Craig S. Miller[2]; [1]*University of Texas at Austin, Austin, TX;* [2]*University of Kentucky, Lexington, KY*

MP 642 **Differential Lectin Capture of Serum Glycoproteins Combined with Pre-Fractionation Methods for Prostatic Disease Biomarker Discovery**; Ellen Schwegler[1]; Gunjan Malik[1]; Michael Ward[1]; Shamina Mitchell[1]; Oliver J Semmes[1]; Richard R Drake[1]; [1]*Eastern Virginia Medical School, Norfolk, VA*

PROTEOMICS: METHODS FOR PHOSPHO PROTEINS

MP 643 **Absolute Quantification (AQUA) of Phosphorylation Levels in Biological Samples using Immobilized Metal Affinity Chromatography Enrichment (IMAC)**; Jeffrey L. Turner[1]; John G. Dapron[1]; Justin Wildsmith[1]; Jessica M. Moeller[1]; Kevin Ray[1]; Graham B. I. Scott[1]; [1]*Sigma-Aldrich Corporation, St. Louis, MO*

MP 644 **Selective Enrichment of Phosphopeptides from Peptide Mixtures by Isoelectric Focusing after Methyl-Esterification**; ChongFeng Xu[1]; Thomas A. Neubert[1]; [1]*New York University School of Medicine, New York, NY*

MP 645 **Ion Mapping Tandem Mass Spectrometry Using either a vMALDI or Nanospray Source Detects More Phosphopeptides than Neutral Loss Experiments;** Dawn Z Chen[1]; Tatiana N. Boronina[1]; Rosa Viner[2]; Robert N. Cole[1]; [1]*Johns Hopkins University, School of Medicine, Baltimore, MD;* [2]*Thermo Electron Co., San Jose, CA*

MP 646 **Separation and Detection of Protein Post-Translational Modifications by Liquid Chromatography Coupled with a Novel Ion Mobility Mass Spectrometer**; Ole N. Jensen[1]; Martin R. Larsen[1]; Jason Wildgoose[2]; Robert H. Bateman[2]; Kevin Giles[2]; Steven Pringle[2]; Chris Hughes[2]; Jim Langridge[2]; [1]*University of Southern Denmark, Odense, Denmark;* [2]*Waters Corp. MS Technologies Centre, Manchester, UK*

MP 647 **Proteomics Analysis of Effect of Casein Phosphopeptides on Metal Ion Binding**; Jiaxi Wang[1]; Kirk Green[1]; Graham McGibbon[1]; Brain McCarry[1]; [1]*McMaster University, Hamilton, Canada*

MP 648 **Complementary Analysis of Phosphorylated Proteins by MALDI and nano ESI-MS/MS**; Rosa Viner[1]; Terry Zhang[1]; Ken Miller[1]; [1]*Thermo Electron, San Jose, CA*

MP 649 **Identification and Quantification of Focal Adhesion Kinase Phosphorylation Sites using Stable Isotope Dilution Nanospray LC/MS and MRM-Initiated Detection and Sequencing**; Eugene Ciccimaro[1]; John M. Hevko Hevko[2]; Ian A. Blair[1]; [1]*Center for Cancer Pharmacology, University of Penn, Philadelphia , PA;* [2]*Applied Biosystems, Foster City, CA*

MP 650 **Identification of Insulin Receptor Phosphorylation Sites using a Novel PhosphoTip Purification Protocol**; Clifford Bolinger[1]; Jamie Graham[1]; Leslie M Frost[1]; [1]*Marshall University, Huntington, WV*

MP 651 **From the Comparison of Phosphoproteomes to a Global Phosphoproteome Database**; Søren Schandorff[1]; Ole Vorm[1]; Hans Jespersen[1]; Alexandre Podtelejnikov[1]; [1]*Proxeon, Odense, Denmark*

MP 652 **Insulin Induced-Changes of the Tyrosine Phosphoproteomes of Brown Preadipocytes and Adipocytes**; Marcus Krueger[1]; Irina Kratchmarova[2]; Blagoy Blagoev[2]; Yu-Hua Tseng[3]; C. Ronald Kahn[3]; Matthias Mann[1]; [1]*Max Planck Institute of Biochemistry, Munich, Germany;* [2]*University of Southern Denmark, Odense, Denmark;* [3]*Joslin Diabetes Center, Harvard Medical School, Boston, MA*

MP 653 **Data Dependent Electron Capture Dissociation (ECD) of Phosphorylated Proteins**; Andrew J. Creese[1]; C. Logan Mackay[2]; Stefan K. Weidt[2]; Pat Langridge-Smith[2]; Nick Morrice[3]; Helen J. Cooper[1]; [1]*University of Birmingham, Birmingham, UK;* [2]*University of Edinburgh, Edinburgh, UK;* [3]*University of Dundee, Dundee, UK*

MP 654 **Dephosphorylation Induced Chromatographic Shift and Isobaric Tagging: an Exquisitely selective and sensitive method for quantitative phosphopeptide profiling**; Duncan L Smith[1]; Andrew JK Williamson[1]; Anthony D Whetton[1]; [1]*University of Manchester, Manchester, UK*

MP 655 **High Probability MS Identification of Phosphopeptides by their Mass Defect**; Erol E. Gulcicek[1]; Mark A. Shifman[1]; Perry Miller[1]; Christopher M. Colangelo[1]; Kathryn L. Stone[1]; TuKiet T. Lam[1]; Can Bruce[1]; [1]*Yale University, New Haven, CT*

MP 656 **Dynamics of in vivo Tyrosine Phosphorylation Events to Elucidate Growth Factor Induced Pathways by High-Accuracy Orbitrap Tandem Mass Spectrometry**; Jesper V. Olsen[1]; Blagoy Blagoev[2]; Sonja Krueger[1]; Florian Gnad[1]; Boris Macek[1]; Peter Mortensen[2]; Matthias Mann[1]; [1]*Max-Planck-Institute of Biochemistry, Martinsried, Germany;* [2]*CEBI - University of Southern Denmark, Odense, Denmark*

MP 657 **Mining Phosphopeptides in LC-MS Data for Protein Phosphorylation Site Determination**; Hsin-Yi Wu[1]; Pao-Chi Liao[1]; [1]*Medical College, National Cheng Kung University, Tainan, Taiwan*

MP 658 **Shotgun^2 Tandem Collision-Induced Dissociation Mass Spectrometry of Phosphotyrosine Peptides**; Yu Shi[1]; Lauren Rosen[1]; Alexis Ramos[1]; Xudong Yao[1]; [1]*University of Connecticut, Storrs, CT*

MP 659 **Discerning Phosphorylation from Tyrosine Sulfation in a Single Polypeptide Using Nanoelectrospray Ionization Tandem Mass Spectrometry**; Lisa A. Marzilli[1]; Erin E. Wiswall[1]; Himakshi K. Patel[1]; Mike A. Jankowski[1]; Jason C. Rouse[1]; [1]*Wyeth BioPharma, Andover, MA*

MP 660 **Enhancement of Ionization Efficiency and Selective Enrichment of Phosphorylated Peptides using Polyhistidine-Tags**; Pegah R Jalili [1]; Deepti Sharma[1]; Haydn Ball[1]; [1]*University of Texas Southwestern Medical Center, Dallas , TX*

MP 661 **Direct Determination of Dialkyl Phosphates (DAPs) by Strong Anion Exchange Atmospheric Pressure Chemical Ionization (APCI) LC-MS-MS**; W. M. Draper, P. Behniwal, D. Wijekoon, *Sanitation and Radiation Laboratory Branch, California Department of Health Services, 850 Marina Bay Parkway, Richmond, CA*

TUESDAY POSTERS

ISOTOPE RATIO MS

TP 9 **Determination of High-Precision Isotope Ratios from Experimental Isotopic Distributions**; Parminder Kaur[1]; Peter B. O'Connor[1]; [1]*Boston University, Boston, MA*

TP 10 **The 13C/12C Ratio Analyses of CO2 in Human Breath of Suspected Helicobactor pylori Infection using Continuous Flow GC/IRMS**; Chul-Min Shin[1]; Won-Gi An[1]; Jong-Jin Lee[1]; Yoon-Jin Lee[1]; Hae-Seon Nam[1]; Sung-Ho Kim[1]; [1]*Soonchunhyang University, Asan, South Korea*

TP 11 **Simultaneous Pulse Counting Detection of Isotopic Ion Beams using a Microchannelplate Array**; Peter J. Todd[1]; Henry S. McKown[1]; [1]*Oak Ridge National Laboratory, Oak Ridge, TN*

TP 12

PARTICLE ANALYSIS

TP 13 **Exploration of the Laser Desorption and Ionization Process of Individual Aerosol Particles**; Erica L. McJimpsey[1]; Paul T. Steele[2]; George R. Farquar[2]; David P. Fergenson[2]; Sue I. Martin[2]; Matthias Frank[2]; Eric E. Gard[2]; Herbert J. Tobias[2]; Carlito B. Lebrilla[1]; [1]*University of California-Davis, Davis, CA;* [2]*Lawrence Livermore National Laboratory, Livermore, CA*

TP 14 **Lithium Ion Attachment as a Soft Ionization Approach for Detection of Organic Species in the Aerodyne AMS**; Achim M Trimborn[1]; John Jayne[1]; Megan Northway[1]; Doug Worsnop[1]; *[1]Aerodyne Research Inc., Billerica, MA*

TP 15 **Spectra Analysis for Aerosol Particles Measured in Parallel with Two Online TOF Laser Mass Spectrometers LAMPAS 2 and SPASS**; Klaus-Peter Hinz[1]; Nicole Erdmann[2]; Carsten Grüning[3]; Bernhard Spengler[1]; *[1]University of Giessen, Giessen, Germany; [2]University of Mainz, Mainz, Germany; [3]Joint Research Center Ispra, Ispra, Italy*

TP 16 **Application of Non-Resonant Laser Ablation Mass Spectrometry for Fast Isotope Analysis of Metal Microparticles**; Kyuseok Song[1]; Bowha Ahn[1]; Sunho Han[1]; Yongjoon Park[1]; Wonho Kim[1]; *[1]Korea Atomic Energy Research Institute, Taejeon, Korea*

HYDROCARBONS AND PETROCHEMICALS BY FTMS

TP 17 **Automated Field Desorption FT-ICR MS for Petroleum Analysis**; Donald F. Smith[1]; Tanner M. Schaub[2]; Christopher L. Hendrickson[2]; Ryan P. Rodgers[2]; Alan G. Marshall[2]; *[1]Department of Chemistry and Biochemistry, Tallahassee, FL; [2]Ion Cyclotron Resonance Program, NHMFL, FSU, Tallahassee, FL*

TP 18 **Analysis of High Boiling Petroleum Products by LC/MS**; Jennifer Huang[1]; Charlie Van Wandelen[1]; Ray Chen[1]; Chris Loran[1]; *[1]Thermo Electron Corp., San Jose, California*

TP 19 **Detailed Compositional Comparison of Acidic NSO Compounds Before and After Bioremediation of Crude Oil-Contaminated Soil**; Samantha A. Galasso[1]; Christine A. Hughey[1]; *[1]Chapman University, Orange, CA*

TP 20 **A Comprehensive Comparison of the Polar NSO Compounds in a Suite of Biodegraded Oils by ESI FT-ICR MS**; Geoffrey C Klein[1]; Ryan P Rodgers[1]; Barry Bennett[2]; Steve R Larter[2]; Alan G Marshall[1]; *[1]NHMFL, Tallahassee, FL; [2]University of Calgary, Calgary, Canada*

TP 21 **Isolation and Characterization of Crude Oil Asphaltenes and Coprecipitants by Negative-Ion Electrospray Ionization FT-ICR Mass Spectrometry**; Do-Gyun Kim[1]; Jeremiah M. Purcell[2]; Ryan P. Rodgers[1]; Alan G. Marshall[2]; *[1]National High Magnetic Field Laboratory, FSU, Tallahassee, Florida; [2]Department of Chemistry and Biochemistry, FSU, Tallahassee, Florida*

TP 22

TP 23 **Detailed Compositional Characterization of Water-in-Oil Emulsion Stabilizers in Canadian Bitumens by ESI FT-ICR MS**; Lateefah A Stanford[1]; Don Smith[1]; Jan Czarnecki[2]; Alex Wu[2]; Ryan P Rodgers[1]; Alan G Marshall[1]; *[1]NHMFL-FSU, Tallahassee, Fl; [2]Syncrude Research, Edmonton, Canada*

METABOLITE PROFILING AND IDENTIFICATION: APPLICATIONS

TP 24 **Identification of An Unusual Defluorination-GSH Conjugate Using Linear Ion Trap Mass Spectrometer**; Ji Ma[1]; Robert Cho[1]; Jianxia Shi[1]; Shichang Miao[1]; Chun Li[2]; Craig Uyeda[1]; Monica Sweany[1]; Meghan Canfield[1]; George Tonn[1]; *[1]Amgen Inc, South San Francisco, USA; [2]Amgen, Thousand Oaks, USA*

TP 25 **Metabolite Identification using LC/LTQ/Orbitrap with Accurate Mass Measurement at 60,000 Resolution of Precursor/Product Ions from Data-Dependent Mass Analysis**; H.K. Lim[1]; Carlo Sensenhauser[1]; Jie Chen[1]; Kevin L. Cook[1]; Vangala Subrahmanyam[1]; *[1]J&J Pharmaceutical Research & Development, Raritan, NJ*

TP 26 **Metabolic Interspecies Comparison, by LCMS and Principle Component Analysis**; Elliott Jones[1]; Ji Ma[2]; Sasaki Tania[1]; Robert Cho[2]; *[1]Appliedbiosystems, Foster City, CA; [2]Amgen, South San Francisco, CA*

TP 27 **A Novel DynamicFlow System for Sensitive Radioisotope Detection and Structural Elucidation**; Dian Y. Lee[1]; Kevin Hsu[1]; *[1]AIM Research Co., Hockessin, DE*

TP 28 **MS/MS Characterization of New Sulfate Metabolites of Aristolochic Acid I**; Robert A. Rieger[1]; Horacio Priestap[1]; Tomoko Freshwater[2]; David R. Taft[2]; M.Cecilia Torres[1]; Charles R. Iden[1]; *[1]State University of New York at Stony Brook, Stony Brook, NY; [2]Long Island University, Brooklyn, NY*

TP 29 **Investigation of Metabolic Pathways in *Desulfovibrio v.* by ESI FT-ICR;** Francesco Pingitore[1]; Yinjie Tang[1]; Aindrila Mukhopadhyay[1]; Jay Keasling[1]; *[1]University of California, Berkeley, Berkeley, CA*

TP 30 **Analysis of Ceramides in Body Fluids by Electrospray LC/MS/MS**; Jie Chen[1]; Srinivas B. Narayan[1]; Michael J. Bennett[1]; *[1]Children's Hospital of Philadelphia, Philadelphia, PA*

TP 31 **Profiling of Urinary Metabolites;** Vladimir V. Tolstikov[1]; Kindra D. Brooks[1]; Robert H. Weiss[2]; *[1]UC Davis Genome Center, Davis, CA; [2]Div. Of Nephrology, UC Davis, Davis, CA*

TP 32 **Stereoselective metabolism of methadone by human liver microsomes and cDNA-expressed P450s**; Yan Chang[1]; Shen-Nan Lin[1]; David E Moody[1]; *[1]University of Utah, Salt Lake City, UT*

TP 33 **Chiral and Achiral LC/MS for Studies on the Formation of Hydroxylated Metabolites of Ketamine**; Joelle Onorato[1]; Peter Bullock[2]; Maria E. Rodriguez-Rosas[1]; Irving Wainer[1]; *[1]NIH/NIA, Baltimore, MD; [2]Panacos, Rockville, MD*

TP 34 **Identification of a metabolite of atrazine, N-ethyl-6-methoxy-N'- (1-methylethyl)-1,3,5-triazine-2, 4-diamine, upon incubation with rat liver microsomes**; Aiqun Li[1]; Matthew P. May[1]; James C Bigelow[1]; *[1]Idaho State University, College of Pharmacy, Pocatello, Idaho*

TP 35 **High Performance Liquid Chromatography followed by Post Source Decay Laser Desorption Ionization Mass Spectrometry for Retinoid Characterization from Retinol Metabolism**; Moo-Jin Suh[1]; Xiaohan Tang[1]; Lorraine J Gudas[1]; *[1]Weill Medical College of Cornell University, New York, NY*

TP 36 **Metabolite Detection and Characterization by High-Resolution Orbitrap Mass Spectrometry: Application of Mass Defect and Product Ion Filtering Techniques**; Qian Ruan[1]; Scott Peterman[2]; Mark A. Szewc[2]; Li Ma[1]; Dan Cui[1]; W. Griffith Humphreys[1]; Mingshe Zhu[1]; *[1]Bristol-Myers Squibb Company, Princeton, NJ ; [2]Thermo Electron Corp, Somerset, NJ*

TP 37 **LC-FTMS for High-Throughput Analysis of Oxidative Stress Biomarkers in Human Plasma**; Jennifer M. Johnson[1]; Frederick H Strobel[1]; Dean P. Jones[1]; *[1]Emory University, Atlanta, GA*

TP 38 **Characterization of Microsomal Metabolism of BML-190, a CB2 Selective Agonist by HPLC-MS/MS**; Qiang Zhang[1]; Peng Ma[1]; Richard B Cole[2]; Guangdi Wang[1]; *[1]Xavier University of LA, New Orleans, LA ; [2]University of New Orleans, New Orleans, LA*

TP 39 **Qualitative Reaction Phenotyping of P450 Isozymes involved in the Metabolism of Selegiline to Desmethylselegiline and Methamphetamine**; Salete Benetton[1]; Che Fang[1]; Yanou Yang[1]; Ramya Alok[1]; Mey Year[1]; Chin-Chung Lin[1]; Li-Tain Yeh[1]; *[1]Valeant Research & Development, Costa Mesa, CA*

TP 40 **Combining MDF and PeakMatch Techniques for Comprehensive and Selective Detection of Drug Metabolites in Vivo**; Haiying Zhang[1]; Mingshe Zhu[1]; Li Ma[1]; Kan He[1]; W. Griffith Humphreys[1]; Mark Sanders[1]; *[1]Bristol-Myers Squibb, Princeton, NJ*

TP 41 **Drug Metabolism of Curcumin by Liquid Chromatography Tandem Mass Spectrometry (LC-MS-MS) on a hybrid quadrupole linear ion trap system**; Constantin Tamvakopoulos[1]; Zacharias D. Sofianos[1]; Spiros D. Garbis[1]; James Wyche[2]; Zhiyong Han[2]; Panayotis Pantazis[1]; [1]*Biomedical Research of the Academy of Athens, Athens, Greece;* [2]*Oklahoma University Health Sciences Center, Oklahoma City, OK*

TP 42 ***In vitro* Metabolism of Abyssinone II, a Potential Anticancer Agent from *Broussonetia papyrifera* (L.)**; Yan Pang[1]; John M. Pezzuto[2]; Richard B. van Breemen[1]; [1]*University of Illinois College of Pharmacy, chicago, Illinois;* [2]*Purdue University School of Pharmacy, West Lafayette, Indiana*

TP 43 **Metabolite Identification of Ac-CHAVC-NH2 in Human Plasma using LC-MS/MS**; Qiao Zhan[1]; Mark Bednarcik[2]; Jonathan Green[1]; [1]*Research Triangle Institute, International, RTP, NC;* [2]*Adherex Technologies Inc., Durham, NC*

TP 44 **The Power of Hyphenated Technologies Combined with Traditional Approaches in Degradation Chemistry Investigation: A Case Study on Vitamin D**; Fa Zhang[1]; [1]*Johnson & Johnson CPWW, Skillman, NJ*

TP 45 **Identification of in vitro and in vivo Metabolites of Degarelix, a GnRH (Gonadotropin-Releasing Hormone) Receptor Blocker, by LC-MS**; Anders Sonesson[1]; Birgitte Buur Rasmussen[1]; [1]*Ferring Pharmaceuticals A/S, Copenhagen, Denmark*

METABOLITE PROFILING AND IDENTIFICATION METHODS

TP 46 **A High Throughput Approach for Metabolite Profiling and Characterization Using a Linear Ion Trap Mass Spectrometer**; Min He[1]; Alicia Du[1]; Gargi Choudhary[1]; Diane Cho[1]; [1]*Thermo Electron, San Jose, CA*

