. Thorsten Benter, University of Wupperta	
10:00 AM	**High spatial resolution laser ablation sampling/ionization under ambient conditions using a hybrid laser microdissection/liquid vortex capture/mass sp** Dr. Gary Van Berkel, Oak Ridge National Laboratory	
10:30 AM	**Obtaining complete structural identification of lipids by using low-energy electrons in a novel branched radio-frequency ion trap** Dr. Takashi Baba, Sciex	

11:00 AM	**Matrix-assisted laser desorption ionization distance-of-flight mass spectrometry** Dr. Steven Ray, State University of New York at Buffalo	
11:20 AM	**Echo-MS: a versatile platform for ultrafast mass spectrometry analysis in drug discovery** Dr. Martin Bachman, AstraZeneca	
11:40 AM	**Direct enantiomer selective mass spectrometry of multi-component chiral mixtures by MS-PECD** Dr. Maurice Janssen, MassSpecpecD BV	
12:00 PM – 12:15 PM	**Closing ceremony and presentation by IMSC 2018**	Hall A, Level 300
12:15 PM – 1:00 PM	**Farewell reception**	Exhibits Hall B, Level 300

Posters

Advanced chromatographic methods in environmental analysis

M-T-001

Ozone-induced DNA damage: a pandora box of oxidatively modified DNA bases

Dr. Guru Swamy Madugundu, PERFORM Centre, Concordia University

M-T-002

Chemical speciation of secondary organic aerosol using electrospray ionization-ion mobility time of flight mass spectrometer

Mr. Jianhuai (Jackie) Ye, University of Toronto

M-T-003

Sequential ultrasonic extraction of a Chinese coal and characterization of nitrogen-containing compounds in the extracts using HPLC/ESI-TOF-MS

Dr. Xing Fan, China University of Mining and Technology

M-T-004

Screening for dioxin-like compounds in sediment using modified QuEChERS and a GC-qTOF mass spectrometer with atmospheric pressure chemical ionization

Mr. Liad Haimovici, Ontario Ministry of the Environment

M-T-005

Phytosterols and phytoestrogens of red propolis determined by GC-MS

Ms. Begoña Gimenez-Cassina Lopez, UNICAMP

M-T-006

An accurate analysis of the internal concentration of pesticide in whole larvae tissue of Japanese medaka using LC-QqQ-MS without clean-up step

Mr. Hattan Alharbi, Toxicology Graduate Program at University of Saskatchewan

Advances in analytical separations for MS

M-T-007

Kinetic study of azobenzene E/Z isomerization using ion mobility-mass spectrometry

Dr. Salomé Poyer, University of Evry - LAMBE

M-T-008

Using differential mobility spectrometry to study chiral compounds

Dr. J. Larry Campbell, SCIEX

M-T-009

Utilising unusual ionisation and SFC to solve a taxing problem

Dr. John Langley, University of Southampton

M-T-010

High throughput non-depletive SPME method for LC-MS/MS determination of free and total concentrations of multi-residue in small sample volumes

Dr. Ezel Boyaci, University of Waterloo

M-T-011

Metabolic distributions of vitamin D metabolites in dried blood spots after chemical derivatization and LC-MS/MS

Ms. Miriam Mueller, Institute of Bioanalytical Chemistry

M-T-012

Can ASAP Provide a quantitative screen for rapid detection of drugs in saliva?

Ms. Julie Herniman, University of Southampton

M-T-013

Ionisation enhancement through use of a supercritical fluid and a novel ionisation technique

Dr. John Langley, University of Southampton

M-T-014

Digital microfluidic immunoprecipitation for the microscale targeted analysis of proteins from biological samples using mass spectrometry

Mr. Brendon Seale, NSERC CREATE York University and University of Toronto

M-T-015

Multimode gradient HPLC-MS method for metabolomics and environmental monitoring

Dr. Marc Suter, Eawag

M-T-016

An automated method for microcystins analysis using two-dimensional liquid chromatography-quadrupole time-of-flight mass spectrometry (2DLC-QTOFMS).

Dr. Xavier Ortiz, Ontario Ministry of the Environment and Climate Change

M-T-017

CE-nanoESI-MS for Untargeted proteomic characterization of small neuron populations

Mr. Sam Choi, George Washington University

M-T-018

Optimal selection of separation chemistry for 3D-LC-MS/MS in bottom-up proteomics

Dr. Oleg Krokhin, University of Manitoba

M-T-019

Expanded analytical capability through the application of open access UHPSFC-APPI-MS

Ms. Julie Herniman, University of Southampton

M-T-020

Solid-phase microextraction low temperature plasma mass spectrometry for the direct and rapid analysis of complex mixtures

Mr. Morphy Dumlao, School of Chemistry, University of New South Wales

M-T-021

Ultra-fast analysis of allergens using capillary electrophoresis coupled to mass spectrometry and ultraviolet photodissociation

Mr. Ken Miller, Thermo Fisher Scientific

M-T-022

Cellular metabolomic analysis using photo-controlled probes coupled with ambient mass spectrometry

Dr. Lin Wang, Beijing University of Technology

M-T-023

Rapid LC method development for multiple drug classes by using a new four-channel LC

Dr. Pengxiang Yang, Thermo Scientific

M-T-024

The detection of allergens in foods using 2D-LC-MS/MS

Dr. Sophie Thurlow, LGC

M-T-025

Effect of mobile phase pH: implications for the LC-MS/MS bioanalysis of vitamin D –sulfate compounds

Ms. Nur Sofiah Abu Kassim, The University of Queensland

M-T-026

Identification of Dechloranes by gas chromatography coupled to tandem mass spectrometry with atmospheric pressure chemical ionization (GC-APCI-MS/MS)

Dr. Ronan Cariou, LABERCA-Oniris, France

M-T-027

Determination of phthalates in baby food by gas chromatography–mass spectrometry

Ms. Adriana Godoy, University of Campinas

M-T-028

A multi-class drug and metabolite screen of 231 analytes by LC-MS/MS

Mr. Justin Steimling, Restek Corporation

M-T-029

Harnessing the efficiency of N_2 as GC carrier gas with an atmospheric pressure MS source

Mr. Adam Ladak, Waters

M-T-030

Comprehensive profiling of various platycosides in Platycodi radix by UPLC-QTOF/MS

Dr. DaeYoung Lee, Department of Herbal Crop Research, National Institute of Horticultural and Herbal Science, Rural Development Administration

M-T-031

A Novel nanoLC-MRM workflow for analyzing deoxycholic acid (DOC)-solubilized protein digests from biological samples

Mr. Luc Tessier, National Research Council

M-T-032

Automated protein digestion on a RTC-PAL system directly coupled to nano-LC-MS^2

Dr. Andrea Vojs Stanova, University of Bern

M-T-033

High-performance separation techniques in combination with high-resolution mass spectrometry in the study of MHGF-68

Dr. Magdalena Zimnicka, Comenius University in Bratislava, Faculty of Natural Sciences, Department of Analytical Chemistry

M-T-034

Diversity of peptide diastereoisomers examined by ion mobility mass spectrometry (IM-MS)

Dr. Magdalena Zimnicka, Institute of Organic Chemistry Polish Academy ofSciences

M-T-035

Detection and semi-quantitative determination of designer benzodiazepines in serum using LC-MS^n

Mrs Laura Maria Huppertz, Institute of Forensic Medicine, Medical Center – University of Freiburg, Faculty of Medicine, University of Freiburg, Germany

M-T-036

Quantitation of Synthetic cannabinoids in serum: a comprehensive and sensitive multiplex assay for 99 compounds by LC-MS/MS

Dr. Andrea Kiehne, Bruker Daltonik GmbH

M-T-037

Comprehensive two-dimensional gas chromatography (GC×GC) with simultaneous TOFMS and flame ionization detector analysis of petroleum products

Mr. Joe Binkley, LECO Corporation

M-T-038

Determination of the antibiotic residues in meat by optimized liquid chromatography tandem mass spectrometry

Ms. Hye Young Park, Ministry of food and drug safety

M-T-039

Improving the sensitivity for an immunocapture LC-MS assay of Infliximab in rat plasma using trap-and-elute MicroLC-MS

Dr. Johnny Cardenas, SCIEX

M-T-040

A sensitive two dimensional LC-MS approach for the characterization of free drug impurities in antibody-drug conjugates

Dr. Alexander Muck, Waters Corp.

