

19th Lake Louise Workshop on Tandem Mass Spectrometry

Thursday - November 30			
Chair	Paul D'Agostino		
8:15	Gary Glish	Introductory Remarks	
8:20	Robin Black	Tandem MS in the Analysis of Chemical Warfare Agents, Their Degradation Products And Biomarkers of Exposure	Defence Science & Technology Laboratory
9:05	Donald V. Kenny ¹ , Raj Mangaraj ¹ , Anne M. Gregg ¹ , David Mickunas ² , Eric Koglin ³ , Nancy Adams ³	Real-Time Analysis of CWA's in Air Using APCI-MS/MS	¹ Battelle Memorial Institute, ² U.S. EPA – Environmental Response Team, ³ National Homeland Security Research Center – U.S. EPA
9:35	J.A. Laramée ¹ , H.D. Durst ² , J.M. Nilles ¹	DART: The Appliance of Science	¹ SAIC, ² ECBC
10:05	Discussion		
10:10	Break		
10:40	Beata M. Kolakowski ¹ , Margaret A. McCooeye ¹ , Zoltan Mester ¹ and Paul A. D'Agostino ²	Rapid Separation and Identification of CW Agents in Food by ESI-FAIMS-MS/MS	¹ NRC; ² DRDC
11:00	Allen E. Haddrell, Alice Kardjaputri, Stephen van Eeden, George R. Agnes	Understanding The Adverse Health Effects of Air Pollution One Particle at a Time Using Off-line Tandem Mass Spectrometry	Simon Fraser U.
11:20	Susan D. Richardson ¹ , F. Gene Crumley ¹ , Francesca Fasano, Michael J. Plewa ² , Elizabeth Wagner ² , Ron Orlando ³	Mass Spectrometry and Toxicity Characterization of Drinking Water Fractions: Are High Molecular Weight DBPs Toxic	¹ U.S. EPA, ² U. Illinois, ³ U. Georgia
11:40	Michael J. Y. Jarvis, Gregory K. Koyanagi, Diethard K. Bohme	Scrubbing Ions with Molecules: Kinetic Studies of Chemical Noise Reduction in Mass Spectrometry by Ion-Molecule Reactions	York U.
12:00	Discussion		
Chair	Susan Richardson		
14:00	Alfred Yergey, Jennifer Campbell, Paul Blank, Stephen Stein	Recent Observations on Ion Formation in a MALDI TOF-TOF	NIH
14:45	Paul Kebarle, Udo H. Verkerk	Ion Pairing and Ion Molecule Reactions at the Surface of Proteins in ESIMS	U. Alberta
15:05	Don Douglas	Gas phase protein / small-molecule complexes that retain their solution binding: Cex in a vacuum	U. British Columbia
15:25	John Klassen	Protein-ligand binding affinity and stoichiometry determined by the direct ES-MS assay	U. Alberta
15:45	Discussion		
15:50	Break		
16:20	Lars Konermann	Protein Structure and Dynamics Studied by Hydrogen/Deuterium Exchange ESI-MS/MS	Department of Chemistry, The University of Western Ontario
16:40	Evgeniy V. Petrotchenko ¹ , Kunhong Xiao ² , Robert J. Lefkowitz ^{2,3} , Christoph H. Borchers ^{1,4}	MALDI photo-cleavable crosslinker combined with tandem-MS for structural proteomics	¹ U. North Carolina; ² Duke U.; ³ Howard Hughes Medical Institute; ⁴ U. Victoria