TP 47 **Metabolomics: Using Electrochemistry / MS to Investigate Biological Metabolite Identification**; David F. Meyer[1]; Michael C. Granger[1]; Qi Zhang[1]; Milind P. Nagale[1]; Ian Acworth[1]; Paul H. Gamache[1]; [1]*ESA Biosciences, Chelmsford, MA*

TP 48 **Identification of in vivo Metabolites: Challenges and Solutions using an LTQ Orbitrap**; Young G. Shin[1]; Teresa Dong[1]; Alica Du[2]; Vlad Zabrouskov[2]; Yan Chen[2]; Patrick J. Rudewicz[1]; [1]*Genentech, South San Francisco, CA;* [2]*Thermo Electron, San Jose, CA*

TP 49 **Custom Software to Expedite Qualitative and Quantitative Profiling of Drug Metabolites**; Robert Langish[1]; Jonathan Josephs[1]; Mary Grubb[1]; Petia Shipkova[1]; Mark Sanders[2]; [1]*Bristol-Myers Squibb, Hopewell, NJ;* [2]*Bristol-Myers Squibb, Lawrenceville, NJ*

TP 50 **Metabolite Identification using Multivariate Data Analysis and Energy Resolved Mass Spectrometry**; Shom N. Paul[1]; Sarah Rutan[1]; [1]*Virginia Commonwealth University, Richmond, VA*

TP 51 **Accurate Mass Measurements of Product Ions for Metabolite Identification on Unit Mass Resolution Mass Spectrometers**; Jianyao Wang[1]; Ming Gu[2]; Yongdong Wang[2]; [1]*Wyeth Pharmaceuticals, Collegeville, PA;* [2]*Cerno Bioscience, Monmouth Junction, NJ*

TP 52 **The Impact of the "Reversed Energy Ramp" Scan Function on Metabolite Identification at or Below 1uM on a Triple Quadrupole**; Louis Maljers[1]; [1]*Thermo Electron, San Jose, CA*

TP 53 **Semiquantitation of Diclofenac Metabolites using a Triversa Nanospray Source Interface and Comparison with a Conventional Electrospray Interface**; Mary F. Grubb[1]; Jonathan Josephs[1]; Gary A. Schultz[2]; [1]*Bristol-Myers Squibb, Pennington, NJ;* [2]*Advion BioSystems, Inc., Ithaca, NY*

TP 54 **Binding Affinity of the Immobilized β-Cyclodextrin with Urinary Androgens and Estrogens**; Ju-Yeon Moon[1]; Man Ho Choi[1]; [1]*Korea Institute of Science and Technology, Seoul, Korea*

TP 55 **Withdrawn**

TP 56 **Online Class-based HPLC Separation/Time-of-flight Mass Spectrometry for Profiling of Structural Lipids and Oxylipins of *Arabidopsis thaliana*;** Michael C. Stagliano[1]; A. Daniel Jones[1]; Heidi Appel[2]; Jack C. Schultz[2]; [1]*Michigan State University, East Lansing, MI;* [2]*The Pennsylvania State University, University Park, PA*

TP 57 **Detection and Enhanced Characterization of Low-Level Metabolites by Peak Parking And LC-MSn**; Miao Zhuang[1]; Prakash Chandra[1]; [1]*Pfizer Global Reserach & Development, Groton, CT*

TP 58 **Identification of Metabolites from Phosphate Based HPLC Systems using 96 Well Fraction Collection, Off Line Counting and LC/MSn**; Richard Clayton[1]; Brian Morrison[1]; [1]*Covance Laboratories, Harrogate, United Kingdom*

TP 59 **Biosynthesis,Isolation and Stability of Retigabine N-Glucuronide by HPLC and LC-MS/MS**; Hong Kim[1]; Nanqun Zhu[1]; Chin-Chung Lin[1]; Li-Tain Yeh[1]; [1]*Valeant Pharmaceutical, Costa Mesa, CA*

TP 60 **Automated Data Dependent™ Precursor Ion MS³ for Identification of Biotransformations using an Ion Trap Mass Spectrometer**; Marta Kozak[1]; Gargi Choudhary[1]; Diane Cho[1]; [1]*Thermo Electron, San Jose, CA*

METABOLISM XENOBIOTICS

TP 61 **A Novel Approach to Metabolite Detection and Identification by the Use of UPLC-Hybrid Quadrupole-Travelling Wave-IMS-oaTof**; Jose Castro-Perez[1]; John Shockcor[1]; Kevin Giles[2]; Steve Pringle[2]; Robert Bateman[2]; Alan Millar[2]; Iain Beattie[3]; Jason Wildgoose[2]; [1]*Waters Corporation, Milford, MA;* [2]*Waters MS Technology, Manchester, UK;* [3]*AstraZeneca, Loughborough, UK*

TP 62 **Complete Characterization of ML3403 Metabolites from Liver Microsomes using ESI-Qq-TOF-MS and LC-SPE-cryo NMR/MS**; Holger Scheible[1]; Stefan Laufer[1]; Wolfgang Albrecht[2]; Gabriela Zurek[3]; Manfred Spraul[4]; Markus Godejohann[4]; Bernd Kammerer[1]; [1]*University of Tübingen, Tuebingen, Germany;* [2]*Merckle GmbH, Ulm, Gerrmany;* [3]*Bruker Daltonik GmbH, Bremen, Germany;* [4]*Bruker BioSpin GmbH, Rheinstetten, Germany*

TP 63 **Automated on-Line Column-Switching HPLC-MS/MS Method for the Determination of Five Parabens in Urine**; Xiaoyun Ye[1]; Amber Bishop[1]; Larry L. Needham[1]; Antonia M. Calafat[1]; [1]*Centers for disease control and prevention, Atlanta, GA*

TP 64 **Systematic Approaches in Phytochemical Determination using Mass Spectrometry**; Qingguo Tian[1]; Mark Failla[1]; Gary Stoner[1]; Steven Schwartz[1]; [1]*The Ohio State University, Columbus, OH*

TP 65 **Structure Elucidation of M15, a Motexafin Gadolinium (MGd) Metabolite**; Purvi Jejurkar[1]; Wenchen Luo[1]; Alice Lin[1]; Chitra Mani[1]; Garry Boswell[1]; Dale Miles[1]; [1]*Pharmacyclics, Inc., Sunnyvale, CA*

TP 66 **Simultaneous Measurement of Multiple Hemoglobin Adducts of Environmental Chemicals by HPLC/MS/MS**; Maria P. Ospina[1]; Enada Archibold[1]; Tunde Meyers[1]; Antoinette Smith[1]; Leigha Ingham[1]; Gary L. Myers[1]; Hubert Vesper[1]; [1]*CDC, Atlanta, GA*

TP 67 **Etoposide Glucuronidation is Specifically Catalyzed by Human UGT1A1: Structural Characterization of Glucuronide Conjugates and Estimation of Enzyme Kinetics by LC-ESI-MS**; Zhiming Wen[1]; Melanie N. Tallman[1]; Shazia Y. Ali[1]; Philip C. Smith[1]; [1]*University of North Carolina at Chapel Hill, Chapel Hill, NC*

TP 68 **Identification of Plant Metabolites Using Accurate Mass, MS/MS, and MSn Data**; Sara J. Linder[1]; Jeffrey R. Gilbert[1]; Roobina I. Baloch[1]; Jesse L. Balcer[1]; Carla N. Yerkes[1]; Gerrit J. Deboer[1]; [1]*Dow AgroSciences, Indianapolis, IN*

TP 69 **Development of Automated Software for Creation of Metabolite LC/MS Methods for a QQQ/LIT Hybrid Mass Spectrometer;** Claire J Bramwell-German[1]; Eva Duchoslav[2]; Elliott Jones[1]; Robert Campbell[3]; [1]*Applied Biosystems, Foster City, CA;* [2]*Sciex, Concord, ON, Canada;* [3]*Theravance, South San Francisco, CA*

TP 70 **The Use of Liquid Chromatography Tandem Mass Spectrometry to Identify Drug Metabolites Produced by Cunninghamella elegans**; Annica Tevell[1]; Marina Lushnikova[2]; Ulf Bondesson[3]; Mikael Hedeland[3]; [1]*Uppsala University, Uppsala, Sweden;* [2]*HFL, Fordham, United Kingdom;* [3]*National Veterinary Institute, Uppsala, Sweden*

TP 71 **On-Line Solid-Phase ESI-MS/MS Analyses Revealed the Association between Glutathione S-Transferase Genetic Polymorphism and the Urinary Metabolic Profile of Benzene Exposure**; Lung-Cheng Lin[1]; Yin-Mei Chiung[2]; Wan-Jou Cheng[1]; Tung-Sheng Shih[2]; Pao-Chi Liao[1]; [1]*National Cheng Kung University, Tainan, Taiwan;* [2]*Institute of Occupational Safety and Health, Taipei, Taiwan*

TP 72 **Optimization of a Linear Ion Trap Mass Spectrometer for Structural Elucidation of Metabolites**; Jim M Schmidt[1]; Aixia Sun[1]; Charles P Cruz[1]; Ling Li[1]; Liam B. Moran[1]; [1]*Lexicon Genetics, The Woodlands, TX*

TP 73 **Increased Sensitivity of the Altrenogest Glucuronide in Liquid Chromatography Tandem Mass Spectrometry by Chemical Derivatization**; Matilda Lampinen Salomonsson[1]; Elin Beckman[1]; Ulf Bondesson[2]; Mikael Hedeland[2]; [1]*Uppsala University, Uppsala, Sweden;* [2]*National Veterinary Institute, Uppsala, Sweden*

TP 74 ***In Vitro*** **Metabolism of Vorinostat (Suberoylanilide Hydroxamic Acid), a Novel Anticancer Agent**; Natasa D. Pajkovic[1]; Kenneth A. Koeplinger[1]; Maribeth P. Baker[1]; Eric D. Soli[2]; Scott E. Fauty[1]; Punam Sandhu[1]; [1]*Merck Research Laboratories, West Point, PA;* [2]*Merck Research Laboratories, Rahway, NJ*

TP 75 **Collision-Induced Dissociation of Metal Complexes to Identify Isomeric Flavonoid Glucuronide Metabolites**; Barry D. Davis[1]; Paul W. Needs[2]; Paul A. Kroon[2]; Jennifer S. Brodbelt[1]; [1]*The University of Texas at Austin, Austin, TX;* [2]*The Institute of Food Research, Norwich, United Kingdom*

QUANTITATIVE ANALYSIS OF DRUGS AND METABOLITES II

TP 76 **A Highly Sensitive and Specific LC/MS/MS Method for Quantitation of Methotrexate and Its 7-Hydroxy Metabolite in Human Plasma**; Yong-Xi Li[1]; Dawei Zhou[1]; [1]*XenoBiotic Laboratories, Inc., Plainsboro, NJ*

TP 77 **Study of Atmospheric Pressure Chemical Ionization and Electrospray Ionization Mass Spectrometric Quantitative Analysis for Lopinavir and Ritonavir**; Jun Zhang[1]; Qin Ji[1]; Tawakol El-Shourbagy[1]; [1]*Abbott Laboratories, Abbott Park, IL*

TP 78 **LC/MS/MS Determination of Fluoxetine and Norfluoxetine in Equine Biological Fluids**; Jhoana A. Mendoza[1]; Keith D. Zientek[2]; Patrick T. Colahan[3]; Cynthia A. Cole[2]; John R. Eyler[1]; [1]*University of Florida, Gainesville, FL;* [2]*UF, College of Vet. Med., Racing Laboratory, Gainesville, FL;* [3]*UF, College of Veterinary Medicine, Gainesville, FL*

TP 79 **Simultaneous Determination of Ribavirin and Ribavirin Base in Monkey Plasma Using Liquid Chromatography with Tandem Mass Spectrometry**; Wenkui Li[1]; Suyi Luo[1]; Shaoyong Li[1]; Lawrence Athill[1]; Amy Wu[1]; Tapan Ray[1]; Wei Zhou[1]; June Ke[1]; Francis Tse[1]; [1]*Novartis Pharmaceuticals Corporation, East Hanover, NJ*

TP 80 **Quantitation of Norelgestromin in Human Plasma via HPLC with MS/MS Detection**; Moucun Yuan[1]; Jingduan Chi[1]; Rand Jenkins[1]; Bruce Hidy[1]; [1]*PPD, Richmond, VA*

TP 81 **Solving the Plasma Mycophenolic Acid Analytical Challenges: A Validated Liquid Chromatography/Tandem Mass Spectrometry Quantitation Method**; Ling Zhu[1]; Andrew Cooper[1]; J.J. Thiessen[2]; [1]*Allied Research International, Mississauga, Canada;* [2]*School of Pharmacy, University of Waterloo, Waterloo, Canada*

TP 82 **A Novel APCI LC-MS/MS Method for the Determination of Finasteride in Human Plasma**; Michael Deng[1]; Heather Wan[1]; Andrew Cooper[1]; J.J. Thiessen[2]; [1]*Allied Research International, Mississauga, Canada;* [2]*School of Pharmacy, University of Waterloo, Waterloo, Canada*

TP 83 **High Performance Liquid Chromatography-Tandem Mass Spectrometric Determination of N-methyl-4-isoleucine-cyclosporin (NIM811) in Human Whole Blood**; Suyi Luo[1]; Lawrence Athill[1]; Wenkui Li[1]; Michael Hayes[1]; Handan He[1]; Francis Tse[1]; [1]*Novartis Pharmaceuticals Corporation, East Hanover, NJ*

TP 84 **Trouble-Shooting and Redevelopment of an Assay for Compound A with an Analog Internal Standard in Rabbit Plasma using LC/MS**; Jingduan Chi[1]; Neal Simmons[1]; Rand Jenkins[1]; [1]*PPD, Richmond, VA*

TP 85 **Determination of Chlorpromazine in Rat Plasma and Brain Tissue by LC MS/MS**; Guodong Zhang[1]; Alvin V. Terry[1]; Michael G. Bartlett[1]; [1]*Department of PBS, School of Pharmacy, UGA, Athens, GA*

TP 86 **Stability Studies of Vorinostat and Its Two Metabolites in Human Plasma, Serum and Urine**; Lihong Du[1]; Donald Musson[1]; Amy Wang[2]; [1]*Merck Research Lab, west point, PA;* [2]*GlaxoSmithKline Pharmaceutical, King of Prussia, PA*

TP 87 **Single Mass Spectrometry Method for the Determination of Nevirapine in Human EDTA K_2 Plasma using Automated SPE Extraction;** Jean Couture[1]; Nadia Smith[1]; Marie-Claude Théberge[1]; François Vallée[1]; [1]*SFBC Anapharm, Ste-Foy, QC, Canada*

TP 88 **Quantitative Analysis of Valacyclovir Following Automated Protein Precipitation**; Matthew Amundson[1]; Melissa Meyer[1]; Darren Hoffman[1]; Laura Baum[1]; Andrew Osenga[1]; Dan Aufman[1]; Ardeshir Khadang[1]; [1]*PRACS Institute, Fargo, ND*

TP 89 **Advantages of using Tetrahydrofuran-Water Mobile Phases in Quantitative Determination of Cyclosporin A in Monkey Plasma**; Yinghe Li[1]; Austin C. Li[1]; Wilson Z. Shou[1]; Xiangyu Jiang[1]; [1]*Covance Laboratories, Inc., Madison, WI*

TP 90 **Simultaneous Quantification of Tenofovir Diphosphate and Emtricitabine Triphosphate in Human and Macaque Primary Lymphocytes**; David C Delinsky[1]; Brenda I Hernandez-Santiago[1]; Raymond F Schinazi[1]; [1]*Emory University / VA Medical Center, Decatur, GA*

TP 91 **Overcome Selectivity Issues in Developing a Rugged LC-MS/MS Method for Dextromethorphan and Dextrorphan in Human Plasma**; Ernest YK Wong[1]; Dezhong Liu[1]; Anita Towers[1]; Nicola Hughes[1]; [1]*Biovail Contract Research, Toronto, Ontario, Canada*

TP 92 **Determination of Steviosede in Mouse Plasma by Use of Automated 96-Well SPE and LC/MS/MS**; Seung Kwon Yang[1]; Moon-Sun Jang[1]; Kyung Ryul Lee[2]; Hee Joo Lee[1]; Seungwoo Kang[1]; [1]*BioCore Co., Ltd, Seoul, Korea;* [2]*Seoul Medical Science Institute, Seoul, Korea*

TP 93 **High-Throughput LC-MS/MS Analysis of Sirolimus in Whole Blood by Automated Protein Precipitation and Solid-Phase Extraction**; Aimin Tan[1]; Peter Hang[1]; Rajah

Uthaya[1]; Jean Couture[2]; Saleh Hussain[1]; Francois Vallee[2]; *[1]SFBC Anapharm (Richmond Hill), Richmond Hill, ON, Canada; [2]SFBC Anapharm (Quebec), Ste-Foy, QC, Canada*

TP 94 **Determination of an Immunosuppressant Mycophenolic Acid and Its Prodrug Mycophenolate Mofetil in Human Plasma by A High Throughput LC/MS-MS Platform**; V Srivatsan[1]; A K Dasgupta[1]; Prashant Kale[1]; Sandeep Sharma[1]; Gunjan Soni[1]; *[1]Lambda Therapeutic Research Ltd., Ahmedabad, INDIA*

TP 95 **A Novel Approach to Quantify Unbound Cisplatin, Carboplatin and Oxaliplatin in Human Plasma Utlrafiltrate by Measuring Platinum-DDTC Complex Using LC/MS/MS;** Min Meng[1]; Ryan Kuntz[1]; Al Fontanet[1]; Patrick K. Bennett[1]; *[1]Tandem Labs, Salt Lake City, UT*

TP 96 **Strategy for Negative and Positive ESI Assay for High Throughput Analysis of Levosimendan and Its Metabolites in Human Plasma Samples**; Qin Ji[1]; Jun Zhang[1]; Tawakol El-Shourbagy[1]; *[1]Abbott Laboratories, Abbott Park, IL*

TP 97 **An Unusual High Percentage of Aqueous Mobile Phase to Achieve Maximum Sensitivity in LC-MS Bioanalysis of Penciclovir**; Guy Thériault[1]; Vincent Moreau[1]; Malika Madi[1]; Troy Bradley[1]; Fabio Garofolo[1]; *[1]Algorithme Pharma, Laval (Montreal), Canada*

TP 98 **Exploring Different Ionization Techniques in LC-MS/MS to Optimize the Sensitivity of Tacrolimus**; Marie-Pierre Taillon[1]; Malika Madi[1]; Troy Bradley[1]; Fabio Garofolo[1]; *[1]Algorithme Pharma, Laval (Montreal), Canada*

QUANTITATIVE ANALYSIS OF DRUGS: METHOD DEVELOPMENT II

TP 99 **A General Strategy Using Mass Spectrometry as a Powerful Tool to Handle Metabolite Issues from the Drug Biotransformation**; Véronique Gauvreau[1]; Malika Madi[1]; Troy Bradley[1]; Fabio Garofolo[1]; *[1]Algorithme Pharma, Laval (Montreal), Canada*

TP 100 **Significantly Improving Quantitative LC-MSMS Analysis for Large Number of Analytes (>500) with Scheduled-MRM**; Nic Bloomfield[1]; J.C. Yves Le Blanc[1]; Byron Kieser[1]; Andre Schreiber[1]; *[1]Applied Biosystems|MDS Sciex, Concord, Canada*

TP 101 **Accelerator Mass Spectrometry (AMS) in Early Drug Development: An Ultrasensitive ADME/PK Study of a Diabetes Compound in Mice**; Ali Arjomand[1]; Ugo Zoppi[1]; Michael Chansler[1]; *[1]Accium BioSciences, Seattle, WA*

TP 102 **The Application of High Resolution Mrm in Rountine Quantitative Bioanalysis**; Mike J Redrup[1]; Caroline Clegg[1]; Derek Lewis[1]; Kun N Cheng[1]; *[1]BioDynamics Research Ltd, Rushden, Northants, United Kingdom*

TP 103 **Development of a Bioanalytical LC/MS/MS Method for the Selective Quantitation of Small Organic Acids In Plasma**; Michael G. Ma[1]; Salma Sarwary[1]; Kyung Kwon[1]; Michael B. Martin[1]; *[1]Arena Pharmaceuticals Inc., San Diego, CA*