M-T-041

Comparison of two protein precipitation methods for vitamin D LC/MS assay of human serum

Ms. Nur Sofiah Abu Kassim, The University of Queensland

Ambient ionization methods

M-T-042

ASAP and DART mass spectrometry analysis for the understanding of polymers degradation mechanisms

Diane Lebeau, Den-Service d'Etude du Comportement des Radionucléides (SECR), CEA, Université Paris-Saclay, F-91191, Gif-sur-Yvette, France

M-T-043

Application of ambient mass spectrometry to high-throughput detection of drugs binding to proteins

Dr. Jin Ouyang, College of Chemistry, Beijing Normal University

M-T-044

Imaging volatile and semi-volatile compounds by low-temperature plasma MS

Dr. Robert Winkler, CINVESTAV Unidad Irapuato

M-T-045

An ambient ionization toolbox: comparison of helium and argon DART with complementary ambient ionization methods

Dr. Robert (Chip) Cody, JEOL USA, Inc.

M-T-046

The assessment of volatile organic compounds in foods using APCI-MS and chemometric methods

Dr. Mathew Turner, Centre for Analytical Science, Loughborough University

M-T-047

Characterization of the oxidation products of Shengli lignite using mass spectrometers with "hard", "soft" and ambient ion sources

Dr. Xing Fan, China University of Mining and Technology

M-T-048

Integrating digital microfluidic sample preparation with desorption atmospheric pressure photoionization-mass spectrometry

Mr. Gowtham Sathyanarayanan, University of Helsinki

M-T-049

Development of a flowing atmospheric pressure afterglow (FAPA) ionisation source to extend the capability of ion trap and Orbitrap mass spectrometry

Dr. Christopher Williams, EPSRC NMSF

M-T-050

Negative ion generation in the FAPA source: formation processes and auxiliary gas addition effect

Dr. Jaime Orejas, University at Buffalo

M-T-051

DESI-HRMS leaf analysis for classification and characterization of mycorrhizal rosemary plants

Ms. Raquel Seró Llor, University of Barcelona

M-T-052

Identification of organotin compounds in a molluscicide product by DESI-HRMS

Ms. Raquel Seró Llor, University of Barcelona

M-T-053

pH effects on electrospray ionization efficiency

Mr. Jaanus Liigand, University of Tartu

M-T-054

Rapid determination of pharmacokinetic profiles of caffeine and its metabolites collected on skin by ambient mass spectrometry

Dr. Jentaie Shiea, National Sun Yat-Sen University , Taiwan

Biomolecular structure: covalent labeling and crosslinking

M-T-055

A single approach to quantify protein-protein, protein-RNA interactions and posttranslational modifications

Dr. Florian Richter, Goethe University, Medical School

M-T-056

MALDI mass spectrometry and HCCA labeling as a powerful tool for peptide quantitation in biology

Mr. Maxime ROSSATO, University of Montpellier

M-T-057

Multidimensional mass spectrometry of peptides and proteins conjugated with poly(ethylene glycol)

Dr. Chrys Wesdemiotis, The University of Akron

M-T-058

Biochemistry of redox regulation of apoptosis signal-regulating kinase 1: identification and isolation of disulfide-linked intermediates

Mr. Johannes Weijman, Department of Biochemistry, University of Otago, NZ

M-T-059

Optimization of crosslinked peptide analysis on an Orbitrap Fusion Lumos mass spectrometer

Mr. Julian Saba, Thermo Fisher Scientific

M-T-060

Formaldehyde versus established cross-linkers in examining a transient protein complex using mass spectrometry

Dr. Juergen Kast, University of British Columbia

Chemical proteomics

M-T-061

Venom composition's study from genus Lonomia caterpillars, using SDS-PAGE and HPLC-MS/MS

Mr. Danny Alejandro Díaz Moscoso, Los Andes University

M-T-062

Proteomic analyses of Nm23-H1/NDPKA activator induced cellular responses in triple negative breast cancer cells

Dr. Jae-Jin Lee, EWHA woman's univ

M-T-063

Characterization of formaldehyde-induced modifications in diphtheria toxoid

Mr. Joost Uittenbogaard, Intravacc

Clinical proteomics

M-T-064

Quantifying signalling pathway activity from tissue lysates using immuno-MALDI

Mr. Robert Popp, University of Victoria - Genome BC Proteomics Centre

M-T-065

Alternative proteins : the hidden world of potential biomarkers

Dr. Julien Franck, University of Lille

M-T-066

Performance and Bioanalytical applicability of MALDI-compatible protein chips prepared by ambient ion soft landing

Dr. Petr Novak, Institute of Microbiology

M-T-067

Functionalized surfaces for direct immuno-affinity mass spectrometry - detection of haptoglobin phenotypes

Dr. Petr Pompach, Institute of Biotechnology

M-T-068

Towards a new diagnostic tool for human urinary tract infection using LCMS data independent acquisition (DIA) analysis and specific spectral libraries

Mrs Florence Roux-Dalvai, CHU Quebec Research Center

M-T-069

Novel automated quantitative microproteomics approaches for analyzing minute sample amounts in tumour heterogeneity

Dr. Erik de Graaf, Fondazione Pisana per la Scienza

M-T-070

Droplet-based liquid extraction for spatially-resolved microproteomics analysis from tissue sections

Mr. Maxence Wisztorski, Univ. Lille, INSERM U1192, PRISM

M-T-071

Novel therapeutic targets of spinal cord injury based on spatio-temporal proteomics analysis

Dr. Michel Salzet, University of Lille - France

M-T-072

The discovery of HDL-associated protein biomarkers to predict stroke

Dr. Chao-Jung Chen, Graduate institute of integrated medicine, China Medical University

M-T-073

Fully automated sample preparation of whole blood for TDM and diagnostics procedures by LC/MS/MS using a commercial autosampler with tool change

Dr. Lucas Luethy, CTC Analytics AG

M-T-074

Epitope identifiication and affinity characterization of human alpha-Galactosidase A to a monoclonal antibody by SPR-affinity mass spectrometry

Mr. Zdenek Kukacka, Steinbeis Centre for Biopolymer Analysis and Biomedical Mass Spectrometry

M-T-075

Mass spectrometry and computational approach for proteomic characterization of amniotic fluid in polyhydramnios pregnancies