17:00	John Chik ¹ , Gordon Slys ¹ , Dan Sackett ² , David Schriemer ¹	Deriving Drug Mechanism using HDX in MS and MS/MS Space: New Insights into Microtubule Poisons	¹ U. Calgary; ² NIH
17:20	Andrew R.S. Ross	Identification of Proteins and Protein Phosphorylation Sites in Plant Seeds and Embryos using Gel Electrophoresis and Q-TOF LC-MS/MS	NRC
17:40	Discussion		
Chair	Orval Mamer		
20:00	O. Krokhin, V. Spicer, W. Ens, K. Standing, J. Wilkins	Reducing the need for MSMS - protein identification by LC-MS mass fingerprinting with a retention time constraint	U. Manitoba
20:20	Diem Ly Van; George R. Agnes	Ionic Matrix Sample Preparation Using Levitated Droplets for Complementary Sequence Coverage in Model Membrane Proteins by MALDI	Simon Fraser U.
20:40	Andrew Leslie, Dietrich Volmer	Fundamental and technical aspects of quantitative MALDI of small molecules	Institute for Marine Biosciences
21:00	Discussion		
21:05	Poster Session		
	John Headley, Kerry Peru and Jing-Long Du	Determination of Photolysis Rates of Selected Sulfonylurea Urea Herbicides Utilizing ESI LC/MS/MS.	Environment Canada
	Alan A. Doucette	The Best of Both Worlds: Intact Protein Separation for Targeted Proteome Analysis on the vMALDI-LTQ	Dalhousie U.
	Julie Marr ¹ , Michael Zumwalt ¹ , John Hughes ¹ , Matthew Slawson ² , Chad Borges ² , Dennis Crouch ²	Analysis of Anabolic Substances Using the Agilent G6410A Triple Quadrupole LC/MS/MS	¹ Agilent Technologies, ² U. Utah
	Robert Read	Quantitative LC-MS-MS methods applied to the study of percutaneous poisoning by the organophosphorus nerve agent VX	Defence Science & Technology Laboratory
	Brigitte L. Simons ¹ , Guanghui Wang ² , Rong-Fong Shen ² , and Mark A. Knepper ¹	In Vacuo Isotope Coded Alkylation Technique (IVICAT); a novel approach for LC-MS/MS quantitative phosphotyrosine proteomics of the rat kidney inner medullary collecting duct	NIH
	Hoe Chee Chua	Screening of Nitrogen Mustards and their degradation products in water and decontamination emulsion using LC/MS	DSO National Laboratories
	Doug Olson, Uma Aryal, Steve Ambrose, Andrew Ross	S-Top And Go Extraction (STAGE) Tips for Enhanced PMF and PSD Analysis of Proteins from Silver-stained Gels	NRC
	Stacey Owen, Monika Lafond, Patricia Bowen, Carl Bogdanoff, Wilhelmina Kalt, Charles Forney, Suzanne Abrams	Plant Hormone Profiling: Quantification of Abscisic Acid and its Metabolites in Berries by LC-MS/MS	NRC
	Angela Jackson, Derek Smith, Terry Pearson, Leigh Anderson, Christoph Borchers.	Enrichment of Lower Abundance Proteins in Human Plasma Using Stable Isotope Standards and Capture by Anti-Peptide Antibodies (SISCAPA)	U. Victoria
	Mark Wall, John Tran, Chris MacDonald and Alan Doucette	An Alternative to Gels and Shotgun Proteomics: Integrated Multidimensional Parallel LC and Digestion of Intact Proteins analyzed by MALDI MS/MS	Dalhousie U.

	John C. Tran, Chris J. B. McDonald, Alan A. Doucette	Tap-ID: Targeted Protein Identification. An Algorithm Incorporating the Intrinsic Information from Gel-Free Proteome Separations and Peptide Sequencing on the vMALDI-LTQ	Dalhousie U.
	J. Larry Campbell, ¹ Paula P. Pittock, ¹ Hongfeng Yin, ² Kevin Killeen, ² Reid Brennen, ² Gilles A. Lajoie ¹	Combining Microfluidic HPLC Chip Technology with a Hybrid Triple Quadrupole Fourier Transform Ion Cyclotron Resonance Mass Spectrometer for Novel "Bottom-up" and "Top-Down" Protein Analyses	¹ U. Western Ontario; ² Agilent
	Chris McDonald, Mark Wall, Alan Doucette	A parallel LC/MALDI interface for high throughput proteomics analysis	Dalhousie U.
	Jonathan Bailey, Allan J. Cessna, John V. Headley, Marley J. Waiser, Kerry M. Peru, Sandra L. Kuchta	Investigation of the Chemical Stability of Chlortetracycline in Prairie Wetlands by LC-MS/MS	National Hydrology Research Centre
	Gordon A. Simms ¹ , John S. Klassen ² , Igor Sinelnikov ²	Influence of Internal Energy on the Dissociation of Multimeric Protein Complexes in the Gas Phase. Unraveling the subunit unfolding process	¹ Dalhousie U; ² U. Alberta
	Juan Fan, Vy Ha, Nada Kurt Stojkovic, Anita Towers, Iffat Balkhi, Chrysantha Xavier, Nicola Hughes	Method Development and Validation for the Simultaneous Determination of Carvedilol, its Metabolites O-Desmethylcarvedilol (M2), 4'-Hydroxyphenylcarvedilol (M4) and 5'-Hydroxyphenylcarvedilol (M5) in Human Plasma by LC/MS/MS	Biovail Contract Research
	Yves LeBlanc	Scheduled MRM: Quantifying Thousands of Analytes by LC/MS/MS	MSD Sciex
	J.F. Carriere; B. de Haan, R. Swart, R. van Ling	Performance of Polystyrene-Divinylbenzene Monolithic ESI Needles for Nano LC-MS/MS Peptide Sequencing	Dionex
	Paul A. D'Agostino, Claude L. Chenier, James R. Hancock, Carmela R. Jackson Lepage	Analysis of Chemical Warfare Agents by DESI-MS/MS	DRDC
	James Kapron, Bay Sheldrick	Improved Signal-to-noise Ratio in the Analysis of Clenbuterol in Urine using LC – FAIMS – H-SRM	Thermo Electron
Friday – December 1			
Chair	Gord McKay		
8:15	Liang Li	Development of Mass Spectrometric Methods for Proteomics	U. Alberta
9:00	Hannah Johnson ¹ , Stephen Wong ¹ , Robert J Beynon ² , Simon J Gaskell ¹	QconCAT Quantification of Proteins Achieved by Double Notch Isolation of Isotopic Pairs Using FT-ICR MS	¹ U. Manchester; ² U. Liverpool
9:20	Diane Mataija, Alan Doucette	Analysis of the Human Urine Proteome by MALDI-MS/MS via i) 2D-SDS-PAGE-MS/MS and ii) Solution Phase Isoelectric Focusing –Reversed Phase Liquid Chromatography-MS/MS (SPIEF-RPLC-MS/MS). Which Method is Best for Urinalysis	Dalhousie U.
9:40	Leroi V. DeSouza ¹ ; Valerie Dube ² ; Shaun Ghanny ¹ ; Joerg Grigull ¹ ; Alexander D. Romaschin ³ ; Terence J. Colgan ² ; K.W. Michael Siu ¹	Mass-Tagging Approaches to Discovery and Identification of Endometrial Cancer Biomarkers and Their Subsequent Validation Using Immunochemistry	¹ York U.; ² Mt. Sinai Hospital; ³ St. Michael's Hospital
10:00	Discussion		