TP 104 **Ultra Low Limits of Quantitation Utilizing LC-MS/MS with a Novel High Throughput Autosampler Technology;** Mauro Aiello[1]; Thomas Londo[2]; Thomas Covey[1]; Peter Kovarik[1]; Byron Kieser[3]; *[1]MDS Sciex, Concord, Canada; [2]Parker Life Sciences, Hollis, NH; [3]Applied Biosystems/MDS Sciex, Concord, Canada*

TP 105 **Automated Column/Mobile Phase Screening System to Achieve Optimum Chromatographic Separation and Sensitivity during LC-MS/MS Bioanalytical Method Development**; Yuan-Qing Xia[1]; Zheng Ouyang[1]; Mohammed Jemal[1]; *[1]Bristol-Myers Squibb Company, Princeton, NJ*

TP 106 **Validation of an LC-MS/MS Method for a Schering-Plough Development Compound using the Symbiosis Pharma with Direct Addition of Internal Standard**; James E. Schiller[1]; Hui Lin[1]; Roger N. Hayes, Ph.D. [1]; Dirk Hiemstra[2]; Steven Eendhuizen[2]; Valerie Cloutier[2]; *[1]Schering-Plough Research Institute, Kenilworth, NJ; [2]Spark Holland, Plainsboro, NJ*

TP 107 **Elimination of Carryover in Determination of a Cyclic Hexapeptide using LC/MS**; Michael H. Wang[1]; Kimberly Algayer[1]; Kimberly Manser[1]; Danielle Euler[1]; Henry Wu[1]; *[1]Merck & Co., Inc., West Point, PA*

TP 108 **Comparison of UPLC, TFC, and Conventional HPLC for Bioanalytical Quantitation of Preclinical Drug Candidates in the Presence of Interfering Metabolites**; Marc Browning[1]; Michael Donegan[1]; Daniel Morgan[1]; *[1]Bristol-Myers Squibb, Wallingford, CT*

TP 109 **Quantitative Analysis of HIV-1 Protease Inhibitors in Biological Matrices by MALDI-TOF Mass Spectrometry;** Jeroen J.A. van Kampen[1]; Peter C. Burgers[1]; Ronald de Groot[2]; Theo M. Luider[1]; *[1]Erasmus Medical Center, Rotterdam, The Netherlands; [2]UMC st. Radboud, Nijmegen, The Netherlands*

TP 110 **Quantitative Determination of Hydrophilic Ionic Compounds Using Gradient Chromatofocuing-Cation-Exchange LC-ESI-MS/MS**; Jianhua Tang[1]; Lian Shan[2]; Xiang Zhou[1]; Anderson J. David[1]; *[1]Cleveland State University, Cleveland, OH; [2]Frantz BioMarkers, Cleveland, OH*

TP 111 **Speed vs. Sensitivity? The Influence of Peakwidth and Flow Rate on Sensitivity in UHPLC-MS for Bioanalytical Quantitation;** Guenter Boehm[1]; Michel Wagner[1]; Paul-Gerhard Lassahn[2]; *[1]Flux Instruments AG, Basel, Switzerland; [2]Spectronex AG, Basel, Switzerland*

TP 112 **Selected Techniques for Increasing Sensitivity in Quantitative LC-MS/MS**; Mike Larson[1]; Mary Pelzer[1]; Tom Addison[1]; Xiangyu Jiang[1]; *[1]Covance Laboratories, Inc., Madison, WI*

TP 113 **Better Understanding of MALDI-MS/MS for Quantitative Analysis**; Emily D Adarayan[1]; *[1]Merck Research Labs, West Point, PA*

TP 114 **Automated and Parameter-Free Peak Integration for LC/MS/MS Quantitation**; Ming Gu[1]; Dawei Zhou[2]; Zheming Gu[2]; Yongdong Wang[1]; *[1]Cerno Bioscience, Monmouth Junction, NJ; [2]XenoBiotic Laboratories, Plainsboro, NJ*

TP 115 **Optimized High Resolution SRM Quantitative Analysis using a Calibration Correction Method on a Triple Quadrupole System;** Ya-Mei Liu[1]; Kristi Akervik[1]; Louis Maljers[1]; *[1]Thermo Electron Corporation, San Jose, CA*

TP 116 **Performance of a Novel Parameter-Less Integrator with Built-In Peak Quality Validation for Reliable Unsupervised Integration of Triple Quadrupole MRM Data**; Lee H. Altmayer[1]; Frank E. Kuhlmann[1]; *[1]Agilent Technologies Inc., Santa Clara, CA*

TP 117 **Method Development of Minimizing Carry Over in LC/MS/MS -Novel Cleaning Technique and Device**; Jun Watanabe[1]; Hiroshi Hike[2]; Yoshifumi Kogure[1]; Hansjoerg Cueni[3]; Yasuhiko Bando[2]; *[1]TAKARA BIO INC., Shiga, Japan; [2]AMR, Inc., Tokyo, Japan; [3]CTC Analytics AG, Zwingen, Switzerland*

TP 118 **Chemometric Optimization of LC-MS-MS Assay for Quantification of Candidate Drug and Three Metabolites in Plasma**; Margret Thorsteinsdottir[1]; Baldur B Sigurdsson[1]; Gisli Bragason[1]; Thorkell Andresson[1]; *[1]deCODE Genetics, Reykjavik, Iceland*

TP 119 **Quantitation of Nipride (Sodium Nitroprusside Dihdrate) in Human Plasma by ICP-MS**; Jing Ke[1]; Qian Liu[1]; Allan Xu[1]; *[1]SFBC Analytical Laboratories, Inc., North Wales, PA*

TP 120 **MALDI TOF/TOF MS and MS/MS Analysis of Fluorescently Tagged Peptides with the Fluorogenic Agent 3-(2-furoyl)-quinoline-2-carboxaldehyde**; David A. Michels[1]; *[1]Amgen Inc, Seattle, WA*

TP 121 **Guidelines for Non-Linear Regression in LC-MS Analysis**; Stephanie F. Baldrey[1]; John L. Burrows[1]; Tony A. Bates[1]; Graeme T. Smith[1]; Ian Flack[1]; Timothy P. Sangster[2]; *[1]Huntingdon Life Sciences, Alconbury, Huntingdon, United Kingdom; [2]Huntingdon Life sciences, Princeton, New Jersey*

TP 122 **Experimental Factors Affecting Accuracy and Precision in Quantitative MS Analyses**; Michael S. Alexander[1]; *[1]BASi Northwest Laboratory, McMinnville, Oregon*

REACTION INTERMEDIATES

TP 123 **Development and Application of Mass Spectrometric Methods for the Investigation of Organocatalytic Reactions**; Wolfgang Schrader[1]; Peni Handayani[1]; *[1]Max-Planck-Institut für Kohlenforschung, Mülheim / Ruhr, Germany*

TP 124 **Novel Carbon-Nitrogen (CN) ortho-Benzynes**; Michael J. Yurkovich[1]; Karinna Campbell[1]; John J. Nash[1]; Hilkka I. Kenttamaa[1]; *[1]Purdue, University, IN*

TP 125 **A d,d,d–Triradical Cation:The 2,4,6–Tridehydropyridinium Ion**; Nelson R. Vinueza[1]; Bartlomiej J. Jankiewicz[1]; Anthony Adeuya[1]; Michael J. Yurkovich[1]; John J. Nash [1]; Hilkka I. Kenttamaa[1]; *[1]Purdue University, West Lafayette, Indiana*

TP 126 **Characterization of an Exception to the "Even Electron Rule" In Negative Ion Electrospray Mass Spectrometry**; Yang Cai[1]; Zhenzhen Mo[1]; Bruce C. Gibb[2]; Bing Guan[2]; Richard B. Cole[2]; *[1]The Research Institute for Children, New Orleans, LA; [2]University of New Orleans, New Orleans, LA*

TP 127 **FT-ICR Studies on the Reactivity of Aromatic Biradicals toward Amino Acid**; George O. Pates[1]; Hilkka Kenttamaa[1]; *[1]Purdue University, West Lafayette, Indiana*

TP 128 **A Neutralization-Reionization Mass Spectrometric and Computational Study of Arginine Amide Radicals**; Xiaohong Chen[1]; František Turecek[1]; *[1]University of Washington, Seattle, Washington*

TP 129 **Mass Spectrometric Elucidation of The Free Radical Nitric Oxide-Mediated Ras Guanine Nucleotide Dissociation Mechanism using Mass Spectrometric Analyses**; Jongyun Heo[1]; Viorel Mocanu[1]; Kirk C. Prutzman[1]; Sharon L. Campbell[1]; Christoph H. Borchers[1]; *[1]University of North Carolina, Chapel Hill, NC*

TP 130 **Singlet-Triplet Splittings of Substituted Chlorinated Phenyl Nitrene: Negative Ion Photoelectron Spectroscopy;** Maria C Da Fonte[1]; Paul G Wenthold[1]; *[1]Purdue University, West Lafayette, IN*

ION STRUCTURES AND ENERGETICS

TP 131 **Low-Energy Resonant Reactions of Free Electrons and Glycine Oligomers**; Yury V Vasil'ev[1]; Benjamin J Figard[1]; Jeffrey Morré[1]; Valery G Voinov[1]; Douglas F Barofsky[1]; Max L Deinzer[1]; *[1]Oregon State University, Corvallis, OR*

TP 132 **Structure Determination by Surface-Enhanced Raman Scattering of Subzeptomole Quantities of Gas-Phase Ions after Soft Landing on Dry Metal Surfaces**; Michael Volný[1]; Atanu Sengupta[1]; Christopher B. Wilson[1]; E. James Davis[1]; František Tureček[1]; *[1]University of Washington, Seattle, WA*

TP 133 **Ab Initio Studies of Nitramine Radical Anion Fragmentation**; M. Paul Chiarelli[1]; Jan Florian[1]; Denise K. MacMillan[2]; Lan Gao[1]; Vladimir Zhukhovskyy[1]; *[1]Loyola University, Chicago, IL; [2]USACE, Omaha, NE*

TP 134 **Collisionally-Induced Dissociation of Famotidine, Folic Acid and Azithromycin: Mechanisms of Ion Formation Using Hydrogen/Deuterium Exchange and Electrospray Ionization Mass Spectrometry**; Kevin Colizza[1]; Patrick Jeanville[2]; Amin, M Kamel[1]; *[1]Pfizer Global Research and Development, Groton, CT; [2]Thermo Electron Corporation, West Palm Beach, FL*

TP 135 **Studies on Facile McLafferty-type Rearrangements Shown by Certain Substituted Carboxylate Anions**; J. Stuart Grossert[1]; Matthew C. Cook[1]; Robert L. White[1]; *[1]Dalhousie University, Halifax, NS, Canada*

TP 136 **Density Functional Theory Examinations of the Fragmentation Reactions of Amino-Acid Radical-Cations Containing Aromatic Side-Chains (Phenylalanine•+, Tyrosine•+, and Tryptophan•+)**; Chi-Kit Siu[1]; Yuyong Ke[1]; Junfang Zhao[1]; Alan C. Hopkinson[1]; K. W. Michael Siu[1]; *[1]York University, Toronto, Canada*

TP 137 **Sodium Ion Affinities of Commonly Used MALDI Matrices Determined by Guided Ion Beam Tandem Mass Spectrometry and Theoretical Studies**; S.D.M Chinthaka[1]; M.T. Rodgers[1]; *[1]Wayne State University, Detroit, MI*

TP 138 **TPEPICO Investigation of the Acetone Radical;** Emma E. Rennie[1]; Anne-Marie Boulanger[1]; Paul M. Mayer[1]; David M. P. Holland[2]; David A. Shaw[2]; Louise Cooper[3]; Christopher A. F. Johnson[3]; John E. Parker[3]; *[1]University of Ottawa, Ottawa, Canada; [2]Daresbury Laboratory, Daresbury, Warrington, England; [3]Heriot-Watt University, Edinburgh, Scotland*

TP 139 **Relative Ca2+ Affinities of Amino Acids Determined by Using the Kinetic Method**; Ming-Wei Yang[1]; Yen-Peng Ho[1]; *[1]National Dong Hwa University, Hualien, Taiwan, R.O.C.*

TP 140 **Generation and Fragmentation Mechanisms of Two Isomeric Histidine Radical Cations in the Gas Phase**; Junfang Zhao[1]; Yuyong Ke[1]; Udo H. Verkerk[1]; Alan C. Hopkinson[1]; K. W. Michael Siu[1]; *[1]York University, Toronto, Canada*

TP 141 **Theoretical and Experimental Investigation of the Energetics of Cis-Trans Proline Isomerization in Peptide Models**; Jennifer L. Poutsma[1]; Olivia E. Schroeder[2]; Emily Carper[2]; Joshua J. Wind[2]; Felicia A. Etzkorn[3]; John C. Poutsma[2]; *[1]Old Dominion University, Norfolk, VA; [2]College of William and Mary, Williamsburg, VA; [3]Virginia Tech, Blacksburg, VA*

TP 142 **Thermochemical Studies of o-, m- and p-quinomethane**; Silvi A. Chacko[1]; Paul G. Wenthold[1]; *[1]Department of Chemistry, Purdue University, West Lafayette, IN*

TP 143 **Anion Photoelectron Spectroscopy of Collision Cooling Negative Ions**; Xue-Bin Wang[1]; Hin-Koon Woo[1]; Lai-Sheng Wang[1]; *[1]Washington State University, Richland, WA*

TP 144 **Uranyl Nitrate Interactions with Formamide and Acetamide Ligands Studied by Electrospray Ionization Ion Trap Mass Spectrometry**; Garold L. Gresham[1]; Tate R. Crain[1]; Amy Custer[1]; J. Sigrid Barklund[1]; Michael J. Van Stipdonk[2]; Gary S. Groenewold[1]; *[1]Idaho National Laboratory, Idaho Falls, ID; [2]Wichita State University, Wichita, KS*

TP 145 **Gas Phase Acidities of the 20 Protein Amino Acids from the Extended Kinetic Method**; Kathryn E. Colyer[1]; Christopher M. Jones[1]; Rachel A. Metz[1]; Anna K. Pawlow[1]; Emily D. Wischow[1]; John C. Poutsma[1]; *[1]College of William and Mary, Williamsburg, VA*

TP 146 **Collision-Induced Dissociation of Silver(I)Amide Complexes**; Vladimir A. Romanov[1]; Junfang Zhao[1]; Houssain El Aribi[2]; Alan C. Hopkinson[1]; K.W. Michael Siu[1]; *[1]York University, Toronto, Canada; [2]MDS SCIEX, Concord, Canada*

TP 147 **Electron Affinities of Polynuclear Aromatic Hydrocarbons and Chlorinated Hydrocarbons and Their Analysis by Negative Ion Chemical Ionization Mass Spectrometry**; Leon D. Betowski[1]; Mark A. Enlow[2]; Donald H. Aue[3]; *[1]U.S. Environmental Protection Agency, Las Vegas, NV; [2]Applied Research Associates, Inc, Tyndall AFB, FL; [3]University of California at Santa Barbara, Santa Barbara, CA*

TP 148 **Structure and Reactivity of Organolithium Compounds**; Zhixin Tian[1]; Steven R. Kass[1]; *[1]University of Minnesota, Minneapolis, MN*

TP 149 **Influence of Solvents (Water, Methanol, Acetone, and Acetonitrile) on the Binding of Copper Ions to Imidazole and Pyridine**; Nalaka S. Rannulu[1]; M.T. Rodgers[1]; *[1]Wayne State University, Detroit, MI*

TP 150 **Correlation of Bond Dissociation Energies in Ten-Electron Hypervalent Systems to Atomic Properties**; Changtong Hao[1]; Lee S. Sunderlin[1]; *[1]Northern Illinois University, DeKalb, IL*

TP 151 **Experimental and Computational Study of the Formation of Boron Cage Cluster Ions from BBr_3 in a Pulsed Discharge Ion Source**; David A Hales[1]; Jay S VanDenbos[1]; Shawna M Rigsby[1]; Catrin M Mills[1]; R Bret Yarbro[1]; Tony P Tauer[1]; *[1]Hendrix College, Conway, AR*

TP 152 **Examination of the Gas-Phase Ion Structure of Cationized Arginine (Na+, K+) by Infrared Multi Photon Dissociation Spectroscopy and Computational Modelling**; Mathias Schäfer[1]; Nick C. Polfer[2]; Jos Oomens[2]; Dirk Blunk[1]; Rebecca A. Jockusch[3]; *[1]Institute for Organic Chemistry University Cologne, Cologne, Germany; [2]FOM Institute for Plasmaphysics Rijnhiuzen, Nieuwegein, the Netherlands; [3]Department of Chemistry, University of Toronto, Toronto, Canada*

TP 153 **O-Alkylated Nitroalkane Cations in the Gas Phase: Selective Preparation of $C_3H_8NO_2^+$ Isomers and Elucidation of their Unimolecular Chemistry;** Miroslav Polášek[1]; Jirí Kubišta[1]; *[1]J. Heyrovský Institute of Physical Chemistry, Prague, Czech Republic*

TP 154 **Structural Investigation of an Unexpected Impurity Originating from a Polyester Filter Cloth**; John A. Castoro[1]; Albert J. DelMonte[1]; *[1]Bristol-Myers Squibb Company, New Brunswick, NJ*

TP 155 **Collisionally-Induced Dissociation of Methimazole and Acetylsalicylic Acid: Mechanisms of Ion Formation Using Hydrogen/Deuterium Exchange and Electrospray Ionization Mass Spectrometry**; Patrick Jeanville[2]; Kevin Colizza[1]; Amin, M Kamel[1]; *[1]Pfizer Global Research and Development, Groton, CT; [2]Thermo Electron Corporation, West Palm Beach, FL*

TP 156 **Simple Computational Method for Converting Gas-Phase Ion Heats of Formation into Energetics of Ionic Solids**; Lee S. Sunderlin[1]; Nathanial A. Fulton[1]; Paul Weber[1]; Changtong Hao[1]; *[1]Northern Illinois University, DeKalb, IL*

TP 157 **Monitoring Prenucleation in Solid State Formation of Silicates using ESI-MS**; Stefan Pelster[1]; Ferdi Schüth[1]; Wolfgang Schrader[1]; *[1]Max-Planck-Institut für Kohlenforschung, Mülheim / Ruhr, Germany*

TP 158 **Evidence for Ring-size Controlled Competitive Channels in α *vs.*ω-Hydrogen Migration in *N*-(5-Phenylvaleryl)azacycloalkan-2-thiones Probed by Isotope Labeling and Charge Inversion**; Hiroshi Yamaoka[1]; Kei Shiono[1]; Shigeo Hayakawa[1]; Kimio Isa[2]; Naoto Dougawa[2]; Yoshio Takai[3]; Nico M.M. Nibbering[4]; *[1]Osaka Prefecture University, Sakai, Osaka, Japan; [2]University of Fukui, Fukui, Japan; [3]Osaka University, Osaka, Japan; [4]Vrije Universiteit, Amsterdam, The Netherlands*

TP 159 **Experimental and Computational Study of the Gas-Phase Reactivity of Lead(II) Ions Towards D-Glucosamine, N-Ac-D-Glucosamine and Uronic Acids**; Jean-Yves Salpin[1]; Ahlam El Firdoussi[2]; Jeanine Tortajada[1]; *[1]LAMBE - UMR 8587 CNRS/CEA/UEVE, Evry, France; [2]Cadi Ayyad University, Marrakech, Marocco*

ENVIRONMENTAL ANALYSIS: WATER

TP 160 **Determination of Acrylamide in Drinking Water using Direct Injection into LC-ESI/MS/MS**; Daniel Temponi Lebre[1]; Helio Alves Martins-Júnior[1]; Alexandre Yautin Wang[1]; Valéria Chiérice Rodrigues[2]; *[1]Applied Biosystems, Sao Paulo, Brazil; [2]Nestlé Brasil Ltda, Sao Paulo, Brazil*

TP 161 **Investigation of Chlorotetracycline Isomerization using LC-MS/MS**; Jonathan Bailey[1]; Kerry M. Peru[1]; Allan J. Cessna[1]; John V. Headley[1]; *[1]Environment Canada, Saskatoon, Canada*

TP 162 **Analysis of Hydroxylated Metabolites of PCBs and PBDEs in Fish using GC/MS and LC/MS**; Fatin Samara[1]; Diana S. Aga[1]; *[1]State University of New York-University at Buffalo, Buffalo, NY*

TP 163 **Direct Aqueous Injection/Gas Chromatography-High Resolution Mass Spectrometry (DAI/GC-HRMS) of Water Soluble Organic Compounds**; Vince Y Taguchi[1]; Angelina So[1]; Moschoula A Trikoupis[1]; *[1]Ministry of the Environment, Toronto, Canada*