Dr. Ruta Navakauskiene, Institute of Biochemistry, Vilnius University

M-T-076

Rapid discrimination of Aspergillus section Fumigati based on ribosomal protein profiling observed by MALDI-TOFMS

Dr. Hiroaki Sato, National Institute of Advanced Science and Technilogy (AIST)

M-T-077

Proteomic analyses of mouse kidney with systemic lupus erythematosus using mass spectrometry and ion mobility drift-time dependent collision energies

Dr. Kleitos Sokratous, The Cyprus Institute of Neurology & Genetics, Nicosia, Cyprus

M-T-078

Detection of Bordetella pertussis protein pertactin using parallel-reaction monitoring compared to Western Blot Analysis

Dr. Patrick Chong, Public Health Agency of Canada

M-T-080

A quantitative approach using LC-MS in Hepatitis C Virus NS2-3 protease autolysis inhibition

Mr. Maxime Sansoucy, Université du Québec à Montréal

M-T-081

Differential proteomic analysis reveals characteristic protein expression changes in traumatic brain injury

Dr. Ganna Shevchenko, Uppsala University

Emerging and persistent environmental contaminants

M-T-082

Towards an extended application of MALDI-MS in archaeology and artworks: traces of the past in the mass spectra

Ivana K. Levy, CONICET-UMYMFOR, Consejo Nacional de Investigaciones Científicas y Técnicas, Unidad de Microanálisis y Métodos, Físicos aplicados a la química Orgánica, Ciudad de Buenos Aires, Argentina

M-T-083

Comparative assessment of perfluoroalkyl substances (PFASs) levels in drinking water supplies of three South African cities

Adegbenro Daso, adegbenrop@gmail.com

M-T-084

Simultaneous quantitation and confirmation of about 500 pesticide residues in food extracts using LC-QTOF accurate mass spectrometry

Dr. Joe Anacleto, Bruker

M-T-085

A validated high resolution mass spectrometry method for the quantification of T-2 and HT-2 toxins in cereals

Dr. Bryan McCullough, LGC Ltd.

M-T-086

Development of extraction and LC-MS/MS methods for the quantitation of finasteride, levonorgestrel and melengestrol acetate in water and sediment

Dr. Naomi Stock, Water Quality Centre

M-T-087

An LC-MS/MS study of glyphosate and aminomethylphosphonic acid in soil and the reactivities of mono- to triply-deprotonated glyphosate

Dr. Raymond March, Trent University

M-T-088

Monitoring of Baltic Sea sediments for sea-dumped chemical warfare agents using GC–MS/MS and LC–MS/MS

Mr. Martin Söderström, University of Helsinki

M-T-089

Identification and quantitation of legal and illicit drugs in wastewater samples collected during a dance party event

Mr. Andre Schreiber, SCIEX

M-T-090

Data independent acquisition-digital archiving mass spectrometry (DIA-DA MS) with next-generation sequencing for profiling fungal contaminated silage

Ms. Megan Kelman, Western University

M-T-091

Identification and quantitation of underivatized glyphosate and other polar pesticides in water and beer samples using LC-MS/MS

Mr. Andre Schreiber, SCIEX

M-T-092

Reading of accurate mass spectra to find anthropogenic substances in the environment

Dr. Atsushi Yamamoto, Tottori University of Environmental Studies

M-T-093

Parts-per-trillion level high-throughput quantitation of glyphosate, aminomethylphosponic acid (AMPA) and glufosinate in water samples by LC-MS/MS

Dr. Joe Anacleto, Bruker

M-T-094

Identification of potential biomarkers of exposure to diundecyl phthalate

Dr. Manori Silva, Centers for Disease Control and Prevention

M-T-095

A targeted quantitative LC-MS/MS method for 431 positive and negative ion pesticides in a single analysis

Dr. Laurie Allan, Bruker Ltd.

M-T-096

Evaluation of atmospheric pressure ionization techniques for the determination of fluorotelomer alcohols and perfluorinated sulfonamides

Mr. Juan Francisco Ayala Cabrera, University of Barcelona

M-T-097

Mammalian metabolism of the C-P bond in perfluorinated phosphinates (PFPiAs) and identification of resulting metabolites

Ms. Shira Joudan, University of Toronto

M-T-098

Phytochelatin production and sequestration of heavy metals as a detoxification pathway in Chara australis for use in phytoremediation

Mr. Jerod Hurst, University of Buffalo

M-T-099

Determination of aqueous film forming foam (AFFF) components using a multivariate analysis approach

Mr. Adam Ladak, Waters

M-T-100

Fast pesticide residue analysis using a novel benchtop time-of-flight mass spectrometer

Mr. Jonathan Byer, LECO Corporation

M-T-101

UHPLC-HRMS determination of palytoxin and ovatoxins from Ostreopsis cf. ovata, a marine microalgae blooming in a Northwestern Mediterranean beach

Ms. Encarna Moyano, University of Barcelona

M-T-102

Using of a high resolution mass spectrometry for the identification of electrochemical degradation products of selected drugs

Ms. Monika Radicova, Comenius University in Bratislava, Faculty of Natural Sciences, Department of Analytical Chemistry

M-T-103

A multi-year study of VOC emissions at a waste disposal facility using mobile LPCI-MS and APCI-MS instruments

Dr. Robert Healy, Ontario Ministry of the Environment and Climate Change

M-T-104

A rapid and robust method for determination of 35 phthalates in influent, effluent and biosolids in wastewater treatment plants

Mehran Alaee, Tommy Bisbicos

M-T-105

Identification of emerging contaminants from a waste water influenced water body using high resolution accurate mass LC/MS and statistical analysis

Dr. Jerry Zweigenbaum, Agilent Technologies, Inc.

FAIMS/DMS and new developments in IMS instrumentation

M-T-106

Investigating tautomers of anilinium with differential mobility spectrometry

Mr. Stephen Walker, University Waterloo

M-T-107

Measuring ion-solvent binding energies with DMS

Mr. Johnathan Steffen, University of Waterloo

M-T-108

Targeted proteomic analyses of MHC peptides using differential ion mobility mass spectrometry

Ms. Sibylle Pfammatter, IRIC - Université de Montréal

M-T-109

An ion mobility screening approach for the detection of toxicologically relevant substances

Dr. Jeff Goshawk, Waters

M-T-110

Sensitive and rapid analysis of biogenic isomers and perfluoro-compounds by high pressure ion mobility spectrometry/time-of-flight mass spectrometry

Dr. Haiyang Li, Dalian Institute of Chemical Physics, Chinese Academy of Sciences

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Ms. Abby Gelb, University of Nebraska-Lincoln

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Ms. Anne Bruinen, M4I - Maastricht University

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Dr. Daniel Beach, National Research Council Canada

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Ms. Jacquelyn Jhingree, Manchester Institute of Biotechnology, University of Manchester

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Dr. Ewa Jurneczko, University of Manchester

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Mr. Chenyu Yao, University of Waterloo

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Mr. David Heywood, Waters Corporation

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Dr. Andrey Trubitsyn, Ryazan State Radio Engineering University

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Dr. Mikhail Dubkov, Ryazan State Radio Engineering University

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Dr. John Fjeldsted, Agilent Technologies

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Dr. Julien De Winter, University of Mons

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Mrs Haidy Metwally, University of Western Ontario

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Dr. Victor Gurov, Ryazan State Radio Engineering University