10:05	Break		
10:35	Jean-Marie Schmitter, Anne Chobelet, Katell Bathany, Maria Urdaci	Characterization of biologically active compounds produced by Bacillus strains.	Institut Européen de Chimie et Biologie
10:55	Sean C Bendall ^{1,2,3} , Morag Stewart ^{2,3} , Dustin George ¹ , Paula Pittock ¹ , Li Li ² , J. Larry Campbell ¹ , Mickie Bhatia ^{2,3} , Gilles Lajoie ¹	The protein microenvironment of human embryonic stem cells: a comprehensive mass spectrometry-based proteomic approach	¹ U. Western Ontario; ² Robarts Research Institute; ³ McMaster U.
11:15	Leroi V. DeSouza, Joydeep Mukherjee, Abhijit Guha, K.W. Michael Siu	Investigation into Differential Expression of Proteins in Glioblastoma Multiforme Mutants	¹ York University, Toronto ² Hospital for Sick Children
11:35	Andrew Stopford, Perdita Barran	A Quantitative Approach to the Structural Analysis of $f\dot{O}$ -Defensins by Collision Induced Dissociation and Molecular Modelling	U. Edinburgh
11:55	Discussion		
16:30	Broomball	Canada v. World	
18:30	Banquet		
Saturday – December 2			
Chair	John Klassen		
8:15	Heather Desaire, Mary L. Bandu	DNA sequencing using ion ratios from MS/MS data	U. Kansas
9:00	Terry Cyr Diane Bertrand, Michel Girard and Barry Lorbetskie	Use of high mass accuracy in the identification of impurities in therapeutic proteins by HPLC/MS/MS	Health Canada
9:20	David M. Horn, Christine A. Miller, Tom A. van de Goor, Bryan D. Miller	The Effect of MS/MS Fragment Ion Mass Tolerance on Peptide Identification in Shotgun Proteomics	Agilent Technologies
9:40	Sean L. Seymour, Ignat V. Shilov, Alpesh A. Patel, Wilfred H. Tang, Alex Loboda, Christie L. Hunter, Lydia M. Nuwaysir, Daniel A. Schaeffer	Advances in Protein Identification Informatics	Applied Biosystem
10:00	Discussion		
10:05	Break		
10:30	Steve Pringle	Using Ion Mobility Separation to Enhance Tandem MS Performance	Waters
10:50	Lester Taylor, Vald Zabrouskov, Andreas Wiegghaus, Ulf Froehlich, Steve Horning	Advances in Orbitrap and FTICR Technologies	Thermo Electron
11:10	Gary Kruppa	Advances in FTMS Instrumentation and Software for Top-Down Proteomics	Bruker Daltonics
11:30	Francesco L Brancia, Li Ding	Exploitation of the potential of rectangular waveforms in a digital ion trap mass spectrometer	Shimadzu
11:50	Philip M. Remes, Gary L. Glish	It is Getting Colder in North Carolina - Operating an Ion Trap at Sub-Ambient Temperatures	U. North Carolina
12:10	Discussion		