TP 164 **Determination of Diethylen Glycole in Marine Water by Nano-FIA Direct EI LC-MS;** Achille Cappiello[1]; Giorgio Famiglini[1]; Pierangela Palma[1]; *[1]Università di Urbino, Urbino, Italy*

TP 165 **From Mass to Structure: Analysis of Aromaticity of Suwannee River Fulvic Acid by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry**; Boris Koch[1]; Matthias Witt[2]; Thorsten Dittmar[3]; *[1]Alfred-Wegener-Institut, Bremerhaven, Germany; [2]Bruker Daltonik GmbH, Bremen, Germany; [3]Florida State University, Tallahassee, FL*

TP 166 **Analysis of Natural Organic Matter by FTMS: Effect of Ionization Techniques for the Analysis of Suwannee River Fulvic Acid**; Matthias Witt[1]; Philippe Schmitt-Kopplin[2]; Moritz Frommberger[2]; Norbert Hertkorn[2]; *[1]Bruker Daltonik GmbH, Bremen, Germany; [2]GSF - National Research Center, Neuherberg, Germany*

TP 167 **Synthesis and Determination of Dicarboxylic Degradation Products of Nonylphenol Polyethoxylates by Gas Chromatography-Mass Spectrometry**; Wang-Hsien Ding[1]; Chin-Yuan Cheng[1]; Wen-Ren Li[1]; *[1]Dept. Chemistry, National Central University, Chung-Li, Taiwan*

TP 168 **Experimental and Theoretical Approaches: Identification of Disinfection Byproducts in Drinking Water with Multidimensional GC/FT-ICR MS**; Touradj Solouki[1]; Indira Silwal[1]; Caleb Heffner[1]; *[1]University of Maine, Orono, ME*

TP 169 **SELDI-TOF-MS Analysis of Circadian Expression of Proteins from *Karenia brevis*, a Harmful Algal Bloom Causing Dinoflagellate**; Brian P. Gregson[1]; Bill Richardson[2]; David P. Fries[1]; *[1]University of South Florida, St. Petersburg, FL; [2]Florida Fish & Wildlife Conservation Commission, St. Petersburg, FL*

TP 170 **Presence of Oligosaccharides in Marine Mucilage Samples and their Characterization by Liquid Chromatography Coupled to Electrospray Tandem Mass Spectrometry**; Pierangela Palma[1]; Helga Trufelli[1]; Giorgio Famiglini[1]; Elisabetta Pierini[1]; Samuela Capellacci[1]; Nunzio Penna[1]; Achille Cappiello[1]; *[1]Università di Urbino, Urbino, Italy*

TP 171 **Mass Spectrometric Identification of Biodegradates of Pharmaceuticals in Wastewater Treatment Systems**; Diana S. Aga[1]; Peter Eichhorn[1]; Sandra Perez[1]; Dawn Celiz[1]; *[1]Univeristy at Buffalo, Buffalo, NY*

TP 172 **Direct injection Detection using LC/MS/MS for the Analysis of Dissociated Organo-Phosphorus Pesticides and their Degradation Products in Water**; Friedrich Werres[1]; Jens Dahlmann[2]; Kristin von Czapiewski[2]; André Schreiber[2]; *[1]Rhenish-Westfalian Institute for Water Research, Mülheim/Ruhr, Germany; [2]Applied Biosystems, Darmstadt, Germany*

TP 173 **Determination of 100 Endocrine Disrupting Compounds in River Water Using LC/MS/MS with a combination of APCI and ESI ionization**; Christopher D Borton[1]; Hesham Ghobarah[1]; Elliott B Jones[1]; Loren Y Olson[1]; Andre Schreiber[2]; *[1]Applied Biosystems, Foster City, CA; [2]Applied Biosystems/MDS Sciex, Toronto, Canada*

TP 174 **Quantitative Analysis of POPs Plastic Debris in the Ocean;** Urja V. Narayan[1]; Lorena M. Rios[1]; Charles Moore[2]; Patrick R. Jones[1]; O. David Sparkman[1]; [1]*University of the Pacific, Stockton, CA;* [2]*Algalita Marine Research Fundation, Long Beach, CA*

TP 175 **Behavior and Presence of Antidepressant Pharmaceuticals and Their Degradates in Municipal Wastewater**; Melissa M. Schultz[1]; Edward T. Furlong[1]; [1]*U.S. Geological Survey, Denver, CO*

TP 176 **Determination of Antibiotics within Various Wastewater Treatment Plants and their Impact on Surrounding Surface Waters**; Angela L. Batt[1]; Sungpyo Kim[1]; Ian B. Bruce[2]; Diana S. Aga[1]; [1]*State University of New York at Buffalo, Buffalo, NY;* [2]*Buffalo State College, Buffalo, NY*

TP 177 **Direct Injection Detection using the API 5000 LC/MS/MS for Analysis of Residual Amounts of Various Phenoxy Acid Herbicides in Water**; Wolfram Seitz[1]; Jens Dahlmann[2]; Axel Besa[2]; Walter Weber[1]; [1]*Zweckverband Landeswasserversorgung, Langenau, Germany;* [2]*Applied Biosystems, Darmstadt, Germany*

TP 178 **Ultra Performance Liquid Chromatography-Tandem Mass Spectrometry (UPLC-LC-MS/MS) for Low ng/L Determination of Quinolone and Macrolide Antibiotics in Wastewater**; Lidija Pozaic Frketic[2]; Mira Petrovic[3]; Damia Barcelo[3]; Francesc Ventura[1]; [1]*AGBAR, Barcelona, Spain;* [2]*PLIVA, Zagreb, Croatia;* [3]*IIQAB CSIC, Barcelona, Spain*

TP 179 **Development of an Electrospray LC/MS Library Identification Protocol for the Screening of Organic Contaminants in Drinking Water**; Lawrence B. Zintek[1]; Joshua D. Neukom[1]; Dennis J. Wesolowski[1]; Jim Krol[2]; [1]*US EPA, Chicago, IL;* [2]*Waters Corporation, Milford, MA*

TP 180 **Mass Spectrometric MRM Technique for Determination of Parts Per Trillion Levels of N-Nitrosamines as Disinfection Byproducts in Drinking Water System**; Yuan-Yuan Zhao[1]; Jessica Boyd[1]; Xing-Fang Li[1]; [1]*University of Alberta, Edmonton, Alberta, Canada*

TP 181 **Hybrid Quadrupole Time of Flight (Q-TOF) for Screening and Confirmation of Pharmaceuticals in Wastewaters**; Damia Barcelo[1]; Mira Petrovic[1]; [1]*IIQAB-CSIC, Department of Environmental Chemistry, Barcelona, Spain*

ENVIRONMENTAL ANALYSIS: AIR

TP 182 **Mass Spectrometry and Electronic Nose. A Complementary Approach in Environmental Odor Characterization and Measurement;** Enrico Davoli[1]; Giancarlo Bianchi[1]; Roberto Fanelli[1]; Laura Capelli[2]; Selena Sironi[2]; [1]*Istituto Mario Negri, Milano, Italy;* [2]*Politecnico di Milano, Milano, Italy*

TP 183 **Mass Spectral Identification of Bioaerosols Through a Novel Capturing and Detection System**; Charlene W. Bayer[1]; Danielle E. Bayer[1]; Victor R. De Jesus[1]; [1]*Georgia Tech Research Institute, Atlanta, GA*

TP 184 **Distinguishing Environmentally-Relevant Isomers using Selected Ion Chemical Ionization in a Quadrupole Ion Trap Mass Spectrometer**; Karen S. Wendling[1]; Gary L. Glish[1]; [1]*The University of North Carolina at Chapel Hill, Chapel Hill, NC*

TP 185 **A Fast and Reliable Method for the Analysis of Respiratory Quinones from Environmental Samples using LC/APCI/MS/MS**; Sung-Chan Jo[1]; Margaret Gan[1]; James M. Cantu[1]; David C. White[1]; [1]*Center for Biomarker Analysis, Knoxville, TN*

TP 186 **Mass Spectrometry Identification of VOCs in the Atmosphere by a Combination of Cartridge Adsorption and SPME**; Alessandro Saba[1]; Andrea Raffaelli[1]; Marco Tumbiolo[2]; Piero Salvadori[2]; [1]*CNR-ICCOM, Pisa, Italy;* [2]*Dipartimento di Chimica e Chimica Industriale, Pisa, Italy*

TP 187 **Determination of Chlorophenols in Aqueous Solution via Headspace Ionic Liquid Coating Sloid-Phase Microextraction Coupled with Gas Chromatography-mass spectrometry**; Tse-Tsung Ho[1]; Maw-Rong Lee[1]; [1]*National Chung-Hsing University, Taichung, Taiwan, ROC*

TP 188 **Field Evaluation of a BTEX Analyzer Using a Mobile TAGA MS/MS System**; Andy Ng[1]; Natalie Stacey[1]; Qing-Feng Chen[1]; Nicholas Karellas[1]; [1]*Ontario Ministry of the Environment, Toronto, Ontario, Canada*

TP 189 **Derivatization Procedures and Determination of Monosaccharide Anhydrides in Atmospheric Aerosols by Gas Chromatography-Mass Spectrometry**; Jia-Lin Wang[1]; Ching-Lin Hsu[1]; Wang-Hsien Ding[1]; [1]*Dept. Chemistry, National Central University, Chung-Li, Taiwan*

TP 190 **The First Parts Per Trillion Detection with SIFT-MS**; Daniel B. Milligan[1]; Barry J. Prince[1]; Gregory J. Francis[2]; Murray J. McEwan[2]; [1]*Syft Technologies Limited, Christchurch, New Zealand;* [2]*University of Canterbury, Christchurch, New Zealand*

TP 191 **Novel High Sensitivity HPLC/ESI-MS/MS Methodology for the Analysis of Amines in Ambient Air**; Mathieu Fournier[1]; Jacques Lesage[2]; Claude Ostiguy[2]; Huu van Tra[1]; [1]*UQAM, Montreal, Canada;* [2]*IRSST, Montreal, Canada*

TP 192 **Determination of Urea Thermal Decomposition Products in Diesel Engine Emissions Using High Performance Liquid Chromatography with Mass Spectrometry Detection**; Valbona Celo[1]; Ewa Dabek-Zlotorzynska[1]; [1]*Environment Canada, ETC, AAQD, Ottawa, ON, K1A 0H3, Canada*

TP 193 **Trace Level Determination of Trichloroethylene in Biological Samples by Headspace Solid Phase Microextraction Gas Chromatography-Mass Spectrometry**; Yongzhen Liu[1]; James V. Bruckner[1]; Michael G. Bartlett[1]; [1]*University of Georgia, Athens, GA*

TP 194 **Environmental Proteomics Study of Elemental Sulfur Oxidation in Anaerobic Conditions**; Ann M Snellinger-O'Brien[1]; Rachael Morgan-Kiss[2]; Thomas Hanson[2]; Murray V Johnston[1]; [1]*Unviersity of Delaware, Newark, DE;* [2]*Delaware Biotechnology Institute, Newark, DE*

TP 195 **Real Time Measurement of Environmental Pollutants by Ion Attachment Mass Spectrometry**; Megumi Nakamura[1]; Harumi Maruyama[1]; Masko Inoue[1]; Yoshiki Hirano[1]; Yasuyuki Taneda[1]; Yoshiro Shiokawa[1]; [1]*Canon ANELVA Technix Corporation, Fuchu-shi, Tokyo, Japan*

SAMPLE PREPARATION FOR LC/MS II

TP 196 **Evaporation-Free Automated Solid Phase Extraction Approach for Faster Bioanalysis by LC/MS/MS in Support of Toxicokinetic and Pharmacokinetic Studies**; Naiyu Zheng[1]; Jianing Zeng[1]; Zheng Ouyang[2]; Stephanie Pasasfarmer[1]; Deborah M. Parker[1]; Adela Buzescu[1]; John Lute[1]; Mohammed Jemal[2]; Mark E. Arnold[1]; Steve E. Unger[1]; [1]*Bristol-Myers Squibb Company, New Brunswick, NJ;* [2]*Bristol-Myers Squibb Company, Princeton, NJ*

TP 197 **Automated, High-Throughput Method Development for HTLC-MS**; Lisa A. Ford[1]; Michael Zhou[1]; [1]*Scynexis, Inc., RTP, NC*

TP 198 **Novel Derivatization Technique for the LC/MS/MS Analysis of Neurosteroids**; Farooq Azam[1]; Neal Simon[2]; Ray Bakhtiar[1]; Rasmy Talaat[1]; [1]*wyeth Research, Collegeville, PA;* [2]*Lehigh University, Bethelehem, PA*

TP 199 **Dealing with Detergents and Dosing Vehicles in Samples Submitted for LC-MS Analysis**; Kathryn Black[1]; Halil Erol[1]; Joseph M. Di Bussolo[2]; [1]*West Chester University of Pennsylvania, West Chester, PA;* [2]*Cohesive Technologies, Franklin, MA*

TP 200 **Semi-Automated Solid Phase Extraction Procedure for high throughput Bioanalytical Assays**; Jianbo Zhang[1]; Hong Gao[1]; Andrew Jayaraj[1]; *[1]Vertex Pharm. Inc., Cambridge, MA*

TP 201 **A Case Study: Adsorptive Losses in a Bioanalytical LC/MS/MS Urine Assay;** Brian T. Hoffman[1]; Sanjeev Bhadresa[1]; Limian Zhao[1]; George Hade[1]; Erika Moore[1]; Stephanie Nowak[1]; Sara Heit[1]; Daniel Mulvana[1]; Mike-Qingtao Huang[2]; Naidong Weng[2]; Steve Unger[2]; *[1]Advion BioServices, Ithaca, NY; [2]Bristol Myers Squibb Company, New Brunswick, NJ*

TP 202 **Evaluation of Cartridge-Saturation versus OTC Drugs Interference When Using Cation-Exchange SPE for Bioanalytical Method Development in LC-MS/MS**; Jean-Nicholas Mess[1]; Audrey Tousignant[1]; Malika Madi[1]; Troy Bradley[1]; Fabio Garofolo[1]; *[1]Algorithme Pharma, Laval (Montreal), Canada*

TP 203 **Comparison of Oasis HLB Extraction to Cohesive Turbulent Flow Online Analysis**; Adlai E. Niggebrugge[1]; Angela Shen[1]; *[1]Charles River Laboratories, Worcester, MA*

TP 204 **A Novel Approach for Tissue Sample Preparation: Enzymatic Disruption of Drug-Receptor Interactions for LC-MS/MS Bioanalysis of RU-486**; Yuhui Yang[1]; Tuyen Ngyuen[1]; Xin Zhang[1]; Jakal Amin[1]; *[1]Charles River Labs, Bioanalytical Chemistry, Worcester, MA*

TP 205 **On-line SPE-LC-MS/MS Method Development: A New Simple and Fast Clean-Up Approach to Improve Sample Throughput**; Emile Koster[1]; *[1]Spark Holland Inc., Plainsboro, NJ*

TP 206 **Evaluation of iTRAQ™ Reagents for Quantitative Amino Acid Analysis of Peptide and Protein Hydrolysates by LC/MS/MS**; Elizabeth S. Ingle[1]; Jennie R. Lill[1]; Claire Bramwell[3]; Scott Daniels[2]; Subodh Nimkar[3]; *[1]Genentech, Inc., South San Francisco, CA; [2]Applied Biosystems, Framingham, MA; [3]Applied Biosystems, Foster City, CA*

TP 207 **Fractionation of the Human Plasma Proteome Prior to Analysis by LC/MS/MS**; Susanne Moyer[1]; Hongbin Liu[1]; Nina Zolotarjova[1]; James Martosella[1]; Peter Mrozinski[1]; Haiying Chen[1]; Jerome Bailey[1]; *[1]Agilent Technologies, Wilmington, DE*

TP 208 **Therapeutic Drug Monitoring of Antiretroviral Drugs by Automated Fast Online XLC-MS/MS as Gold-Standard Technique**; Therese Koal[1]; Alex Berhitu[2]; Emile Koster[2]; Martin Sibum[2]; Volkhard Kaever[1]; *[1]Medical School Hannover Institute for Pharmacology, Hannover, Germany; [2]Spark Holland Inc., Plainsboro, NJ*

TP 209 **Improving Biological Sample Handling and Analyte Response with SPE Technologies for LC/MS/MS Assay**; Raymond J Gonzalez[1]; Irina Miksa[1]; Juan Chen[1]; Michelle Schreier[1]; Denny Christian[1]; *[1]Merck & Co., West Point, PA*

TP 210 **Determination of Lercanidipine in Human Plasma using Automated Online Solid Phase Extraction Combined with Electro Spray Ionization Tandem Mass Spectrometry;** Kwang-Youl Kim[1]; Sang-Man Han[1]; Kwang-Hyeon Kim[1]; John Crutchfield[2]; Robert Mensen[2]; Heon-Soo Lee[1]; *[1]Bio-Medieng, Seoul, Korea; [2]Spark Holland Inc., Plainsboro, NJ*

TP 211 **Novel LC/MS Method of IgG1 Fragments Through Limited Proteolysis and Low Ph Reduction for Identification and Quantification of Post-Translational Modifications**; Gary D Pipes[1]; *[1]Amgen Inc, Thousand Oaks, CA*

TP 212 **LC-MS Analysis of Tricyclic Antidepressants in Human Plasma Using Supported Liquid Extraction Sample Preparation**; Matthew Cleeve[1]; Lee Williams[1]; Scott Merriman[1]; Helen Lodder[1]; Anne Howells[1]; Steve Jordan[1]; Claire Desbrow[1]; Richard Calverley[1]; *[1]Argonaut Technologies, now a Biotage company, Hengoed, UK*

TP 213 **Tandem On-line Extraction LC-MS/MS for Monitoring Drug Levels in Combination Therapy**; Otto Halmingh[1]; Martin Sibum[1]; Emile Koster[1]; *[1]Spark Holland Inc., Plainsboro, NJ*

TP 214 **Reduced Sample Preparation Complexity for the Analysis of Irinotecan and Metabolite SN-38 Utilizing the Sensitivity Gains of the API 5000**; Alexandre Pimenov[1]; Jeff Plomley[1]; Tim Samuels[1]; *[1]Charles River Laboratories, Preclinical Services, Montreal, Canada*

TP 215 **Online and Offline Nanoelectrospray Analysis of Phosphopeptides Purified by TiO2, ZrO2, and Carbon Wall-Coated Pipette Tips**; Christopher J. Toher [1]; Adam W. Perala[1]; Carla J. Marshall-Waggett[1]; Gary A. Valaskovic[1]; Ashok K. Shukla[2]; A.A. Oetting[2]; M.M. Shukla[2]; N. Manohar[2]; *[1]New Objective, Inc., Woburn, MA; [2]Glygen, Inc., Columbia, MD*

TP 216 **A New Method for the Determination of Free Drugs in Mouse Brains By Acoustic Homogenization, Ultracentrifugation and LC-MS/MS**; Philip Wong[1]; Bernd Bruenner[1]; Dean Hickman[1]; *[1]Amgen, Thousand Oaks, CA*

TP 217 **Automated Reversed-Phase Solid-Phase Extraction Optimization of Plasma Samples for LC-MS/MS Bioanalysis of Drugs and Metabolites**; Zheng Ouyang[1]; Yuan-Qing Xia[1]; Mohammed Jemal[1]; *[1]Bristol-Myers Squibb Company, Princeton, NJ*

TP 218 **Stabilization of Reduced Glutathione in Whole Blood and Quantitation of Reduced and Oxidized Glutathione in Human Plasma by LC/MS/MS**; Henry H. Li[1]; Hongzhuan Chen[1]; Yongdong Zhu[1]; Yuan-Shek Chen[1]; Jamie Zhao[1]; Benjamin Chien[1]; Christopher J. Pazoles[2]; *[1]Quest Pharmaceutical Services, Newark, DE; [2]Novelos Therapeutics, Inc., Newton, MA*

TP 219 **Improving the MS Detection of Aflatoxins using a LC/MS system with Automated On-line Solid Phase Extraction and Derivatization**; Juergen Wendt[1]; Norbert Helle[2]; Dirk Bremer[3]; *[1]Agilent Technologies LSCA Sales &Service GmbH, Waldbronn, Germany; [2]TeLA Techn.Lebensmittel- und Umweltanalytik GmbH, Bremerhaven, Germany; [3]Gerstel GmbH & CoKG, Muelheim an der Ruhr, Germany*