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Dr. Kazunari Takaya, Rikkyo university

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Dr. Sven Meyer, Bruker Daltonik GmbH

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Dr. Andrey Trubitsyn, Ryazan State Radio Engineering University

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Dr. Simonetta Fornarini, Università degli Studi di Roma La Sapienza

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Dr. Thiago C. Correra, IQ-USP - Brazil

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Dr. Anzor Mikaia, National Institute of Standards and Technology

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Dr. Frederic Rosu, Univ. Bordeaux. CNRS ums3033

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Mr. Patrick Jäger, Karlsruhe Institute of Technology

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Dr. Farid Benkaci-Ali, University of Sciences and Technology Houari Boumediene, Faculty of Chemistry, Laboratory of Functional Organic Analysis,

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Dr. C K Andy Siu, City University of Hong Kong

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Dr. Michael Burt, University of Oxford

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Dr. Paul Gates, University of Bristol

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Dr. Terry Mcmahon, University of Waterloo

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Mr. Jocky Kung, University of Toronto

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Dr. Jana Roithova, Charles University in Prague

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Mr. Jakob Hitzenberger, Friedrich-Alexander University Erlangen-Nuremberg

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Mr. Ryan Bain, Purdue University

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Ms. Yasaman Jami Alahmadi, Memorial University of NL

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Ms. Suzie Douix, Synchrotron Soleil

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Mr. Bryan Linford, Memorial University

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Mr. Matthew Kusinski, University of Toronto

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Dr. Anna Troiani, Sapienza Rome University, Italy

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Dr. Anzor Mikaia, National Institute of Standards and Technology

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Dr. Jingpei Cao, China University of Mining & Technology

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Ms. Yating Wang, NSERC CREATE York University and University of Toronto

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Mr. Herbert Dias, USP - Univesity of São Paulo

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Mr. Martin Clemen, Christian-Albrechts-Universität zu Kiel

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Dr. Takemichi Nakamura, RIKEN CSRS, Molecular Structure Characterization

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Dr. Jürgen H. Gross, Heidelberg University

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Mr. Gabriel Gaiffe, Université Pierre et Marie Curie

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Mr. Selim Gerislioglu, The University of Akron

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Ms. Sydney Wellman, NSERC CREATE York University and University of Toronto

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Dr. Adel Iakubov, Chemistry Department, Irkutsk State University

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Mr. Corentin Decroo, Umons

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Dr. Martin Czar, Eidgenössische Technische Hochschule Zürich

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Mr. Paolo Benigni, Florida International University

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Dr. Magnus Palmblad, Leiden University Medical Center

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Dr. Sebastien Voisin, Association Plateforme BioPark d'Archamps

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Dr. Nathalie Selevsek, ETH Zurich

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Dr. Sebastien Voisin, Association Plateforme BioPark d'Archamps

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Dr. Olaf Jahn, Proteomics Group, Max-Planck-Institute of Experimental Medicine

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Mr. Maroun El Khoury, Thermo Fisher Scientific

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Dr. Myung Hee Nam, Korea Basic Science Instiyute

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Mr. Maroun El Khoury, Thermo Fisher Scientific

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Dr. Steven Husson, University of Antwerp

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Ms. Débora Sant'Ana, McGill University

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Dr. Daniele F. O. Rocha, post doc student

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Dr. David Peake, Thermo Fisher Scientific

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Mr. Qi Tang, University of Waterloo

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Dr. Zoe Hall, University of Cambridge

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Ms. Kaija Schäpe, Justus-Liebig-University of Giessen

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Ms. Gilian Thomas, Carleton University

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Dr. Jeffrey Agar, Northeastern University

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Dr. Jiejun Wu, Janssen R&D US LLC

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Mr. Sam Shields, Carleton University

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Mr. Juan Aristizabal Henao, University of Waterloo

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Dr. Roy Martin, Waters

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Ms. Helene Mobbs, Department of Biochemistry, University Cambridge

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Mr. Nicolas DEPRETRE, ChemoSens - INRA (France)

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Dr. Raquel Mary Rodrigues Peres, CAISM/UNICAMP

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Mr. Gerson Dirceu Lopez Muñoz, University of los Andes

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Mrs Anik Forest, Montreal Heart Institute

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Mr. Olivier Berdeaux, ChemoSens - INRA (France)

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Ms. Estelle Sibille, ChemoSens - INRA (France)

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Dr. Alexandra Furtos, University of Montreal

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Dr. Damila Morais, Unicamp

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Dr. Andrew Baker, Waters Corporation

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Dr. Heiko Neuweger, Bruker Daltonik GmbH

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Mrs Ghazaleh Moghaddam, Université du Québec à Montréal, Chemistry Department

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Dr. Heiko Neuweger, Bruker Daltonik GmbH

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Dr. Emilien Jamin, MetaboHUB-MetaToul-AXIOM

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Mrs Maria Kakkoura, The Cyprus Institute of Neurology and Genetics, Nicosia, Cyprus

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Dr. Verena Tellstroem, Bruker Daltonics

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Dr. Aiko Barsch, Bruker Daltonics

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Mr. Aaron Boice, Agilent Technologies

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Ms. Mona Hamada, College of Pharmacy and Nutrition, University of Saskatchewan

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Dr. Randy Purves, University of Saskatchewan

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Dr. Verena Tellstroem, Bruker Daltonics

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Ms. Elisa Ollikainen, Faculty of Pharmacy, University of Helsinki

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Ms. Adriana Godoy, University of Campinas

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Ms. Nathaly Reyes-Garces, University of Waterloo

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Ms. Paula Galeano, Universidad de los Andes

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Ms. Encarna Moyano, University of Barcelona

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Ms. Mary Piotrowski, Pfizer

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Dr. Riya Christina Menezes, Max Planck Institute for Chemical Ecology

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Dr. Daisuke Miura, Kyushu University

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Ms. Hanan Elsayed, College of Pharmacy, University of Saskatchewan

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Mr. Lorne Fell, LECO Corporation

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Mrs Mariana Russo, Concordia University

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Dr. Rosa Erra-Balsells, Departamento de Quimica Organica, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires

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Mr. Gustavo Henrique Bueno Duarte, ThoMSon Mass Spectrometry Laboratory

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Mr. Júlio César Santos Júnior, Department of Clinical Pathology, School of Medical Sciences, State University of Campinas – UNICAMP

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Dr. Min Ho Cha, Korea Institute of Oriental Medicine

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A novel targeted metabolomic approach in plant hormone analysis

Mr. Jan Šimura, Laboratory of Growth Regulators & Department of Chemical Biology and Genetics, Centre of the Region Haná for Biotechnological and Agricultural Research, Faculty of Science, Palacký University & Institute of Experimental Botany ASCR

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Dr. Yuqin Dai, Agilent Technologies

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Dr. Kristyna Flokova, Laboratory of Plant Physiology, Wageningen University

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Mr. Fabio Santos, University of Campinas

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Mrs Mi Kyeong Lee, Department of Food Technology and Services, Eulji University

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Dr. Fedor Kryuchkov, University of Bergen

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Ms. Nivedita Bhattacharya, CSIR-National Chemical Laboratory, India

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Dr. Richard B. Cole, Sorbonne Universités, UPMC Univ Paris 06

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Dr. Florian Richter, Goethe University, Medical School

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Dr. Gordon Nicol, MilliporeSigma