TP 220 **Does Column Switching Reduce Phospholipid Ion Suppression in the Analysis of Rapamycin Using HPLC-ESI-MS/MS?**; Cory A. Hawkins[1]; Melissa M. Kiser[1]; Lori D. Payne[1]; *[1]Bioanalytical Systems, Inc. Northwest Laboratory, McMinnville, OR*

CLINICAL CHEMISTRY II

TP 221 **A Rapid UPLC-MS/MS Method for Determining Specific Amino Acids Associated with Maple Syrup Urine Disease and Phenylketonuria Management**; Scott M. Freeto[1]; Donald Mason[1]; Jie Chen[2]; Robert Scott[2]; Srinivas Narayan[2]; Michael Bennett[2]; *[1]Waters Corporation, Beverly, MA; [2]Children's Hospital of Philadelphia, Philadelphia, PA*

TP 222 **Enrichment of Cardiac and Skeletal Muscle Glycogen and Glucose Tetrasaccharide Pools with [$^{13}C_6$]glucose in Pompe Disease Knock-out Mice**; Haoyue Zhang[1]; Sarah P. Young[1]; Baodong Sun[2]; Dwight D. Koeberl[2]; David S. Millington[1]; *[1]Duke University Medical Center, Research Triangle Park, NC; [2]Duke University Medical Center, Durham, NC*

TP 223 **Rapid Quantitation of Steroids from Dried Plasma Spots Using Electrospray Ionization LC-MS/MS;** Susan C. Leonard[1]; Jeffrey D. Miller[1]; *[1]Applied Biosystems, Framingham, MA*

TP 224 **Identification and Quantitation of ß-Lactam Antibiotics in Human by LC/MS/MSIdentification and Quantitation of ß-Lactam Antibiotics in Human Urine by LC/MS/MS**; Anh Pham[1]; David Simons[1]; Gary Myers[1]; Hubert Vesper[1]; *[1]Center for Disease Control, Atlanta, GA*

TP 225 **High Throughput Analysis of Testosterone and Immunosuppressants by Elevated Temperature LC with MS/MS detection**; Bingfang Yue[1]; Mark M. Kushnir[1]; Gwen McMillin[2]; A. Wayne Meikle[2]; Alan L. Rockwood[2]; Stephanie J. Marin[3]; W. Dale Felix[3]; *[1]ARUP Laboratories, Salt Lake City, UT; [2]University of Utah, Salt Lake City, UT; [3]Selerity Technologies, Salt Lake City , UT*

TP 226 **An On-Line Extraction Assay for the Diagnosis of Congenital Adrenal Hyperplasia in Human Serum by LC-MS/MS**; James L. Bruton[1]; *[1]Mayo Clinic, Rochester, MN*

TP 227 **Withdrawn**

TP 228 **Method Development for the Determination of 19-Norandrosterone in Human Urine Using Isotope-Dilution Liquid Chromatography-Tandem Mass Spectrometry**; Susan S. Tai[1]; *[1]NIST, Gaithersburg, MD*

TP 229 **On-Line Analysis of Opiates and Opiod Analgesics in Urine**; Francois A. Espourteille[1]; *[1]Cohesive Technologies, Inc., Franklin, MA*

TP 230 **An Assay for Simultaneous Quantification of Seven Vitamind Derivatives including D2, D3, Mono-Hydroxy Metabolites and Dihydroxy Metabolites in Human Serum**; Yan Ling Zhang[1]; Valerie Burns[1]; Leah Swanson[1]; Michol Rothman[1]; Margaret Wierman[1]; Chester Ridgeway[1]; Uwe Christians[1]; *[1]University of Colorado Health Sciences Center, Denver, CO*

TP 231 **Biomarker Discovery for Renal Clear Cell Carcinoma Using a Two-dimensional (2D) LC-MS Peptidomic Differential Profiling Assay**; Hua Lin[1]; Thomas A. Shaler[1]; Brad Brown[1]; Melissa Chen[1]; Praveen Kumar[1]; Ted Jones[1]; Christopher H Becker[1]; *[1]Biomarker Discovery Sciences, PPD, Inc., Menlo Park, CA*

TP 232 **Measurement of Serum Dihydrotestosterone by LC-MS/MS**; Robert E. Nelson[1]; Ravinder J. Singh[1]; Stefan K. Grebe[1]; *[1]Mayo Clinic, Rochester, MN*

TP 233 **Detection of DNA Methylation in Human Epithelial Cancer Cells Using Electrospray Ionization Mass Spectrometry**; Yun Jiang[1]; Raymond Ranken[1]; Cristina Agasino Ivy[1]; Steven Hofstadler[1]; *[1]Ibis Division, A Division of Isis Pharmaceuticals, Carlsbad, CA*

TP 234 **Simultaneous Measurement of Serum/Plasma Oxcarbazepine and 10-Hydroxycarbazepine by On-line High Turbulence Liquid Chromatography-Tandem Mass Spectrometry**; Qibo Jiang[1]; Sum Chan[1]; Richard E. Reitz[1]; *[1]Quest Diagnostics Nichols Institute, San Juan Capistrano, CA*

TP 235 **A Sensitive, Automated Assay for the Quantification of Biolimus A9 in Blood after Eluting from Coronary Stents: Pushing the Limits**; Yan Ling Zhang[1]; Jamie Bendrick-Peart[1]; Ron Betts[2]; Uwe Christians[1]; *[1]University of Colorado Health Sciences Center, Denver, CO; [2]Biosensors International-USA, Newport Beach, CA*

TP 236 **Quantitative LC-MS/MS Analysis of Endogenous Biomarkers for Clinical Diagnosis in Endocrinology**; Mary K Morr[1]; Andrew D Wagner[1]; Milan Patel[1]; Russell P Grant[1]; *[1]Esoterix inc, 4301 Lost Hills Rd, Calabasas Hills, CA*

TP 237 **Quantitative Measurement of Potential Biomarkers in Schizophrenia: Analysis of D-Serine, L-Serine and Glycine in Biological Matrices using LC-MS/MS**; Thomas J. McLellan[1]; Francis Sweeney[1]; Maria Rosario[1]; Richard O'Sullivan[1]; Holly Soares[1]; *[1]Pfizer Global Research and Development, Groton, CT*

TP 238 **Contribution of LC-Tandem Mass Spectrometry for the Determination of Dansylated Polyamines;** Daniel RUFFIEUX[1]; Hélène BELVA-BESNET[2]; Florence DE FRAIPONT[1]; Véronique DUCROS[1]; *[1]Département de Biologie Intégrée, CHU, GRENOBLE, FRANCE; [2]Appliedbiosystems, Courtaboeuf, FRANCE*

TP 239 **Catecholamine Concentration Determination: iTRAQ™ Derivatization and LC-MS/MS Quantitation**; Peter G. Lodenquai[1]; Susan C. Leonard[1]; Johnie C. Brown[1]; David R. Dupont[1]; Subodh Nimkar[1]; *[1]Applied Biosystems, Foster City, CA*

TP 240 **Multivariate Statistics of LC/UV and LC/MS Data from Urinary Nucleoside Profiles**; Antje Frickenschmidt[1]; Gabriela Zurek [2]; Carsten Baessmann[2]; Jim Cunningham[3]; Hartmut Liebich[4]; Christoph Gleiter[1]; Holger Fröhlich[5]; Andreas Zell[5]; Bernd Kammerer[1]; *[1]Tuebingen University, Tuebingen, Germany; [2]Bruker Daltonik GmbH, Bremen, Germany; [3]Bruker Daltonics, Billerica, MA; [4]University Hospital Tuebingen, Tuebingen, Germany; [5]Centre for Bioinformatics Tuebingen, Tuebingen, Germany*

TP 241 **Comparison of Fenoprofen and Deuterated Ketoprofen as Internal Standards for Ketoprofen Analysis in Microdialysis and Open Flow Microperfusion Samples**; Karin Pickl[1]; Christoph Magnes[1]; Manfred Bodenlenz[1]; Günther Fauler[2]; Thomas R. Pieber[1]; Frank M. Sinner[1]; *[1]Inst. of Medical Technologies a. Health M., Graz, Austria; [2]CIMCL, Medical University Graz, Graz, Austria*

TP 242 **Differentiation of Triiodothyronines by Electrospray Ionization Tandem Mass Spectrometry**; Yuntao Zhang[1]; Abigail H. Conrad[1]; Gary W. Conrad[1]; *[1]Kansas State University, Manhattan, KS*

TP 243 **Simultaneous LC-ESI-MS-MS Determination of Cyclosporine A, Tacrolimus, and Sirolimus in Blood and Mycophenolic Acid in Plasma, using Common Pretreatment Procedure;** Maciej Bogusz[1]; Jamil Abdel-Jawwad[1]; Eid Al-Enazi[1]; Huda Hassan[1]; Mohammed Al-Tufail[1]; *[1]King Faisal Specialist Hospital and Research Centr, Riyadh, Saudi Arabia*

TP 244 **Mass Spectrometric Single Eye Analysis and Contralateral Eye Comparison in a Dry Eye Model**; Bryan M. Ham[1]; Jean T. Jacob[2]; Richard B. Cole[1]; *[1]University of New Orleans, New Orleans, LA; [2]Louisiana State University-Health Sciences Center, New Orleans, LA*

TP 245 **Detection of the Causative Agents of Bacteremia in the Presence of Large Human DNA Background by Electrospary Ionization Mass Spectrometry**; Raymond Ranken[1]; Yun Jiang[1]; Cristina Agasino Ivy[1]; Steven Hofstadler[1]; *[1]Ibis Division, A Division of Isis Pharmaceuticals, Carlsbad, CA*

TP 246 **Enhancing the Limit of Quantitation of Testosterone at Clinically Relevant Levels Using FAIMS**; Jonathan C. McNally[1]; Barbara Ells[1]; James Kapron[1]; *[1]ThermoElectron, San Jose, CA*

TP 247 **Online Glu-C Digestion and Measurement of Hemoglobin A1C and A0 Peptides Using LC/MS**; Kheng B. Lim[1]; Joshua Pengson[1]; Daniel B Kassel[1]; *[1]Takeda San Diego, Inc, San Diego, CA*

IMMUNOLOGY

TP 248 **Identification of Brugia Adult Worm Proteins**; Tiffany Weinkopff[1]; Michael Nold[2]; Jeffrey Silva[2]; James Atwood[1]; George Punkosdy[3]; Brent Weatherly[1]; Ronald Orlando[1]; Patrick Lammie[3]; *[1]University of Georgia, Athens, GA; [2]Waters Corporation, Milford, MA; [3]Centers for Disease Control and Prevention, Atlanta, GA*

TP 249 **Flu Flighters - Proteomics Surveillance of the Influenza Virus with Mass Spectrometry**; Bethny Morrissey[1]; Margaret Streamer[1]; Kevin Downard[1]; *[1]The University of Sydney, Sydney, AUSTRALIA*

TP 250 **Comprehensive Immunopeptome Display of Normal and Leukemic Cells using Multi-Dimensional Nanolc-MS-MS;** Marie-Hélène Fortier[1]; Chantal Baron[1]; Vincent Rineau[1]; Claude Perreault[1]; Pierre Thibault[1]; *[1]IRIC, Université de Montréal, Montréal, Canada*

TP 251 **De Novo Sequencing of a Monoclonal Antibody Using LTQ-FTMS-MS/MS Analysis and Edman Degradation;** Victoria C Pham[1]; David Arnott[1]; Jennie R. Lill[1]; [1]*Genentech Inc., South San Francisco, CA*

TP 252 **Withdrawn**

TP 253 **Identification of Infection-Related Antigenic Peptides Bound to MHC Class I or Class II Molecules Utilizing Dedicated Metabolic Labeling Strategies;** Hugo D. Meiring[1]; Rachel M. Stenger[1]; Betsy Kuipers[1]; Martien C.M. Poelen[1]; Jacqueline A.M. van Gaans-van den Brink[1]; Hans Timmermans[1]; Ad P.J.M. de Jong[1]; Ernst C. Soethout[1]; Cecile A.C.M. van Els[1]; [1]*Netherlands Vaccine Institute, Bilthoven, The Netherlands*

TP 254 **Full length Sequencing of Monoclonal Antibody Light Chains using Nano-LC/MS/MS**; Yan Chen[1]; Jun Lu[1]; Huaiqin Wu[1]; [1]*Abbott Laboratories, Abbott Park, IL*

TP 255 **Mass Spectrometric Characterization of a Discontinuous Epitope of the Hepatitis C Virus (HCV) E2 Protein by Differential Chemical Modification**; Roxana E. Iacob[1]; Steven Foung[2]; Kenneth B. Tomer[1]; [1]*National Institute of Environmental Health Science, RTP, NC;* [2]*Department of Pathology, Stanford University, Stanford, CA*

TP 256 **Analysis of HLA-DR4 Restricted Peptides by Electron transfer Dissociation (ETD) Mass Spectrometry**; Jie Qian[1]; Valentina Robila[1]; Dina Bai[1]; Joy M. Polefrone[1]; Lewis Y. Geer[2]; Victor H. Engelhard[1]; Jeffrey Shabanowitz[1]; Donald F. Hunt[1]; [1]*University of Virginia, Charlottesville, VA;* [2]*National Center for Biotechnology Information, NIH, Bethesda, MD*

TP 257 **Comparing Apples to Pears: Quantitative Comparison Between MHC-Ligand- and mRNA-Ratios Shows Only Faint Correlation;** Andreas Weinzierl[1]; Margret IJ Mueller[1]; [1]*Institute for Cell Biology, Tuebingen, Germany*

TP 258 **Unexpected Abundance of HLA Class II Presented Peptides in Primary Renal Cell Carcinomas**; Joern Dengjel[1]; Maria-Dorothea Nastke[1]; Gitsios Gitsioudis[1]; Oliver Schoor[1]; Florian Altenberend[1]; Margret Müller[1]; Björn Krämer[1]; Anna Missiou[1]; Martina Sauter[2]; Jörg Hennenlotter[3]; Arnulf Stenzl[3]; Hans-Georg Rammensee[1]; Karin Klingel[2]; Stefan Stevanovic[1]; [1]*Immunology, University of Tuebingen, Tuebingen, Germany;* [2]*Molecular Pathology, University of Tuebingen, Tuebingen, Germany;* [3]*Urology, University of Tuebingen, Tuebingen, Germany*

TP 259 **Determination of Interleukin-4 Induced Expression within the Nuclear Proteome of CD4+ Cells using Isotope Tagged Relative and Absolute Quantitation Reagents**; Robert Moulder[1]; Jan-Jonas Filén[1]; Laura Elo[1]; Petri Kouvonen[1]; Tero Aittokallio[2]; Riitta Lahesmaa[1]; Tuula Nyman[3]; [1]*Turku Centre for Biotechnology, Turku, Finland;* [2]*Department of Mathematics, University of Turku, Turku, Finland;* [3]*National Public Health Institute, Helsinki, Finland*

TP 260 **Proteomics-Based Development and Testing of Aspergillus Fumigatus Vaccine Candidates**; Teresa B. Hong[1]; Joseph M. Lyons[1]; Yunan Miao[1]; Terry D. Lee[1]; James I. Ito[1]; Markus Kalkum[1]; [1]*City of Hope National Medical Center, Duarte, CA*

TP 261 **Combining SILAC and iTRAQ for Large Scale Identification of MHC Peptides**; Eilon Barnea[1]; Ilan Beer[2]; Yifat Yanku[1]; Elena Milner[1]; Arie Admon[1]; [1]*Technion-Israel Inst. of Technology, Haifa, Israel;* [2]*IBM Haifa Research Laboratory, Haifa, Israel*

TP 262 **Using NanoLC and HPLC Chip to Identify Novel Membrane Proteins Associated with MHC Class II**; Karen R. Jonscher[2]; Lei Jin[1]; Nichole A. Reisdorph[2]; John Cambier[1]; [1]*National Jewish Medical and Research Ctr, UCHSC, Denver, CO;* [2]*University of Colorado Health Sciences Center, Denver, CO*

TP 263 **Interaction Between Designed Ankyrin Repeat Proteins and CD4 Studied at the Molecular Level by Combined Cross-Linking Chemistry and Mass Spectrometry**; Tatiana Pimenova[1]; Andreas Schweizer[2]; Alexis Nazabal[1]; Patrick Amstutz[3]; Alexandra Trkola[2]; Renato Zenobi[1]; [1]*ETH Zurich, Zurich, Switzerland;* [2]*University Hospital Zurich, Zurich, Switzerland;* [3]*Molecular Partners, Zürich, Switzerland*

TP 264 **Detection of Acetylated-N-Terminal Peptide Hormones Released from the Human MOLT-4 T-Cell Line**; Colette J Rudd[1]; Carol L Soppe[1]; Robert J Barkovich[1]; James H Shofstahl[1]; Diether Recktenwald[2]; [1]*Thermo Electron, San Jose, CA;* [2]*BD BioSciences, San Jose, CA*

MALDI TANDEM MS

TP 265 **Characterization of a Microbial SGNH-Lipase and its Inhibitor-Complexes by MALDI-TOF, ESI-IT, MALDI-IT/RTOF and MALDI-TOF/RTOF Mass Spectrometry**; Martin Zehl[1]; Ivana Lescic-Asler[2]; Filip Kovacic[2]; Marija Abramic[2]; Biserka Kojic-Prodic[2]; Emmanuel Raptakis[3]; Guenter Allmaier[1]; [1]*Vienna University of Technology, Vienna, Austria;* [2]*Ruder Boskovic Institute, Zagreb, Croatia;* [3]*Shimadzu Biotech-Kratos Analytical, Manchester, United Kingdom*

TP 266 **Extending Protein Sequence Information Using a Combination of MALDI in-Source Decay and High Energy CID Fragentation**; Rachel L Martin[1]; Emmanuel Raptakis[1]; [1]*Shimadzu Biotech, Manchester, UK*

TP 267 **Structural Characterization of Pyridylaminated Oligosaccharides and Peptides by Atmospheric Pressure MALDI-QIT-TOF Mass Spectrometry**; Emi Ito[1]; Akio Tominaga[2]; Hiroto Itoi[2]; Shuichi Shinma[3]; Mitsutoshi Setou[3]; Kozo Miseki[2]; Akemi Suzuki[1]; Minoru Suzuki[1]; [1]*RIKEN Frontier, Saitama, Japan;* [2]*Shimadzu Corporation, Kyoto, Japan;* [3]*Okazaki National Research Institutes, Okazaki, Japan*

TP 268 **The Correlation of Milk Peptide and Protein Profiling with the Acute Inflammatory Stage in Cows Affected by Mastitis;** Anna Napoli[1]; Donatella Aiello[1]; Leonardo Di Donna[1]; Dora Spina[1]; Giovanni Sindona[1]; [1]*Department of Chemistry, University of Calabria, Rende , Italy*

TP 269 **Top-Down and Middle-Down Proteome Analysis by MALDI TOF/TOF**; Angela K. Walker[1]; John R. Strahler[1]; Hasand Ghandi[2]; Peggy H. Ostrom[2]; P.C. Andrews[1]; [1]*University of Michigan, Ann Arbor, MI;* [2]*Michigan State University, Lansing, MI*

TP 270 **Increased Sensitivity and Resolution of Low Mass Fragment Ions on a MALDI TOF-TOF via Low Mass Zoom Analysis Mode**; Joanne B. Connolly[1]; Andrew R. Bowdler[2]; Stuart J. McLarnon[3]; [1]*Shimadzu Biotech, Manchester, UK;* [2]*Kratos Analytical, Manchester, UK;* [3]*University of Manchester, Manchester, UK*

METAL IONS IN BIOLOGY

TP 271 **Electron Capture Dissociation of Biological Molecules Complexed with Metal Ions**; Kristina Hakansson[1]; Haichuan Liu[1]; Jiong Yang[1]; Julie T. Adamson[1]; [1]*University of Michigan, Ann Arbor, MI*

TP 272 **Characterization of the Zinc-Binding Properties of Prothymosin-Α**; William B. Monteith[1]; Chris L. Wilson[1]; Colin S. Burns[1]; Allison S. Danell[1]; [1]*East Carolina University, Greenville, NC*

TP 273 **Proteomic Analysis of Calcium- and Phosphorylation-dependent Calmodulin Complexes in Mammalian Cells**; Daojing Wang[1]; Deok-Jin Jang[1]; [1]*Lawrence Berkeley National Laboratory, Berkeley, CA*

TP 274 **Sequencing of Biological Chromium Peptides by Mass Spectrometry**; Carolyn J. Cassady[1]; Jungie Gao[1]; Zhong Li[1]; Dan Pu[1]; [1]*The University of Alabama, Tuscaloosa, AL*

TP 275 **Search for Proteins Involved in Transport of Low-Molecular-Mass Iron**; Petr Pompach[1]; Petr Man[1]; Karel

Valis[2]; Jaroslav Truksa[2]; Jan Kovar[2]; [1]*Institute of Microbiology, Prague, Czech Republic;* [2]*Institute of Molecular Genetics, Prague, Czech Republic*

TP 276 **Top-Down Probing of Protein:Metal and Protein:Nucleic Acid Complexes Via Slow-heating Fragmentation Methods in FTMS**; Katherine A. Kellersberger[1]; Danielle A. Fabris[1]; [1]*University of Maryland, Baltimore County, Baltimore, MD*

TP 277 **Copper Binding of the Prion Protein Studied by Metal-Catalyzed Oxidation Reactions and Mass Spectrometry**; R Srikanth[1]; Juma D Bridgewater[1]; Richard W Vachet[1]; [1]*University of Massachusetts, Amherst, MA*

NATURAL PRODUCTS

TP 291 **Development of a Mass Spectrometry-Based Assay for the Evaluation of Inhibitors of the Cyclooxygenases COX-1 and COX-2**; Yi Tao[1]; Dejan Nikolic[1]; Wenkui Li[1]; Richard B. van Breemen[1]; [1]*University of Illinois College of Pharmacy, Chicago, IL*

TP 292 **The Role of the Hybrid Linear Ion Trap - FTMS in Natural Product Discovery**; Jeffrey R Gilbert[1]; Dennis O Duebelbeis[1]; Paul Lewer[1]; Don R Hahn[1]; [1]*Dow AgroSciences, Indianapolis, IN*

TP 293 **Sequencing Hop (HUMULUS LUPULUS L.) Proanthocyanidin Oligomers by LC/ Electrospray Tandem Mass Spectrometry**; hui-jing Li[1]; Brian Arbogast[1]; Max L. Deinzer[1]; [1]*Department of Chemistry, Oregon State University, Corvallis, OR*

TP 294 **Withdrawn**

TP 295 **Determination of Urinary Phytoestrogens by HPLC-MS/MS: A Comparison of Atmospheric Pressure Chemical Ionization (APCI) and Electrospray Ionization (ESI)**; Michael E. Rybak[1]; Daniel L. Parker[1]; Christine M. Pfeiffer[1]; [1]*Centers for Disease Control and Prevention, Atlanta, GA*

TP 296 **Identification of Nitrogen-Containing Compounds in Black Cohosh (Actaea racemosa L.) by Mass Spectrometric Dereplication**; Dejan Nikolic[1]; David Lankin[1]; Shao Nong Chen[1]; Guido F. Pauli[1]; Richard B. van Breemen[1]; [1]*University of Illinois at Chicago, Chicago, IL*

TP 297 **The Structural Characterisation of Flavonoids by Negative Ion Chip-Based Nanospray Tandem Mass Spectrometry;** Clare Stewart[1]; Mark H Allen[2]; Alistair Sterling[2]; Norberto P Lopes[3]; Paul J Gates[1]; [1]*University of Bristol, Bristol, United Kingdom;* [2]*Advion BioSciences Ltd., Norwich, United Kingdom;* [3]*FCFRP-University of Sao Paulo, Ribeirao Preto, Brazil*

TP 298 **Selective Analytical Determination of Phenolic Compounds in Natural Products by ESI-MS/MS Precursor Ion analyysis**; Claudio Medana[1]; Claudio Baiocchi[1]; Francesco Carbone[1]; [1]*Università di Torino, Torino, Italy*

TP 299 **Chemical Profiling and Quantification of Isoflavone Phytoestrogens in Kudzu Using LC/UV/MSD**; Qing-Li Wu[1]; Yong-Hong Yang[2]; James E. Simon[1]; [1]*Rutgers University, New Brunswick, NJ;* [2]*Yunnan Agricultural University, Kunmin, Yunnan, China*

TP 300 **Natural Product Analysis Utilizing an Ion Trap - Time-of-Flight (IT-TOF) Mass Spectrometer**; Joy M. Ginter[1]; Holly M. Shackman[1]; Joseph P. Fox[1]; Masayuki Nishimura[1]; Masahiko Taniguchi[2]; Yoshihide Usami[2]; Kuo-Hsiung Lee[2]; [1]*Shimadzu, Columbia, MD;* [2]*University of North Carolina, Chapel Hill, NC*

TP 301 **Structure Elucidation of Key Polyphenols in Rosemary Extract by Liquid Chromatography Tandem Mass Spectrometry;** Alun W Davies[1]; Craig S Newby[1]; [1]*GlaxoSmithKline Consumer Healthcare R&D, Weybridge, United Kingdom*

TP 302 **Computer Aided LC/MS oaTOF Analysis Of Complex Pharmaceutical Natural Product Extracts For Structure Elucidation And Ingredient Comparison In Different Subspecies**; Edgar Nägele[1]; [1]*Agilent Technologies R&D and Marketing GmbH & Co., Waldbronn, Germany*

TP 303 **Identification and Structural Characterization of Chlorophyll Catabolites in Senescent Plants using NanoLC-ESI Mass Spectrometry**; Thomas Mueller[1]; Kathrin Breuker[1]; Bernhard Kraeutler[1]; [1]*Inst. of Organic Chemistry, Univ. of Innsbruck, Innsbruck, Austria*

TP 304 **Method Development for Determinations of Two Anti Cancer Bioactive Compounds Isolated from Chinese Herbal Medicine by LC-MS/MS**; Yan Ling Zhang[1]; Zheng Jie Liu[2]; Dale Leitman[2]; Richard Staub[2]; Jenny Jackson[2]; Sylvia Chow[2]; Isaac Cohen[2]; Uwe Christians[1]; [1]*University of Colorado Health Sciences Center, Denver, CO;* [2]*Bionovo, Inc., Emeryville, CA*

TP 305 **LC-MS/MS Analysis of Novel Isoflavone C-Glucosides in Pueraria lobata In Vitro Cultures**; Jeevan K Prasain[1]; Adam Reppert[2]; Ray Moore[1]; Stephen Barnes[1]; Mary A Lila[2]; [1]*University of Alabama at Birmingham, Birmingham, AL;* [2]*University of Illinois Urbana-Champaign, Urbana-Champaign, IL*

TP 306 **Determination of Gibberellic Acid in Plants by Liquid Chromatography – Mass Spectrometry**; Maw-Rong Lee[1]; Jie-Hong Huang[1]; Zu-Guang Li[1]; Shune-Famg Lo[1]; Liang-Jwa Chen[1]; [1]*National Chung-Hsing University, Taichung, Taiwan, ROC*

TP 307 **Protein identification in Pollination Drop of Three Cupressaceous Conifers;** Rebecca E. Wagner[1]; Serena Mugnaini[3]; Darryl Hardie[2]; Patrick von Aderkas[1]; [1]*University of Victoria, Victoria, Canada;* [2]*UVic-Genome BC Proteomics Centre, Victoria, Canada;* [3]*University of Siena, Siena, Italy*

TP 308 **Substrate and Activity Screening of NRPS and PKS Systems by Large Molecule Mass Spectrometry**; Pieter C. Dorrestein[1]; Jonathan Blackhall[1]; Steven van Lanen[3]; Paul Straight[2]; Daniel Edwards[5]; Zachary D. Aron[2]; William H. Gerwick[4]; Roberto Kolter[2]; Ben Shen[3]; Christopher Walsh[2]; Neil Kelleher[1]; [1]*University of Illinois, Urbana, Il;* [2]*Harvard Medical School, Boston, Ma;* [3]*University of Wisconsin, Madison, WI;* [4]*Scripps Institution of Oceanography, San DIego, Ca;* [5]*California State University, Chico, Ca*

TP 309 **Structural Determination of Glycerolipids Isolated from Marine Sponge by FAB Tandem Mass Spectrometry**; Jongki Hong[1]; Min-Sun Kim[1]; Ji-Hye Gil[3]; Jee H. Jung[2]; [1]*College of Pharmacy, Kyung Hee University, Seuol, South Korea;* [2]*College of Pharmacy, Pusan National University, Pusan, South Korea;* [3]*Korea Basic Science Institute, Seoul, South Korea*

TP 310 **Characterization of Iridoids by Metal Complexation using Electrospray-Mass Spectrometry and/or Liquid Chromatography-Electrospray-Mass Spectrometry**; Mathew M Nindi[1]; Andrew Muzila[1]; Moses N. Munkombwe [1]; Titus A. M. Msagati[1]; [1]*University of Botswana, Department of Chemistry, Gaborone, Botswana*

TP 311 **A Combined MS/MS, NMR, and ab initio Computational Study of Flavonoids and Flavonoid Glycosides**; Raymond E. March[1]; Darcy C. Burns[1]; Errol G. Lewars[1]; Hongxia Li[1]; David A. Ellis[1]; [1]*Trent University, Peterborough, ON, Canada*

TP 312 **An LC/MS/MS Approach for Characterization of Silybin, Isosilybin, Silydianin and Silychristin in Milk Thistle Standardized Extract and Human Plasma**; James I. Lee[1]; Di Wu[1]; Bih Hsu[2]; Jeffrey S. Barrett[1]; [1]*The Children's Hospital of Philadelphia, Philadelphia, PA;* [2]*Exelixis, Inc., South San Francisco, CA*

TP 313 **The Use of Exact Mass Measurements at High Resolution to Probe Structural Diversity in Complex Natural**

Products Mixtures; Deborah Zink[1]; Scott Campbell[2]; *[1]Merck Research Laboratories, Rahway, NJ; [2]Sierra Analytics, Inc., Modesto, Ca*

TP 314 **LC-MS/MS Analysis of Glucosinolates and their Enzymatic Degradation Products in Meadowfoam Seed Meal**; Nicholas G. Kesinger[1]; Jeffrey Morré[1]; Stephen Machado[1]; Jan F. Stevens[1]; *[1]Oregon State University, Corvallis, Or*

TP 315 **Structural Analysis of Sepia Melanin Degradation Products by Liquid Chromatography- Tandem Mass Spectrometry**; Weslyn C. Ward[1]; William S. Lee[1]; Lian Hong[1]; John D. Simon[1]; *[1]Duke University, Durham, NC*

TP 316 **Determination of Ginkgolides and Flavonols in Ginkgo Biloba Products and NIST Ginkgo Reference Standard by LC/UV/MS**; Mustafa Ozcan[1]; Pei Chen[1]; *[1]USDA,, Beltsville Hhuman Nutrition Resarch Center, Beltsville, MD*

TP 317 **Rapid Determination of Catechins in Tea and Chocolate using Ultra Performance Liquid Chromatography-Tandem Mass Spectrometry;** Joseph J. Dalluge[1]; Keri L. Ross[1]; Travis T. Tu[1]; *[1]Cargill Incorporated, Minneapolis, MN*

TP 318 **Accurate Mass Quantitation of Ginsenosides in Dietary Supplements using Simultaneous MSn Confirmation**; Helmut Muenster[1]; Mary Blackburn[1]; *[1]Thermo Electron, Somerset, NJ*

TP 319 **Lycopene Uptake and Sub-Cellular Localization in Prostate Cancer Cells**; Ang Liu[1]; Yan Pang[1]; Dongwei Zhu[1]; Richard B. van Breemen[1]; *[1]University of Illinois College of Pharmacy, Chicago, IL*

GLYCOPROTEINS I

TP 320 **Towards Automated Glycoanalysis of Proteomes: Partial Fractionation and Limited Database Deployment**; Lewis K Pannell[1]; Julio C Ruiz[1]; Amra Zuzo[1]; Nathan E Jones[2]; Tina R Hubler[1]; *[1]Cancer Research Institute, USA, Mobile, AL; [2]Penn State University, University Park, PA*

TP 321 **Sequencing of N-Linked Glycans of 1-D SDS-PAGE Separated Glycoprotein: Fragmentation of 3-Aminophthalic Hydrizide-Derivatized Oligosaccharides with MALDI-TOF/TOF**; So Young Jang[1]; Seung Il Kim[1]; Jong-Soon Choi[1]; Young Hwan Kim[1]; *[1]Proteomics Team, Korea Basic Science Institute, Taejeon, South Korea*

TP 322 **Structural Analysis of Rat Epididymal Cysteine Rich Secretory Protein CRISP1**; Joseph L Wooters[1]; Chee-Keng Ng[1]; Mike Nolan[1]; Kenneth Roberts[2]; Kathy Ensrud[2]; David Hamilton[2]; Daniel Johnston[1]; Qiu Yongchang[1]; *[1]Wyeth Research, Cambridge, MA; [2]University of Minnesota, Minneapolis, MN*

TP 323 **Development of Reversed Phase HPLC Methods for Monitoring Fragments and Oxidized Species in Humanized Monoclonal Antibodies**; Jinhua Feng[1]; Mingyan Cao[1]; Ziping Wei[1]; Mark A. Schenerman [1]; *[1]Medimmune, Gaithersburg, MD*

TP 324 **Protein Markers of Pancreatic Cancer in Human Serum Using Lectin Selected Sialic Acid Glycoproteins With Mass Spectrometric Analysis**; Jia Zhao[1]; Diane M. Simeone[1]; Daivd M. Lubman[1]; *[1]University of Michigan, Ann Arbor, MI*

TP 325 **Microwave Assisted Deglycosylation of Antibodies for Accurate Intact Molecular Weight Determination;** Jennie Lill[1]; Wendy Sandoval[1]; Helga Raab[1]; Fred Arellano[1]; David Arnott[1]; Richard Vandlen[1]; *[1]Genentech Inc., South San Francisco, CA*

TP 326 **Glycosylation of Porcine Seminal Plasma Proteins: Selective Enrichment and Characterization**; David S. Selby[1]; Martin R. Larsen[1]; Gareth Evans[2]; Peter Roepstorff[1]; *[1]University of Southern Denmark, Odense, Denmark; [2]The University of Sydney, Sydney, Australia*

TP 327 **Glycosylation Profiling of a Therapeutic Recombinant Monoclonal Antibody with Two Glycosylation Sites by Liquid Chromatography/Mass Spectrometry**; Amareth Lim[1]; Angelia Reed-Bogan[1]; Bryan J. Harmon[1]; *[1]Eli Lilly and Company, Indianapolis, Indiana*

TP 328 **A Method for Peptide Identification during Glycopeptide Analysis using a Prediction Table and Collision Induced Dissociation Mass Spectrometry**; Janet W. Irungu[1]; Dilusha S Dalpathado[1]; Hy-Vy Ha[2]; George R Bousfield[2]; Heather Desaire[1]; *[1]University of Kansas, Lawrence, KS; [2]Wichita State University, Wichita, KS*

TP 329 **On-line Nano-LC-ECD FT-ICR Mass spectrometry for Determination of O-Linked Glycosylation in MUC1 Mucin Reveals Two Variants of Site Occupancy**; Carina Sihlbom[1]; Malin Baeckstroem[1]; Hasse Karlsson[1]; Carol L Nilsson[2]; Gunnar C Hansson[1]; *[1]Institute of Biomedicine, Goteburg University, Goteburg, Sweden; [2]NHMFL and Florida State University, Tallahassee, FL*

TP 330 **ESI-FTICR Studies of a Metalloprotein Laccase: Copper Depletion and Glycoforms**; Asse Marjasvaara[1]; Kristiina Kruus[2]; Pirjo Vainiotalo[1]; *[1]University of Joensuu, Joensuu, Finland; [2]VTT Biotechnology, Espoo, Finland*

TP 331 **Structural Characterization of a Recombinant Antibody Produced in Yeast**; P. Clayton Gough[1]; *[1]Eli Lilly and Company, Indianapolis, IN*

TP 332 **Data-Dependent Neutral Loss Analysis of Glycans and Glycoprotein Digests**; Patrick D. Perkins[1]; Bryan D. Miller[1]; Ning Tang[1]; Christine A. Miller[1]; *[1]Agilent Technologies, Santa Clara, CA*

TP 333 **Automated LC-MALDI Analysis of Glycopeptides from Glycoprotein Digests using DHB as Matrix**; Arndt Asperger[1]; Anja Resemann[1]; Katrin Sparbier[1]; Detlef Suckau[1]; *[1]Bruker Daltonik, Bremen, Germany*

TP 334 **Structural Determination of the *N*- and *C*-Terminus in *gp*41, the Predominant Glycoprotein in the Vitelline Envelope of *Xenopus laevis* Eggs**; Haiqiang Yu[1]; Ruben T. Almaraz[2]; Kenji Murata[2]; Jerry L. Hedrick[2]; Fan Xiang[3]; Andreas H. Franz[1]; *[1]University of the Pacific, Stockton, CA; [2]University of California, Davis, CA; [3]Shimadzu Biotech Corporation, Pleasanton, CA*

TP 335 **Purification and Characterization of a Therapeutic Monoclonal Antibody from Preclinical Serum Samples**; Camille N. Strachan[1]; Michael Lewis[1]; Michael Bond[1]; Qing Mike Tang[1]; *[1]Centocor R&D, Inc., Radnor, PA*

TP 336 **Molecular Basis for Glycoprotein P0 Dimer in Native Membranes of *Xenopus laevis* Peripheral Nerve -Non-covalent Equilibrium Between Dimer and Monomer**; Bo Xie[1]; Xiaoyang Luo[2]; Daniel A. Kirschner[2]; Catherine E. Costello[1]; *[1]1Boston University School of Medicine, Boston, MA; [2]2Boston College, Chestnut Hill, MA*

TP 337 **Analysis of Glycopeptides with ESI Liner Ion Trap FT MS**; Shohei Shioyama[1]; Tomonori Takami[1]; Yasuhiro Yamashita[1]; Rieko Goto[1]; Naoe Yamane[1]; Hisami Murai[1]; Zenzaburo Tozuka[1]; *[1]JCL Bioassay, Nishiwaki, Japan*

TP 338 **Use of High Performance Boronate Affinity Chromatography Combined with LC-MS in Isolation and Identification of Glycoproteins from Human Serum**; Chen Li[1]; David M. Lubman[1]; *[1]University of Michigan, Ann Arbor , MI*

TP 339 **N-linked Glycosylation in Non-Consensus Sequence**; Zhuchun Wu[1]; Luke Bergerud[1]; Angie Deng[1]; Michael Lemar[1]; Mark Hesselberg[1]; Thomas Spitznagel[1]; Michael Byrne[1]; *[1]Human Genome Sciences, Inc., Rockville, MD*

TP 340 **Structural Assignments of N-Glycans and Identification of Peptide Sequence of N-Glycopeptides Using na NonESI/Linear-IT-TOF MS and MS^n Spectral Matching;** Hiroki Ito[1]; Yasuhiro Takegawa[1]; Kisaburo Deguchi[1]; Shinji Nagai[2]; Shinji Yoshioka[2]; Hiroaki Nakagawa[1]; Yasuro Shinohara[1]; Shin-Ichiro Nishimura[1]; *[1]Hokkaido University,*

Sapporo, Japan; [2]Hitachi High-Technologies Corporation, Tokyo, Japan

MODIFIED PROTEINS II

TP 341 **Identification and Characterization of a New Ubiquitin-Like Protein Modification-Neddylation using a Targeted Proteomic Approach**; Jeffrey Jones[1]; Yinying Yang[1]; Kenneth Wu[2]; Cortnie Guerrero[1]; Nadinath Nillegoda[2]; Pan Zhen-Qiang[2]; Lan Huang[1]; *[1]University of California Irvine, Irvine, CA; [2]Mount Sinai School of Medicine, New York, NY*

TP 342 **Intact Protein LC-FTICR MS Identifies Calmodulin as a Substrate for Putative Denitrase in Macrophages**; Natacha M. Lourette[1]; Heather S. Smallwood[1]; Seema Sharma[1]; Curt B. Boschek[1]; David C. Simpson[1]; Thomas C. Squier[1]; Richard D. Smith[1]; Ljiljana Pasa-Tolic[1]; *[1]Pacific Northwest National Laboratory, Richland, WA*