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Ms. Katherine Schumacher, University of Nebraska

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Mr. Frederic Lamoliatte, Institute for Research in Immunology and Cancer, University of Montréal

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Ms. In-kang Song, Ewha womans university

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Mr. Julian Saba, Thermo Fisher Scientific

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Dr. Tomoya Kinumi, National Metrology Institute of Japan (NMIJ)/ AIST

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Mr. David Heywood, Waters Corporation

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Ms. Marialaura Dilillo, Fondazione Pisana per la Scienza

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Dr. Simon Lauter, Bruker Daltonics Germany

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Dr. Catherine Botting, University of St Andrews

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Mr. Ken Miller, Thermo Fisher Scientific

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Ms. Leanne Scharikow, Public Health Agency of Canada

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Dr. Roy Martin, Waters

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Dr. Lyle Burton, Sciex

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Mr. Bernard Delanghe, Thermo Fisher Scientific

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Dr. Thierry Fouquet, National Institute of Advanced Industrial Science and Technology (AIST), Japan

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A combination of on-plate degradation and Kendrick mass defect analysis for characterization of high molecular-weight polyesters by MALDI spiral-TOFMS

Dr. Kanae Teramoto, JEOL Ltd.

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Dr. John Dane, JEOL USA, Inc.

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Mr. Koji Okuda, JEOL USA, Inc.

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Mr. Rongxin Yan, Beijing Institute of Spacecraft Environment Engineering

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Dr. Meiru Guo, Lanzhou Institute of Physics

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Dr. Jack Cornett, University of Ottawa

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Dr. Hiroyuki Hagino, Japan Autmobile Research Institute

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Dr. Inhee Choi, Korea Institute Of Nuclear Safety

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Dr. Bin Deng, York University

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Mr. Ingvar Moller, Department of Health and Medical Sciences, University of Copenhagen

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Conformational differences of the monoclonal antibody Herceptin® demonstrated by Native TWIM-MS, DTIM-MS and HDX-MS

Ms. Rosie Upton, University of Manchester

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The role of conformational dynamics in differing activity and substrate specificity amongst isozymes of glutathione S-transferase

Mr. Nicole McGregor, NSERC CREATE York University and University of Toronto

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Structural differences between Diphtheria toxin and a detoxified single-point mutant CRM197 revealed by HDX-MS

Dr. Peter Liuni, Sanofi Pasteur/York University

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Ms. Ruth Knox, NSERC CREATE York University and University of Toronto

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Ms. Cristina Lento, MS-ESE York University - NSERC CREATE

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Ms. Kate Groves, LGC and University of Leeds

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Mr. Bihac Mazigh, University of Ottawa

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Dr. Yannis-Nicolas Francois, LSMIS- University of Strasbourg

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Dr. Henry Shion, Waters Corporation

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Dr. Christine Enjalbal, Université de Montpellier, Institut des Biomolécules Max Mousseron

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Mr. Adrien Marchand, Inserm, ARNA Lab

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Mrs Piia Liigand, University of Tartu

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Dr. Min Du, Waters Corporation

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Dr. Bin Ma, University of Waterloo

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Dr. Sylvain Letarte, Phytronix Instruments inc.

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Dr. William Alley, Waters

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Mr. Waleed Mohammed Saeid, Drug Design & Discovery Research Group, College of Pharmacy & Nutrition, University of Saskatchewan

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Mr. McDonald Donkuru, University of Saskatchewan

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Dr. Yannis-Nicolas Francois, LSMIS- University of Strasbourg

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Ms. Deborah Michel, University of Saskatchewan

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Dr. Rosana Alberici, Thomson Mass Spectrometry Laboratory-UNICAMP

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Ms. Leslie Welch, Genentech a Member of the Roche Group

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Mrs Wei Sun, Sanofi

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Mr. Chris Spahr, Amgen, Inc.

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Ms. Sydney Wellman, NSERC CREATE York University and University of Toronto

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Dr. Jonathan Josephs, Thermo Fisher Scientific

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Dr. Christopher Anderton, Pacific Northwest National Laboratory

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Dr. Celine Gueguen, Trent University

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Ms. Alena Tierbach, Eawag

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Dr. Hui-Ling Lee, Department of Chemistry, Fu Jen Catholic University

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Mr. Sohidul Islam, Trent University

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Mr. Vaughn Mangal, Trent University

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Dr. Andrew Baker, Waters Corporation

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Mr. Kathirvel Alagesan, Max Planck Institute of Colloids and Interfaces

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Combination of reductive isotope labeling, exoglycosidase digestions and chromatographic separation for glycomics

Dr. Jianjun Li, National Research Council of Canada

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Mrs Mei-Chun Tseng, Institute of Chemistry Academia Sinica

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Ms. Katherine Schumacher, University of Nebraska

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Ms. Abby Gelb, University of Nebraska-Lincoln

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Tandem mass spectrometry determination of the structure of a heterogeneous mixture of Lipid As isolated from the LPS of Aeromonas liquefaciens SJ-19a

Mrs Mervt Almostafa, Memorial University

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Ms. Melissa Bärenfänger, Institute of Organic Chemistry, University of Hamburg

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Dr. Anna Karen Laserna, National University of Singapore

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Dr. Martina Hermannova, Contipro a.s.

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Ms. Chuping Lee, Institute of Atomic and Molecular Sciences, Academia Sinica

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Dr. Nina Ogrinc Potocnik, M4I Institute, Maastricht University

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Dr. Petra Oliva, Sanofi Genzyme

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Metabolomic imaging mass spectrometry of high-risk metastasizing uveal tumors classified upon BAP1 mutational status

Mrs Nasim Bararpour, Centre universitaire romand de médecine légale, Lausanne - Genève (CURML)

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A molecular map of non-alcoholic fatty liver disease progression

Dr. Zoe Hall, University of Cambridge

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imzML: flexibility and exchangeability for mass spectrometry imaging data processing

Dr. Nicolas Desbenoit, Chair of Bioanalytical Science and Food Analysis, University of Bayreuth, Bayreuth, Germany

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Metal-assisted LDI for high resolution imaging MS of neutral lipids from thin tissue sections

Dr. Pierre Chaurand, Université de Montréal

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Mr. Michael Batey, Waters Corporation

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Multimodal mass spectrometry imaging analysis of N-linked glycans and proteins from a single tissue section

Mr. Bram Heijs, Leiden University Medical Center

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Dr. Arash Zarrine-Afsar, Department of Medical Biophysics

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Dr. Brandi West, University of Auckland

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Mr. Ronald Fook Seng Lee, Ecole Polytechnique Federale de Lausanne

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Quantitative imaging mass spectrometry (q-IMS) of tyrosine kinase inhibitor in mouse tissues

Dr. Shuichi Shimma, Osaka University

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Dr. Filip Kaftan, Max Planck Institute for Chemical Ecology

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Imaging mass spectrometry of rat brain tissue using matrix-enhanced surface-assisted laser desorption/ionization with sputter-deposited platinum film

Mr. Satoshi Hamada, Nissan Chemical Industries,LTD.

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Mr. Joseph Kennedy, Prosolia

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Molecular imaging of gangliosides to investigate lysosomal storage diseases using mass spectrometry imaging with ion mobility separation

Dr. Bindesh Shrestha, Waters Corp.

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Dr. Jooyeon Oh, ASTA Inc.