TP 343 **Endogenously Nitrated Proteins in Mouse Brain: Links To Neurodegenerative Disease**; Colette A. Sacksteder[1]; Weijun Qian[1]; Tatyana V. Knyushko[1]; Haixing Wang[1]; Mark H. Chin[2]; Goran Lacan[2]; William P. Melega[2]; David G. Camp II[1]; Richard D. Smith[1]; Desmond J. Smith[2]; Thomas C. Squier[1]; Diana J. Bigelow[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]David Geffen School of Medicine at UCLA, Los Angeles, CA*

TP 344 **Integrated Strategy for Proteomic Analysis of Acetylated Lysine using Tandem Mass Spectrometry**; Morten Beck Trelle[1]; Hye Ryung Jung[1]; Saverio Minucci[2]; Ole Nørregaard Jensen[1]; *[1]University of Southern Denmark, Odense, Denmark; [2]European Institute of Oncology, Milan, Italy*

TP 345 **Homocysteine Thiolactone Modification of Fibrinogen Analyzed by Mass Spectrometry and its Implication to Impaired Fibrinolysis**; Maria E. Warren[1]; Derrick L. Sauls[2]; Carol E. Parker[1]; Maureane Hoffman[3]; Christoph H. Borchers[1]; *[1]University of North Carolina, Chapel Hill, NC; [2]Durham Vereran's Affiars Medical Center, Durham, NC; [3]Duke University, Durham, NC*

TP 346 **Withdrawn**

TP 347 **Seyting Histone Lysine Methyltransferases and Heterochromatin Straight**; Tara L. Muratore[1]; Yifan Liu[2]; Jeffrey Shabanowitz[1]; C. David Allis[2]; Donald F. Hunt[1]; *[1]University of Virginia, Charlottesville, VA; [2]The Rockefeller University, New York, NY*

TP 348 **Screening for Chemoprevention Agents in the Botanical Dietary Supplement *Angelica sinensis* using Mass Spectrometry**; Dongting Liu[1]; Yan Luo[1]; Birgit M. Dietz[1]; Aimee L. Eggler[1]; Judy L. Bolton[1]; Guido F. Pauli[1]; Andrew D. Mesecar[1]; Richard B. van Breemen[1]; *[1]University of Illinois College of Pharmacy, Chicago, IL*

TP 349 **Extensive Age-Related Deamidation of Human ?S Crystallin at a Single Site Determined Quantitatively by Top Down Mass Spectrometry**; Vlad Zabrouskov[1]; Noah E. Robinson[2]; Jennifer Zhang[1]; Kirsten J. Lampi[3]; Arthur B. Robinson[2]; *[1]Thermo Electron, San Jose, CA; [2]Oregon Institute of Science and Medicine, Cave Junction, OR; [3]Oregon Health and Science University, Portland, OR*

TP 350 **Reprogramming of Post-translational modifications on Histones H3 and H4 by Egg Extracts from Xenopus Laevis**; Raghu K. Chitta[1]; David F. Shechter[2]; Benjamin A. Garcia[1]; Jeffrey Shabanowitz[1]; C. David Allis[2]; Donald F. Hunt[1]; *[1]University of Virginia, Charlottesville, VA; [2]Rockefeller University, New York, NY*

TP 351 **Improving Dynamic Range on the LTQ-FT Instrument using Hypothesis-Driven Mass Spectrometry**; Nadezhda A Galeva[1]; Yakov M Koen[1]; Viktor S Sharov[1]; Christian Schöneich[1]; Robert B Hanzlik[1]; Todd D Williams[1]; *[1]University of Kansas, Lawrence, KS*

TP 352 **Characterization and Quantitation of Glycated Hemoglobins**; Brian Imai[1]; Xianglin Yuan[1]; Nagarajan Chandramouli[1]; Haiteng Deng[1]; *[1]Rockefeller University, New York, NY*

TP 353 **Top Down Mass Spectrometric Analyses of Human Histone H4: Determination of Cancer-Specific and Cell-cycle Correlated Modification Profiles;** James J. Pesavento[1]; Craig A. Mizzen[1]; Neil L. Kelleher[1]; *[1]University of Illinois - Urbana, Urbana, IL*

TP 354 **Identification and Structure Determination of Tyrosine Nitration in Human Eosinophils using High Resolution Mass Spectrometry in Combination with Immunoanalytical Methods**; Alina Petre[1]; Reinhold Weber[1]; Martina Ulrich[2]; Gerd Doering[2]; Michael Przybylski[1]; *[1]University of Konstanz, Konstanz, Germany; [2]University of Tübingen, Tübingen , Germany*

NEUROPEPTIDES

TP 355 **Application of MALDI-FTMS to Determine Variations in Peptide Isoforms Between Individuals using Single Tissues or Organs from Decapod Crustaceans**; Christopher R. Cashman[1]; Yun-Wei A. Hsu[2]; Daniel I. Messinger[2]; Patsy S. Dickinson[1]; Andrew E. Christie[2]; Elizabeth A. Stemmler[1]; *[1]Bowdoin College, Brunswick, ME; [2]University of Washington, Seattle, WA*

TP 356 **Identification of Potential Biomarkers for Multiple Sclerosis in Cerebrospinal Fluid using SELDI and MALDI-TOF MS**; Ashley S. Beasley[1]; David Wheeler[1]; Avindra Nath[1]; David Irani[1]; Douglas Kerr[1]; Peter Calabresi[1]; Robert J. Cotter[1]; *[1]Johns Hopkins University School of Medicine, Baltimore, MD*

TP 357 **Qualitative and Quantitative *in situ* Analysis of Neuropeptides Involved in Feeding**; Stephanie S. DeKeyser [1]; Kimberly K. Kutz-Naber[1]; Lingjun Li[1]; *[1]University of WI, Madison, WI*

TP 358 **Mass Spectrometric Measurements from Neurons Cultured in Microfluidic Devices**; Michael L Heien[1]; Lucas B Thompson[1]; Ralph G Nuzzo[1]; Jonathan V Sweedler[1]; *[1]University of Illinois, Urbana-Champaign, IL*

TP 359 **Characterizing Cell-to-Cell Signaling Molecules in the Mammalian Brain**; Suresh P Annangudi[1]; Nathan G Hatcher[1]; Elena V Romanova[1]; Stanislav S Rubakhin[1]; Jonathan V Sweedler[1]; *[1]University of Illinois, Urbana-Champaign, IL*

TP 360 **On-Target Reduction and Alkylation of Disulfide-Bond Containing Peptides**; Kimberly K. Kutz-Naber[1]; Shelly K. Heinzelman[1]; Lingjun Li[1]; *[1]University of Wisconsin, Madison, WI*

TP 361 **Rat Neuropeptidomics by LC/MS/MS and MALDI-FTMS: Enhanced Extraction Techniques Coupled with 2D RP-RP HPLC Separation**; James Dowell[1]; Lingjun Li[1]; *[1]School of Pharmacy, University of Wisconsin, Madison, WI*

TP 362 **Capillary LC-MALDI-TOF-MS at the Attomole Level for Discovering Endogenous Peptides in Rat Brain**; Hui Wei[1]; Kerstin Nolkrantz[1]; Kristin Schultz[1]; Minshan Shou[1]; Robert T. Kennedy[1]; *[1]University of Michigan, Ann Arbor, MI*

TP 363 **The Effect of Reserpine on the Levels of Striatal Neuropeptides - A Time Course Study**; Anna Nilsson[1]; Karl Sköld[1]; Maria Fälth[1]; Marcus Svensson[1]; Per Svenningsson[2]; Per E. Andrén[1]; *[1]Uppsala University, Uppsala, Sweden; [2]Karolinska Institute, Stockholm, Sweden*

TP 364 **Accurate Mass Mapping and Sequencing of Corpus Cardiacum Neuropeptides by Means of LC-MALDI-oaTOF MS/MS and UPLC-oaTOF MS;** Peter D. Verhaert[1]; Gerold Schwarz[2]; Arthur R. Kroon[1]; James L. Langridge[2]; Johannes P.C. Vissers[2]; *[1]Delft University of Technology, Delft, Netherlands; [2]Waters Corporation - MS Technologies Centre, Manchester, UK*

TP 365 **Coupling Microdialysis to NanoLC-MS for *In Vivo* Monitoring of Neuropeptides**; Heidi L. Behrens[1]; Lingjun Li[1]; [1]*University of Wisconsin-Madison, Madison, WI*

TP 366 **Optimization of Peptide Extraction Conditions for Peptidomic Studies**; Fa-Yun Che[1]; Lloyd D Fricker[1]; [1]*Albert Einstein College of Medicine, Bronx, New York*

TP 367 **Mass Spectrometric Approaches for the Analysis of Biomarkers of Cocaine Addiction-Related Behaviors**; Elena V. Romanova[1]; Jessica Stanis[1]; Joshua M. Gulley[1]; Stanislav S. Rubakhin[1]; Jonathan V. Sweedler[1]; [1]*University of Illinois, Urbana, IL*

TP 368 **Immunoaffinity-Based Mass Spectrometric Characterization of the RFamide Neuropeptide Family in the Pericardial Organ of Cancer borealis**; Mingming Ma[1]; Kimberly K. Kutz-Naber[1]; Lingjun Li[1]; [1]*School of Pharmacy, University of Wisconsin, Madison, WI*

PROTEIN CONFORMATION I: HYDROGEN EXCHANGE

TP 369 **Conformational Studies on the Tachykinin and Related Peptides using Hydrogen/Deuterium Exchange Coupled with Mass Spectrometry**; Tarun Gheyi[1]; Chhabil Dass[1]; [1]*The University of Memphis, Memphis, TN*

TP 370 **Conformational Properties of Full Length HIV and SIV Nef by Mass Spectrometry**; James M. Hochrein[1]; Thomas E. Wales[1]; Edwina C. Lerner[2]; Anthony P. Schiavone[2]; Thomas E. Smithgall [2]; John R. Engen[1]; [1]*University of New Mexico, Albuquerque, NM;* [2]*University of Pittsburgh School of Medicine, Pittsburgh, PA*

TP 371 **Hydrogen Exchange FT-ICR Mass Spectrometry Study on Intact Human SOD1**; Murat Karabacak[1]; Mike Aguiar[2]; Jeffrey Agar[1]; Bernard F. Gibbs[2]; [1]*Brandeis University, Waltham, MA;* [2]*McGill University, Montreal, Canada*

TP 372 **Activator Binding Site of Arp2/3 Complex Probed by Hydrogen Exchange and Mass spectrometry**; Wendy Zencheck[1]; Hui Xiao[1]; Steven Almo[1]; [1]*Albert Einstein College of Medicine, Bronx, NY*

TP 373 **Ligand-Induced Conformational Changes in Human Serum Transferrin probed by SUPREX**; Petra L. Roulhac[1]; Michael C. Fitzgerald[1]; [1]*Duke University, Durham, NC*

TP 374 **Novel Application of Supercritical Fluid Chromatography to Eliminate Back Exchange after Solution-Phase Hydrogen/Deuterium Exchange;** Mark R. Emmett[1]; Sasa Kazazic[1]; Alan G. Marshall[1]; Wei Chen[2]; Stone D.-H Shi[2]; Ben Bolanos[2]; Michael J. Greig[2]; [1]*Ion Cyclotron Resonance Program, NHMFL-FSU, Tallahassee, FL;* [2]*Global Research & Development, Pfizer Inc., San Diego, CA*

TP 375 **H/D Exchange MS Study of Peroxiredoxin**; Ji-Eun Yi[1]; Leslie B. Poole [2]; Claudia S. Maier[1]; [1]*Oregon state university, Corvallis, OR;* [2]*Wake Forest university, winston-salem, NC*

TP 376 **Time Resolved H/D Exchange of Gas-Phase Protein Ions in a Linear Ion Trap**; P. John Wright[1]; D.J. Douglas[1]; [1]*University of British Columbia, Vancouver, BC*

TP 377 **The Interaction of Thrombin and its DNA Ligand Investigated by PLIMSTEX**; J. Micah Wilcox[1]; Michael L. Gross[1]; [1]*Washington University in St. Louis, Saint Louis, MO 63130*

TP 378 **Investigation of Various Ligands Interactions with Human RXR&Alpha Ligand Binding Domain by Hydrogen/Deuterium Exchange and Mass Spectrometry**; Xuguang Yan[1]; David Broderick[1]; Jeff Morre[1]; Michael Schimerlik [1]; Max Deinzer[1]; [1]*Oregon State University, Corvallis, OR*

TP 379 **Site Specific H/D Exchange Analysis of Protein by Mass Spectrometry Coupled with Carboxypeptidase Digestion**; Tatsuya Yamamoto[1]; Shunsuke Izumi[1]; Jorge Fernandez-de-Cossio[2]; Toshifumi Takao[3]; Kunihiko Gekko[1]; [1]*Hiroshima University, Higashi-Hiroshima, Japan;* [2]*Center for Genetic Engineering and Biotechnology, Havana, Cuba;* [3]*Institute for Protein Research, Osaka University, Suita, Japan*

TP 380 **Conformational Analysis of Α- and Β-Neo-Endorphins in Membrane-Mimetic Environments by Hydrogen/Deuterium Exchange and ESI-MS/MS;** Hari Kosanam[1]; Chhabil Dass[1]; [1]*The University of Memphis, Memphis, TN*

TP 381 **Toward Conformer-Specific Characterization of Protein Structure and Dynamics: Combination of Hydrogen Exchange and Tandem Mass Spectrometry**; Rinat Abzalimov[1]; Igor Kaltashov[1]; [1]*University of Massachusetts at Amherst, Amherst, MA*

TP 382 **Structural Analysis of a Metal-Binding Protein Domain by Hydrogen/Deuterium Exchange and ESI-MS/MS**; Peter L Ferguson[1]; Jingxi Pan[1]; Brian R Dempsey[1]; Gilles A Lajoie[1]; Brian H Shilton[1]; Lars Konermann[1]; [1]*University of Western Ontario, London, ON CANADA*

TP 383 **Non-Covalent Small Heat Shock Protein Complex Studied by Hydroxyl radical Modification, H/D Exchange and Native Nanospray**; Guilong Cheng[1]; David Hambly[2]; Christopher M. Jones[1]; Elizabeth Vierling[1]; Michael L. Gross[2]; Vicki H. Wysocki[1]; [1]*University of Arizona, Tucson, AZ;* [2]*Washington University in St. Louis, St. Louis, MO*

TP 384 **Hydrogen/Deuterium Exchange (HDX) is an Indispensable Tool in determining Regions of Destabilization in ALS-Causing SOD1 Mutant proteins;** Armando Durazo[1]; Bryan F. Shaw[1]; Kym F. Faull[1]; Julian P. Whitelegge[1]; Joan S. Valentine[1]; [1]*University of California, Los Angeles, CA*

TP 385 **Local H/D Exchange Kinetics of Calmodulin and Human Centrin 2 Reveal Differences in Calcium Binding**; Justin Sperry[1]; Michael L. Gross[1]; Rajiv Kumar[2]; [1]*Washington University in St. Louis, Saint Louis, MO;* [2]*Mayo Clinic, Rochester, MN*

TP 386 **Use of Two Different Proteases to Improve the Spatial Resolution in the H/D Exchange Study of the Creatine Kinase Dynamics**; Hortense Mazon[2]; Christian Vial[2]; Eric Forest[1]; [1]*Institute of Structural Biology, Grenoble, France;* [2]*University Claude Bernard, Lyon, France*

TP 387 **Identification and Characterization of EX1 Kinetics in H/D Exchange Mass Spectrometry by Peak Width Analysis**; Matthew Hotchko[1]; David D. Weis[2]; Lynn F. Ten Eyck[1]; John R. Engen[2]; [1]*University of California - San Diego, La Jolla, CA;* [2]*University of New Mexico, Albuquerque, NM*

TP 388 **Conformational Dynamics of Enzymes during Catalysis Studied by Hydrogen-Deuterium Exchange and ESI-MS**; Yuhong Liu[1]; Lars Konermann[1]; [1]*The University of Western Ontario, London, Canada*

TP 389 **Conformational Analysis of the Tip Protein from Herpesvirus Saimiri with Hydrogen Exchange and Mass Spectrometry**; Jennifer M. Carter[1]; R. P. Trible[2]; Lori A. Emert-Sedlak[2]; Edwina C. Lerner[2]; Jeremy J. Applen[1]; Daniel F. Cimino[1]; David D. Weis[1]; Bartholomew M. Sefton[3]; Thomas E. Smithgall[2]; John R. Engen[1]; [1]*University of New Mexico, Albuquerque, NM;* [2]*University of Pittsburgh School of Medicine, Pittsburgh, PA;* [3]*The Salk Institute for Biological Studies, La Jolla, CA*

TP 390 **Mapping the Interaction Between Human Choroinic Gonadotropin and its Receptor by Hydrogen Exchange and Mass Spectrometry**; Yongsheng Li[1]; Ron Orlando[1]; David Puett[1]; [1]*University of Georgia, Athens, GA*

TP 391 **Conformational Analysis of Type III Secretion Pilins by HDX and Mass Spectrometry**; Olivia Guerre[1]; Jason M. Criscione[1]; Michael D. Stein[1]; Joel S. Lwande[1]; J. Throck Watson[1]; William J. Wedemeyer[1]; [1]*Michigan State University, East Lansing, MI*

TP 392 **Binding Induced Changes in Backbone Dynamics for the Hck YEEI:HIV Nef Protein Complex Observed by HX**

MS; Thomas E. Wales[1]; James M. Hochrein[1]; Edwina C. Lerner[2]; Anthony P. Schiavone[2]; Thomas E. Smithgall[2]; John R. Engen[1]; *[1]University of New Mexico, Albuquerque, NM; [2]University of Pittsburgh School of Medicine, Pittsburgh, PA*

TP 393 **HXMS Reveals Phosphorylation-Dependent Conformational Changes in the catalytic Domain of Lymphocytic Cell Kinase**; David D. Weis[1]; Lori A. Emert-Sedlak[2]; Thomas E. Smithgall[2]; John R. Engen[1]; *[1]University of New Mexico, Albuquerque, NM; [2]University of Pittsburgh, Pittsburgh, PA*

TP 394 **Automated Hydrogen Deuterium Exchange with High Resolution FT-ICR MS Analysis and Enhanced Automated Data Reduction**; Saša Kazazic[1]; Mark R. Emmett[1]; Gregory T. Blakney[1]; Christopher L. Hendrickson[1]; Alan G. Marshall[1]; *[1]ICR Program, NHMFL, Florida State University, Tallahassee, FL*

PEPTIDES: FRAGMENTATION AND SEQUENCING II

TP 395 **Abundant B-Type Ions produced in Electron Capture Dissociation (ECD) of Peptides Without Basic Amino Acid Residues**; Haichuan Liu[1]; Kristina Hakansson[1]; *[1]Department of Chemistry, University of Michigan, Ann Arbor, MI*

TP 396 **The CID and ECD Behavior of Sulfur-Containing Peptides**; Robert J. Chalkley[1]; Katalin F. Medzihradszky[1]; Al L. Burlingame[1]; *[1]UCSF, San Francisco, CA*

TP 397 **B-Ions and Other Odd Fragments in Electron Capture Dissociation**; Kim F. Haselmann[1]; *[1]University of Southern Denamrk, Odense, Denamrk*

TP 398 **Differentiating between Y-ions and B-ions in a CID Spectrum using Positive to Negative Charge Inversion**; Joshua F. Emory[1]; Scott McLuckey[1]; *[1]Purdue University, West Lafayette, Indiana*

TP 399 **Electron Capture Dissociation (ECD) of Bipyridine Capped Peptides and Metal Directed Protein Bundles**; Jace W. Jones[1]; Frank Turecek[1]; David R. Goodlett[1]; Tomikazu Sasaki[1]; *[1]University of Washington, Seattle, WA*

TP 400 **Comparison of Electron Capture Dissociation (ECD) Behaviors of Alanine-Rich Peptides that Contain Lysine Homologues**; Sunyoung Lee[1]; Soojin Park[1]; Han Bin Oh[1]; *[1]Sogang Univestiy, Seoul, South Korea*

TP 401 **A Comparison of Electron-Transfer Dissociation to Collision-Activated Dissociation Tandem Mass Spectrometry for Peptide (1 – 5 kDa) Sequencing**; David M. Good[1]; Matthew Wirtala[1]; Graeme C. McAlister[1]; Danielle L. Swaney[1]; Jae C. Schwartz[2]; Joshua J. Coon[1]; *[1]University of Wisconsin-Madison, Madison, WI; [2]Thermo Electron Corporation, San Jose, CA*