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Dr. Jun Aoki, Osaka University

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An investigation of DESI imaging at varying acquisition rates with real time display for optimized tissue imaging

Mr. Michael Batey, Waters Corporation

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Laser ablation atmospheric pressure photoionization (LAAPPI) for ambient mass spectrometry imaging of low polarity compounds in animal tissue

Mr. Juha-Pekka Hieta, University of Helsinki

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Dr. Akiko Kubo, Keio University

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Dr. Anna Maria Fernandes, ThoMSon Mass Spectrometry Laboratory

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The key point extraction technique for amniotic fluid proteome characterization

Dr. Ruta Navakauskiene, Institute of Biochemistry, Vilnius University

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Cool-MALDI: matrix-free mass spectrometric imaging of metabolites in snap-frozen tissue sections using IR-laser ablation and UV-laser postionization

Mr. Jens Soltwisch, Institut for Hygiene, University of Muenster

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Back to basics - revisiting sprayer design for desorption electrospray ionisation mass spectrometry imaging (DESI-MSI) of biological tissues

Ms. Jocelyn Tillner, Imperial College

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Mr. Marcel Wiegelmann, Biomedical mass spectrometry, University of Münster, Germany

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Mr. Florian Brenner, Vienna University of Technology

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Dr. John Hammond, Physical Electronics USA

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Ms. Emmanuelle Claude, Waters Corporation

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Dr. Shannon Cornett, Bruker

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Dr. Rima Ait-Belkacem, Fondazione Pisana per la Scienza ONLUS

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Mr. Benjamin Bartels, IMPRS

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A next-generation ultrafast detector for imaging mass spectrometry: the pixel imaging mass spectrometry (PImMS) sensor

Dr. Jason Lee, University of Oxford

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Dr. Zheng Ouyang, Tsinghua University

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Dr. Mark Bier, Carnegie Mellon University

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Dr. Gökhan Baykut, Bruker Daltonik GmbH

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Dr. Romain Huguet, Thermo Fisher Scientific

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Dr. Viatcheslav Artaev, LECO Corporation

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Dr. Xi Luo, Japan advanced institute of science and technology

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Dr. Christian Rolando, Université Lille 1, Sciences et Technologies

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Ms. Annika Koch, University of Münster, Biomedical Mass Spectrometry

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Dr. Chuan-Fan Ding, Department of Chemistry, Fudan University

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Dr. Ping Chen, Dalian Institute of Chemical Physics, Chinese Academy of Sciences

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Dr. R. Graham Cooks, Purdue University

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Dr. I-Chung Lu, Department of Chemistry, Wayne State University

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Dr. Binghe Gu, The Dow Chemical Company

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Dr. Michael Przybylski, Steinbeis Centre for Biopolymer Analysis and Biomedical Mass Spectrometry

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Mr. Eric Dziekonski, Purdue University

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Dr. Philip Remes, Thermo Fisher Scientific

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Mr. Guido Zeegers, ETH Zürich

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Mr. Matthew Soyk, LECO Corporation

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Dr. Simon Lauter, Bruker Daltonics Germany

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Dr. Daniel Eikel, Advion Inc.

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Ms. Päivi Pöhö, Division of Pharmaceutical Chemistry and Technology, Faculty of Pharmacy, University of Helsinki

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Dr. Christine Joblin, University Toulouse 3 / CNRS, IRAP

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Dr. David Langridge, Waters Corporation

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Dr. Aviv Amirav, Tel Aviv University

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Dr. Alexander Fialkov, Tel Aviv University

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Mr. Philipp Laufer, Technische Universität Dresden - Institute for Aerospace Engineering

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Dr. Josef Cvačka, Institute of Organic Chemistry and Biochemistry, Prague

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Mr. Björn Raupers, Institute of pysical chemistry, University of Kiel

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Dr. Martin Bachman, AstraZeneca

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Dr. Dimitris Papanastasiou, Fasmatech Science & Technology

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Dr. Kermit Murray, Louisiana State University

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Dr. Sharon Curtis, John Holmes Mass Spec Facility Ottawa

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Dr. Michael Durr, Justus Liebig University Giessen

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Dr. Aviv Amirav, Tel Aviv University

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Mr. Robert Goguen, IonSense

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Dr. Li Ding, SRL (Europe) Ltd.

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Dr. Xuejing Shen, NCS Testing technology Co., Ltd

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Ms. Zilan Xiao, NCSTestingTechnology Co., Ltd

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Mr. Hou-Yu Lin, Institute of Atomic and Molecular Sciences Academia Sinica

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Mr. Lorne Fell, LECO Corporation

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Mrs Christina Kelly, LECO Corporation

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Mr. Logan Plath, Carnegie Mellon University

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A novel benchtop GC-TOFMS for fast targeted allergen screening and non-targeted characterization for personal care products

Mr. Bernie Yeung, LECO Corporation

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Time of flight SIMS quantification of bromine based insecticide in mosquito netting

Dr. Chuanzhen Zhou, Analytical Instrumentation Facility at NCSU

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Dr. Anneli Kruve, University of Tartu

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Mr. Jian Jun Li, University of Calgary

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The distinction of cis and trans fatty acids in food products with a novel benchtop time of flight GC-MS system

Mr. Bernie Yeung, LECO Corporation

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Comparison of weird and wild" jelly bean flavors using HS SPME - gas chromatography - mass spectrometry"

Mr. Joe Binkley, LECO Corporation

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Multidimensional mass spectrometry to characterize by-products generated during MALDI of polystyrenes synthesized by controlled radical polymerization

Mr. Christophe Chendo, Aix-Marseille Université – CNRS, UMR 7273, Institut de Chimie Radicalaire, Marseille – France

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Mrs Christina Kelly, LECO Corporation

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Dr. William Wallace, National Institute of Standards and Technology

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Ms. Natalie Dean, University of Victoria

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Mr. Eric Janusson, University of Victoria

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Dr. Nicole Rijs, Karlsruhe Institute of Technology

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Mrs Renske Penning, Utrecht University

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Dr. James Schofield, University of Southampton, UK

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Dr. Wai Him Kwok, Racing Laboratory, The Hong Kong Jockey Club

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Mr. Andreas Dannhorn, Imperial College London

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Dr. Lijiang Song, University of Warwick

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Mr. Tobias Lieblein, Goethe-University Frankfurt

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Mr. Michael Wleklinski, Purdue University

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Making ESI-MS/MS newborn screening simplier and much less expensive

Mrs Andréia Porcari, ThoMSon Mass Spectrometry Laboratory, Institute of Chemistry, University of Campinas, UNICAMP, Campinas, SP, Brazil

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Dr. Petr Halada, Institute of Microbiology AVCR

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Dr. Arnd Ingendoh, Bruker Daltonics

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Mr. Shahrokh Ghobadloo, University of Ottawa

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Dr. Pawel Jaruga, National Institute of Standards and Technology

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Mr. Lukas Bregy, ETH Zurich

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Ms. Marialaura Dilillo, Fondazione Pisana per la Scienza

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Dr. Sangeeta Tanna, De Montfort University

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Dr. R. Graham Cooks, Purdue University

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Dr. Damila Morais, Unicamp

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Dr. Geoffrey Rule, ARUP Laboratories

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Mr. Davide Pellegrini, NEST, Scuola Normale Superiore

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Mr. Adrien Marchand, Inserm, ARNA Lab

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Mrs Stefanie Ickert, Federal Institute for Materials Research and Testing

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Dr. Chuan-Fan Ding, Department of Chemistry, Fudan University

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Dr. Jiang Zhou, Peking University

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Dr. Satoko Akashi, Yokohama City University

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Dr. Xinhua Guo, College of chemistry, Jilin University

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Dr. Maxim Berezovski, University of Ottawa

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Dr. Pascal Gerbaux, University of Mons

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Ms. Zoja Nagurnaja, University College London

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Ms. Liliana Pedro, Eskitis Institute for Drug Discovery, Griffith University

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Ms. Ulrike Anders, ETH Zurich

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Dr. Guru Swamy Madugundu, PERFORM Centre, Concordia University

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Ms. Kerene Brown, NSERC CREATE York University and University of Toronto

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Dr. Besnik Bajrami, Broad Institute of MIT and Harvard

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Mr. Toru Takarada, Kobe Pharmaceutical University

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Mrs Agni Faviola Mika Gavriilidou, ETH Zurich

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Mr. Shaan Rashid, University of Ottawa

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Dr. Natalie Wielsch, Max Planck Institute for Chemical Ecology

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Ms. Mays Al-Dulaymi, University of Saskatchewan

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Ms. Ulrike Warzok, Freie Universität Berlin

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Mrs Soha Ahmadi, University of Toronto

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Dr. Jiang Zhou, Peking University

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Dr. Magdalena Zimnicka, Institute of Organic Chemistry Polish Academy ofSciences

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Mr. Vincent Guerineau, CNRS ICSN

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Dr. Meital Kupervaser-Cohen, Weizmann Institute of Science

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Dr. Chang Liu, SCIEX

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Dr. Mariam ElNaggar, Prosolia

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Mrs Aleksandra Michalik-Onichomowska, Bundesanstalt für Materialforschung und -prüfung (BAM)

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Dr. Pu Wei, Purdue University

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A novel benchtop time of flight GC/MS system for high throughput qualitative and quantitative analysis of drugs of abuse in human urine

Mr. David Alonso, LECO Corporation

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Utilizing new reverse search library program and DART-MS for targeted screening of food and supplements for adulterants

Mr. Frederick Li, IonSense, Inc.

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Medical swab analysis using desorption electrospray ionization mass spectrometry (DESI-MS) – a novel, non-invasive approach for mucosal diagnostics

Ms. Pamela Pruski, Imperial College London

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Spatially resolved analysis of symbiotic soybean-rhizobia interactions by laser ablation-electrospray ionization mass spectrometry

Dr. Christopher Anderton, Pacific Northwest National Laboratory

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Mobile membrane introduction mass spectrometry for real-time geo-spatial resolution of atmospheric trace organics

Dr. Erik Krogh, Applied Environmental Research Labs, Department of Chemistry

W-T-204

Temperature-regulated thermal desorption and pyrolysis coupled with direct analysis in real time mass spectrometry (DART)

Dr. Robert (Chip) Cody, JEOL USA, Inc.

W-T-205

Metabolic phenotyping of cell lines by rapid evaporative ionization mass spectrometry

Ms. Emmanuelle Claude, Waters Corporation

W-T-206

Real time detection of fish fraud using rapid evaporative ionisation mass spectrometry (REIMS)

Dr. Olivier Chevallier, Queen's University Belfast

W-T-207

Fast identification of counterfeit medicines – a comparison of two MS systems

Dr. Graham Lawson, De Montfort University

W-T-208

The effect of sampling pipeline on the measure gas partial pressure with mass spectrometer in molecule flow

Mr. Rongxin Yan, Beijing Institute of Spacecraft Environment Engineering

W-T-209

Molecularly imprinted polymers with desorption electrospray ionization mass spectrometry for faster environmental monitoring of neonicotinoids

Mr. Jeremy Gauthier, Memorial University of Newfoundland

W-T-210

Evaluation of thorium and uranium concentrations and isotope ratios by quadrupole-ICP-MS in naturally occurred radioactive materials

Ms. Juhyun Lee, Korea Institute of Nuclear Safety

W-T-211

Analysis of evolved hydrogen gas from industrial materials by using a quadrupole mass spectrometer

Mr. Koji Okuda, JEOL USA, Inc.

W-T-212

Open probe fast GC-MS – real time analysis with separation

Dr. Alexander Fialkov, Tel Aviv University

W-T-213

Fresh approaches to the analysis of small polar N-nitrosamines in water using MIP-DESI-MS

Dr. Christina Bottaro, Department of Chemistry, Memorial University

W-T-214

Polymer inclusion membranes with condensed phase membrane introduction mass spectrometry (CP-MIMS): improved analytical response time and sensitivity

Dr. Chris Gill, Applied Environmental Research Laboratories - Vancouver Island University

Novel high throughput techniques

W-T-215

Scout-MRM; a method to acquire large numbers of MRM without predefined retention times

Dr. David Cox, SCIEX

W-T-216

Evaluating quadrupole detection FTMS for complex mixture profiling

Dr. Michael Easterling, Bruker Daltonics

W-T-217

Measurement of Estradiol in human serum by LC-MS/MS using a novel estrogen-specific derivatization reagent

Mrs Reena Desai, Anzac Research Institute, Sydney, Australia

W-T-218

Generic sample extraction workflow for analysis of complete drugs of abuse panel by LDTD-MS/MS (screening) and LC-MS/MS (confirmation)

Mr. Alex Birsan, Phytronix Technologies Inc.

W-T-219

Now a reality: sub second quantitative mass spectrometry analysis with Acoustic sample deposition and fiber coupled LDTD-MS/MS

Dr. Pierre Picard, Phytronix Technologies Inc

W-T-220

Direct insertion probe coupled to a high resolution time of flight mass spectrometer for rapid targeted and non-targeted analysis of drugs of abuse

Mr. David Borton, LECO Corporation

W-T-221

Non-aqueous capillary electrophoresis-electrospray ionization mass spectrometry on thiol-ene-based microchips

Ms. Sari Tähkä, Division of Pharmaceutical Chemistry and Technology, Faculty of Pharmacy, University of Helsinki, Finland

W-T-222

2D-patterning technique for analysis of post-translationally modified proteins using LC-MS with different chromatographic separations

Mr. Akira Tarui, School of Materials Science, Japan Advanced Institute of Science and Technology

W-T-223

Ultra high throughput screening by MALDI-TOF MS in drug discovery – exceeding one million samples per week

Dr. Sergei Dikler, Bruker Daltonics Inc.

W-T-224

Long term test on a new four-channel HPLC

Dr. Byungchul Cha, Thermo Fisher Scientific

W-T-225

A continuous flow sampling interface for high-throughput SPME-MS/MS analysis of in-vitro ADME samples

Mr. John Janiszewski, Pfizer Inc.

W-T-226

Microscale isolation of cytokinins by magnetic microparticle-based immunopurification

Dr. Ondrej Novak, Laboratory of Growth Regulators, IEB & UP Olomouc

W-T-227

Screening of αvβ6 antagonists using ultrafiltration-liquid chromatography-mass spectrometry

Mr. Nkazimulo Tshuma, University of Nottingham

W-T-228

Capillary gap sampler: a new microfluidic platform directly coupled to ESI-MS for fast analysis of low sample amounts

Mrs Sahar Ghiasikhou, ETH Zurich

W-T-229

Enzymatic assay development using novel MALDI high-throughput screening system

Dr. Sergei Dikler, Bruker Daltonics Inc.

W-T-230

A high-throughput LC/MS biochemical assay for monitoring activity of the early wall teichoic acid pathway gene product TarO

Mr. Paul Tawa, Merck & Co

W-T-231

High throughput microflow LC/MS: sensitivity gains on a practical timescale

Dr. Michael Donegan, Waters Corp

W-T-232

Rapid determination of protein binding affinity using solid phase micro extraction (SPME)

Dr. Sara Smith, MilliporeSigma

Phosphoproteomics

W-T-233

Identification of proteins and phosphorylation events associated with Leishmania stage differentiation

Dr. Mariette Matondo, Institut Pasteur

W-T-234

Visualizing mechanisms of BRAF-mutant melanoma drug resistance using PhosphoPath

Ms. Linsey Raaijmakers, Utrecht University

W-T-235

Proteomic and phosphoproteomic analysis of cell response to photon and particle irradiation

Mr. Martin Winter, German Cancer Research Center

W-T-236

High sensitivity and high throughput phosphoproteomics with micro-scale TMT labeling

Mr. Kosuke Ogata, Graduate School of Pharmaceutical Sciences, Kyoto University

W-T-237

Analysis of protein pyrophosphorylation by CID and EThcD mass

Dr. Eberhard Krause, Leibniz-Institut für Molekulare Pharmakologie Berlin

W-T-238

Comparison of the cellular effects two classes of Erk inhibitors in A375 mutant melanoma cells using a phosphoproteomic readout

Dr. Finn Holding, Astex Pharmaceuticals

W-T-239

Phosphoproteomic pipeline for the identification of non-genomic signaling pathways activated by contaminant exposure in aquatic species

Dr. Tara Sabo-Attwood, University of Florida

Protein-protein complexes

W-T-240

New developments in intact mass analysis of proteins and protein complexes

Dr. Chris Becker, Protein Metrics Inc.

W-T-241

Epitope binning by hydrogen deuterium exchange mass spectrometry: Understanding epitope-driven effects

Dr. Chris Morgan, Sanofi Genzyme

W-T-242

A novel two-dimensional (2-D) proteomic platform for proteome-wide protein-protein interaction studies

Dr. Reza Pourhaghighi, University of Toronto

W-T-243

Slightly bigger is better: protein interaction analysis with 100um ID columns

Mr. Brett Larsen, LTRI

Quantitation and structural elucidation of metabolites and covalent adducts

W-T-244

Fast and reliable quantitation of Z-drug hypnotics and benzodiazepines in serum using accurate mass LC-QTOF mass spectrometry

Dr. Jim Kapron, Bruker

W-T-245

A multi-analyte method using liquid chromatography with high resolution accurate mass spectrometry for aerosol constituents in 3D tissue cultures

Mr. Quentin Dutertre, Philip Morris

W-T-246

Clinical evaluation of prostaglandin D2 and E2 metabolites in urine

Dr. Atsuko Takeuchi, Kobe Pharmaceutical University

W-T-247

Determination of folate vitamers in feces and serum of Crohn´s disease patients using isotope-dilution UPLC-ESI-MS/MS

Dr. Wolfram Engst, German Institute of Human Nutrition Potsdam- Rehbrücke (DIfE)

W-T-248

Sensitive and robust method for the quantification of dimethylacetamide and its primary metabolite monomethylacetamide in human plasma

Ms. Fadwa Benkessou, Karolinska Institutet

W-T-249

The fate of platinum(IV) anticancer prodrugs in different biological fluids by LC-ICP-MS

Dr. Sarah Theiner, Insitute of Analytical Chemsitry, University of Vienna

W-T-250

On-line, absolute quantitation of analytes from 20-40 µm microdissections by laser microdissection-liquid vortex capture-mass spectrometry

Dr. John Cahill, Oak Ridge National Laboratory

W-T-251

In vitro metabolism of ketamine-derived designer drug methoxetamine by human liver microsomes using LC-HR-MS

Dr. Kyoung-Moon Han, NIFDS, MFDS, Republic of Korea

W-T-252

Thermal degradation of sulfamethoxazole during food cooking

Dr. Laurent Debrauwer, Axiom Platform - UMR 1331 INRA Toxalim - Toulouse - France

W-T-253

Validation of a U-HPLC-ESI-MS/MS method for the quantification of reactive aldehydes produced by lipid peroxidation in the intestinal lumen

Dr. Sylvie Chevolleau, Axiom platform - UMR 1331 Toxalim INRA Toulouse - France

W-T-254

Data and prediction driven convergent analysis for metabolite identification in drug discovery

Dr. Richard Lee, Advanced Chemistry Development, Inc. (ACD/Labs)

Radical peptides

W-T-255

Isomerizations and dissociations of FGW radical cations

Dr. Kai Chi Lau, MS-ESE York University - NSERC CREATE

W-T-256

Dissociation of [b5-H]$^{\bullet+}$ derived from alpha-methyltryptophan-containing hexapeptides

Mr. Bai Han Wu, NSERC CREATE York University and University of Toronto

W-T-257

Nucleophilic substitution in the aromatic rings of $[zn - H]^{\bullet+}$ ions via amide nitrogen

Dr. Cheuk Kuen Lai, MS-ESE York University - NSERC CREATE

Top-down proteomics

W-T-258

Reliable discrimination of Leucine and Isolucine in high throughput peptide sequencing

Dr. Albert Lebedev, Lomonosov Moscow State University

W-T-259

Development of an all-recombinant intact protein standard for LC MS application development and system suitability testing

Mr. Paul Fayad, Thermo Fisher Scientific

W-T-260

Proteomic and metabolomic analysis of wort: differentiation of malting barley cultivars

Dr. Martin Dusek, Research Institute of Brewing and Malting

W-T-261

Characterization of virulent Bacillus cereus species using top-down proteomics

Mr. Christian Malosse, Institut Pasteur

W-T-262

Profiling of intact proteins in the CSF of Alzheimer's disease patients

Mr. Victor Fursey, Bruker Daltonics Inc

W-T-263

In-source decay and pseudo-MS3 top-down analysis of peptide and protein ions using an AP-UV-MALDI source coupled to a Q Exactive mass spectrometer

Dr. Rima Ait-Belkacem, Fondazione Pisana per la Scienza ONLUS

W-T-264

Performance considerations for ultraviolet photo-dissociation using the Nd:YAG 5th harmonic (213nm)

Dr. Chad Weisbrod, Thermo Fisher Scientific

W-T-265

A quantum chemical tool for the prediction of mass spectra and the identification of fragmentation pathways: unexpected fragmentations in tripeptides

Ms. Julie Cautereels, University of Antwerp

W-T-266

Identification of biomarkers related to potential critical quality attributes (pCQA) for a new vaccine formulation.

Dr. Olena Masui, MS-ESE York University - NSERC CREATE

W-T-267

Identification of novel cysteine-containing peptides in tropical ant venoms using 3D mass mapping

Mr. Luuk van Oosten, Heidelberg University

W-T-268

Method for clinical application of MALDI imaging driven top-down microproteomics for discovery of tumor biomarkers

Mr. Vivian Delcourt, Université Lille 1 INSERM U-1192 PRISM - Université Sherbrooke