TP 402 **Electron Capture Dissociation Proceeds With a Low Degree of Intramolecular Migration of Amide Hydrogens**; Thomas J.D. Jorgensen[1]; Jesper V. Olsen[3]; Matthias Mann[3]; Peter Roepstorff[1]; Henrik Gardsvoll[2]; Michael Ploug[2]; *[1]University of Southern Denmark, Odense, Denmark; [2]Finsen Laboratory, Rigshospitalet, Copenhagen, Denmark; [3]Max-Planck-Institute of Biochemistry, Martinsried, Germany*

TP 403 **Generation of b-/y- and Atypical Internal Fragment Ions in Electron Capture Dissociation of Peptides**; Eva Yi Man Fung[1]; Kelly Wai Yi Chan[1]; Dominic Tak-Wah Chan[1]; *[1]The Chinese University of Hong Kong, HKSAR, China*

TP 404 **Tryptic Peptide Fragmentation Using Time-Delayed Fragmentation For Specific Y-ion Series Generation;** Alan Morrish[1]; K.W. Michael Siu[1]; *[1]York University, Toronto, Canada*

TP 405 **Electron Transfer Dissociation of Disulfide Linked Polypeptides:Effect of Charge State and Charge Site**; Harsha P. Gunawardena[1]; Scott A. McLuckey[1]; *[1]Purdue University, West Lafayette, IN*

TP 406 **A Novel SID/TOF Source for MALDI-IM-SID-oTOF MS**; Wenjian Sun[1]; David H. Russell[1]; *[1]Texas A&M University, College Station, TX*

TP 407 **Phospho-peptide Fragmentation with Electron Transfer Dissociation Mass Spectrometry**; An Chi[1]; Dina Bai[1]; Lewis Y. Geer[2]; Jeffrey Shabanowitz[1]; Donald F. Hunt[1]; *[1]University of Virginia, Charlottesville, VA; [2]National Center for Biotechnology Information, Bethesda, MD*

TP 408 **Thermally-Induced Fragmentation of Peptide and Protein Ions at Atmospheric Pressure**; Hao Chen[1]; Livia Eberlin[1]; R. Graham Cooks[1]; *[1]Purdue University, West Lafayette, IN*

TP 409 **Mechanisms of Electron Capture Dissociation and Collision-Activated Dissociation are truly Complementary**; Frank Kjeldsen[1]; Mikhail M. Savitski[1]; Michael L. Nielsen[1]; Roman A. Zubarev[1]; *[1]Uppsala University, Uppsala, Sweden*

TP 410 **Electron Transfer Dissociation of Multiply Charged Peptides: Investigation of the Z. + 33Da Adduct**; David E. Erickson[1]; Yu Xia[1]; Paul Chrisman[1]; Sharon Pitteri[1]; Scott A. McLuckey[1]; *[1]Purdue University, West Lafayette, IN*

TP 411 **Dissociation Induced by Electron Transfer of Multiply Charged Ions on Collision with Rare Gas and Alkali Metal Targets**; Shigeo Hayakawa[1]; Akihiro Kitaguchi[1]; Satoko Kameoka[1]; Michisato Toyoda[2]; Toshio Ichihara[2]; *[1]Osaka Prefecture University, Sakai, Osaka, Japan; [2]Osaka University, Toyonaka, Osaka, Japan*

TP 412 **Improved Sequencing of Oxidized Peptides Using Electron Transfer Dissociation in a 3-D Quadrupole Ion Trap**; Richard W. Vachet[1]; Juma D. Bridgewater[1]; Jonathan Wilson[2]; Ali Kettani[2]; *[1]University of Massachusetts, Amherst, MA; [2]Bruker Daltonics, Inc., Billerica, MA*

TP 413 **Comparison of Collision-Induced Dissociation (CID) Fragmentation with Electron Capture Dissociation (ECD) fragmentation of the phospho peptide;** Tomonori Takami[1]; Shohei Shioyama[1]; Rieko Goto[1]; Naoe Yamane[1]; Hisami Murai[1]; Zenzaburo Tozuka[1]; *[1]JCL Bioassay, Nishiwaki, Japan*

TP 414 **Electron Transfer Dissociation for Sequence Characterization of Larger Peptides and Small Proteins**; Jonathan Wilson[1]; Andreas Brekenfeld[2]; Carsten Baessmann[2]; Ralf Hartmer[2]; *[1]Bruker Daltonics, Billerica, MA; [2]Bruker Daltonik, Bremen, Germany*

TP 415 **Mechanistic Elements on the Hydrogen Transfers Occuring during the Electron Capture Dissociation (ECD) of Peptides**; Guillaume van der Rest[1]; Julia Chamot-Rooke[1]; *[1]Ecole Polytechnique, Palaiseau, France*

TP 416 **The Effect of Collision Gas Pressure on the STEP Analysis for Two Mass Spectrometers- Triple quadrupole and Ion Trap**; Dilusha S Dalpathado[1]; Qing Chang[1]; Colleen M Burkett[1]; Mary Bandu[1]; Heather Desaire[1]; *[1]University of Kansas, Lawrence, KS*

TP 417 **Probing the Long-lived Radical Intermediates in Electron Capture Dissociation with a Double Resonance Experiment**; Cheng Lin[1]; Jason J. Cournoyer[1]; Peter B. O'Connor[1]; *[1]Boston University, School of Medicine, Boston, MA*

TP 418 **Electron-Transfer Ion/Ion Reactions of Triply and Doubly Protonated Peptides: Effect of Cooling Gas Pressure**; Hongling Han[1]; Xiaorong Liang[1]; Harsha Gunawardena[1]; Yu Xia[1]; Scott A. McLuckey[1]; *[1]Purdue University, West Lafayette, IN*

PEPTIDES: QUANTITATION

TP 419 **High throughput Quantitative Analysis of Hematide dimer by LC/MS/MS**; JooSoo Hyun[1]; Xun Cheng[1]; Douglas L. Cole[1]; Jing J. Zhang[1]; *[1]Affymax, Inc, Palo Alto, CA*

TP 420 **Identification and Quantitation of Proteins in Plasma and Serum using a Non-Isobaric Labeling Technique**; James E Carlson[1]; Margorie S Minkoff[1]; Scott N Daniels[1]; Brian L Williamson[1]; *[1]Applied Biosystems, Framingham, MA*

TP 421 **Accomplishing Trace Level Quantitation During Bioanalytical Method Development of a Large Peptide**; Greg Rahn[12]; Gene Miller[12]; Todd Branch[12]; Larry Davey[12]; Tom Parish[12]; *[1]Procter & Gamble Pharmaceuticals, Norwich, NY; [2]Procter & Gamble Pharmaceuticals, Mason, OH*

TP 422 **Withdrawn**

TP 423 **Fast and Accurate Protein Quantitation in Biological Samples - an Alternative of ELISA**; Judit Krenyacz[1]; Laszlo Drahos[1]; Zoltan Takats[1]; Karoly Vekey[1]; *[1]Chemical Research Center Hung. Acad. Sci., Budapest, Hungary*

TP 424 **A Method for the Determination of Terlipressin and the Monitoring of Lys8-Vasopressin (analogs of ADH) in Human Plasma via LC-MS/MS;** Lee Winchester[1]; Yousef Basir[1]; Alan Dzerk[1]; Chad Briscoe[1]; Curtis Sheldon[1]; *[1]MDS Pharma Services, Lincoln, NE*

TP 425 **Sensitive Quantification of the Disease Associated Prion Protein PrPSc Using Standard Peptides and Selected Reaction Monitoring**; Dorothea Rutishauser[1]; Erich Brunner[2]; Ralph Schlapbach[1]; Adriano Aguzzi[3]; *[1]Functional Genomics Center Zurich, Zurich, Switzerland; [2]Institute of Zoology, Zurich, Switzerland; [3]Institute of Neuropathology, University Hospital, Zurich, Switzerland*

TP 426 **Quantitation of PYY [3-36] in Human plasma by On-line SPE LC/MS/MS**; Miryam Kadkhodayan[1]; Kevin McCowen[1]; Deirdre Hauser[1]; *[1]Amylin Pharmaceuticals Inc., San Diego, CA*

TP 427 **Online-LC GLAD for Partition Coefficient Determination of Tau-Related Peptides**; Jessica Bereszczak[1]; Federico A. Rojas Quijano[2]; Warren J. Goux[2]; Francesco L. Brancia[1]; *[1]Shimadzu Research Laboratory, Manchester, UK; [2]The University of Texas at Dallas, Richardson, Texas*

TP 428 **Quantitation of Hepcidin in Urine using Deuterated and Non-Deuterated Vinylpyridine Alkylation and SELDI**; Kenyon M Evans-Nguyen[1]; Amanda Ray[1]; Richard D Semba[1]; Luigi Ferrucci[2]; Robert J Cotter[1]; *[1]Johns Hopkins University School of Medicine, Baltimore, MD; [2]National Institute on Aging, Baltimore, MD*

TP 429 **Determination of the Relative and Absolute Stoichiometry of Proteins in Mixtures using Quantitative Mass Spectrometry of Fluorescent Concatenated Peptide Standards**; Dhaval Nanavati[1]; Marjan Gucek[1]; Melinda McFarland[1]; Jacqueline Milne[2]; Sriram Subramaniam[2]; Sanford P. Markey[1]; *[1]National Institute of Mental Health, Bethesda, MD; [2]National Cancer Institute, Bethesda, MD*

TP 430 **Quantitation of Low Abundance Proteins in Human Plasma using Stable Isotope Standards and Capture by Anti-Peptide Antibodies (SISCAPA)**; Angela M Jackson[1]; Derek S Smith[1]; Terry W Pearson[1]; Jamie M Thomas[1]; Leigh N Anderson[2]; *[1]University of Victoria, Victoria, Canada; [2]Plasma Proteome Institute, Washington, DC*

TP 431 **Quantification of Voltage Dependant Anion Channel (VDAC) Protein in Human Alzheimer's disease Brain Mitochondrial Sample by Immunoaffinity Purification and LC-MS/MS;** Anup P. Thakur[1]; Mark A. Lovell[1]; Bert C. Lynn[1]; *[1]University of Kentucky, Lexington, KY*

TP 432 **Quantitative Determination of Methionine Oxidation Product Levels in PEGylated Peptides by LC-MS**; Xun Cheng[1]; JongSoo Hyun[1]; Pallavi Golla[1]; Shan Lin[1]; Douglas L. Cole[1]; Jing J. Zhang[1]; *[1]Affymax, Inc, Palo Alto, CA*

TP 433 **Quantification of Intermediate Abundance Proteins in Serum by Multiple-Reaction-Monitoring (MRM) Mass Spectrometry In a Single-Quadrupole Ion Trap**; Shanhua Lin[1]; Thomas Shaler[1]; Christopher Becker[1]; *[1]PPD, Menlo Park, CA*

TP 434 **Quantitation of Antimicrobial Peptides in Human Saliva**; Michael S. Gardner[1]; Yinfai Amy Siu[1]; James L. Stephenson[1]; *[1]RTI International, Research Triangle Park, NC*

TP 435 **Targeted Protein Absolute Quantification using Isotopic Dilution with Heavy Peptides**; Stéphanie Kirsch[1]; Joëlle Widart[1]; Edwin De Pauw[1]; *[1]University of Liege, Liege, Belgium*

TP 436 **Quantitation of Substance P in Biofluids by LC/ESI, LC/MALDI and Elisa - a Comparative Study**; Klaus C Rumpel[1]; Hendrik Neubert[1]; Marina Lumbreras[1]; Andrew D Scott[1]; *[1]Pfizer Global R&D, Sandwich, Kent, UK*

TP 437 **Stable Isotope Dilution LC-Negative ESI/MS/MS and Immunoaffinity Purification for Analysis of Amyloid Beta Peptides in Alzheimer's Disease**; Tomoyuki Oe[1]; Koichi Inoue[1]; Carlos Garner[2]; Brad L. Ackermann[2]; Ian A. Blair[1]; *[1]Center for Cancer Pharmacology, University of Penn, Philadelphia, PA; [2]Drug Disposition, Eli Lilly and Company, Indianapolis, IN*

PEPTIDES: POST-TRANSLATIONAL MODIFICATIONS I

TP 438 **Using Complementary Hydrazide Chemistry Based Methods with Precursor-Ion Scanning to Characterize Potential in Vivo Sites of HNE Modification**; Mikel R. Roe[1]; Hongwei Xie[1]; Sricharan Bandhakavi[1]; Timothy J. Griffin[1]; *[1]University of Minnesota, St. Paul, MN*

TP 439 **Characterization Of Human Growth Hormone Oxidation Using LC/MS and Peptide Mapping**; Charles Pan[1]; Jane Pepper[1]; Frances Liu[1]; Rosario LoBrutto[1]; Hans Wallny[2]; Alan Jones[1]; Richard Vivilecchia[1]; *[1]Novartis Pharmaceuticals Corporation, East Hanover, New Jersey; [2]Novartis AG, Basel, Switzerland*

TP 440 **Hybrid Linear Ion Trap-FTICR Mass Spectrometer-Based Examination of Histone Post-Translational Modifications in Neurospora Crassa;** D. C. Anderson[1]; Kristina Smith[1]; Ray Green[2]; Eric U. Selker[1]; *[1]Institute of Molecular Biology, Univ. of Oregon, Eugene, OR; [2]Mercer University, Atlanta, GA*

TP 441 ***In vitro* Model of Muscle Aging: Functional, Structural and Chemical Effects of Hydrogen Peroxide Oxidation on Skinned Muscle Fibers**; Daniel J. Spakowicz[1]; Ewa Prochniewicz[1]; Dawn A. Lowe[1]; LeeAnn Higgins[1]; Deborah A. Ferrington[1]; LaDora V. Thompson[1]; David D. Thomas[1]; *[1]University of Minnesota, Minneapolis, MN*

TP 442 **Defining Specificity for Four Previously Uncharacterized Histone Acetyltransferases (HATs) in Arabidopsis;** Rachel A. Reuther[1]; Keith W. Earley[1]; Craig S. Pikkard[1]; Michael L. Gross[1]; *[1]Washington University, St. Louis, MO*

TP 443 **Improved Methods for Comprehensive Sample Analysis Using Protein Prospector**; Peter R Baker[1]; Robert J Chalkley[1]; Katalin F Medzihradszky[1]; June O Snedecor[1]; Alma L Burlingame[1]; *[1]UCSF, San Francisco, CA*

TP 444 **Characterisation, Identification and Prediction of n-Terminus Acetylated Proteins;** Samuel Kanor[1]; Ioannis Xenarios[3]; Anne Estreicher[4]; Manfredo Quadroni[1]; Willy V Bienvenut[2]; *[1]Protein Analysis Facility, University of Lausanne, Epalinges, Switzerland; [2]The Beatson Institute for Cancer Research, Glasgow, United-Kingdom; [3]Serono pharmaceutical research institute, Plan-les-Ouates, Switzerland; [4]Swiss Institute of Bioinformatics, Geneva, Switzerland*

TP 445 **Mapping Sites of Asparagine Deamidation in Recombinant Proteins by MALDI TOF and MALDI tandem TOF mass spectrometry**; Peter S. Backlund[1]; Pradeep Gupta[2]; Stephen H. Leppla[2]; Alfred L. Yergey[1]; *[1]NICHD, National Institutes of Health, Bethesda, MD; [2]NIAID, National Institutes of Health, Bethesda, MD*

TP 446 **Specific Modification of Citrulline Containing Peptides and their Characterization by MALDI- and ESI Mass Spectrometry**; Anders Holm[1]; Nicole Sessler[1]; Frode Rise[2]; Ludvig M Sollid[1]; Kjell Undheim[2]; Burkhard Fleckenstein[1];

[1]*University of Oslo, Institute of Immunology, Oslo, Norway;* [2]*University of Oslo, Department of Chemistry, Oslo, Norway*

TP 447 **Modification of Peptides by Lipid Peroxidation Products Studied by MALDI-MS/MS using a TOF/TOF Instrument**; Jianyong Wu[1]; Claudia Maier[1]; [1]*Oregon State University, Corvallis, OR*

TP 448 **Direct Detection of Covalent Lipidations of Mammalian Plasma ApoA-I**; Frederic J. Halgand[1]; Lang Yam[1]; Sara Bassilian[1]; Pedram Ghasri[1]; Puneet Souda[1]; Kym F. Faul[1]; Verne Schumaker[1]; Don Puppione [1]; Julian P. Whitelegge[1]; [1]*The Pasarow Mass Spectrometry Laboratory, UCLA, Los Angeles, CA*

TP 449 **Comprehensive Analysis of Aldehyde Modifications by LC-ESI LTQ-FT MS Methods**; Erin M Shonsey[1]; Shannon M Eliuk[1]; Marion Kirk[1]; Helen Kim[1]; Matthew Renfrow[1]; Stephen Barnes[1]; [1]*University of Alabama at Birmingham, Birmingham, AL*

TP 450 **Two-Pass Searches Using Protein-Specific Custom Databases to Determine Protein Truncation Sites**; Jason C. Rogalski[1]; Matthew J. Sniatynski[1]; Sebastian G.B. Furness[1]; Kelly M. McNagny[1]; Juergen Kast[1]; [1]*The Biomedical Research Centre, Vancouver, Canada*

TP 451 **Identification and Characterization of Deamidation in anti-EGFR Monoclonal Antibody Cetuximab**; Li Yang[1]; Tun Liu[1]; Jay Charlebois[1]; Yuemei Ma[1]; Babita Saxena[1]; Ann Daus[1]; S.Joseph Tarnowski[1]; Qinwei Zhou[1]; [1]*ImClone Systems Incorporated, Branchburg, NJ*

TP 452 **Electron Capture Dissociation and Electron Transfer Dissociation for Identification of p53 Dependent Histone Modifications Following Topoisomerase I Mediated DNA Damage**; C. Logan Mackay[1]; Stefan Weidt[1]; Emma Carrick[2]; Mike Lang[2]; J. Kenicer[2]; Yves Pommier[3]; Ted Hupp[2]; Pat Langridge-Smith[1]; R. Larry Hayward[2]; [1]*SIRCAMS, University of Edinburgh, Edinburgh, UK;* [2]*Edinburgh Cancer Centre, Edinburgh, UK;* [3]*Laboratory of Molecular Pharmacology, Bethesda, MD*

TP 453 **LC/MS/MS Characterization of Oxidized Amyloid Beta Peptides as Potential Biomarkers of Alzheimer's Disease**; Koichi Inoue[1]; Carlos Garner[2]; Brad L. Ackermann[2]; Tomoyuki Oe[1]; Ian A. Blair[1]; [1]*University of Pennsylvania, Philadelphia, PA;* [2]*Lilly Corporate Center, Indianapolis, IN*

TP 454 **Reliable Identification of Deamidations from Tandem Mass Spectrometry Data Using Corrected Parent Ion Masses and Chromatographic Time Differences;** Surendra Dasari[1]; Phillip A. Wilmarth[2]; D. Leif Rustvold[2]; Larry L. David[2]; Srinivasa R. Nagalla[1]; [1]*School of Medicine, Oregon Health & Science Univ., Portland, OR;* [2]*School of Dentistry, Oregon Health & Science Univ., Portland, OR*

TP 455 **Characterization of Stable Cysteine Sulfenic Acid in a Synthetic Peptide PRCGVPDVA of Pro-Matrix Metalloproteinase-7 (Pro-MMP-7)**; Vivekananda Shetty[1]; Thomas A Neubert[1]; [1]*New York UniVersity School of Medicine, New York, NY*

TP 456 **Analysis of Dynamic Changes in Post-Translational Modifications of Human Histone During Cell Cycle by Mass Spectrometry**; Débora Bonenfant[1]; Harry Towbin[1]; Michèle Coulot[1]; Adrian Salathé[1]; Patrick Schindler[1]; Jan Van Oostrum[1]; [1]*Novatis Institutes of Biomedical Research, Basel, Switzerland*

TP 457 **Histone Post-translational Modification Analysis Using High Energy Collisions on a Tandem TOF/TOF Mass Spectrometer with a Curved Field Reflectron**; Robert Cotter[1]; Omar Belgacem[2]; Wendell Griffith[1]; Rachel Martin[2]; Emmanuel Raptakis[2]; [1]*Johns Hopkins University School of Medicine, Baltimore, MD;* [2]*Shimadzu Biotech, Manchester, United Kingdom*

PHOSPHOPEPTIDE ENRICHMENT

TP 458 **Cell Cycle-Defined Phosphoproteome Analysis of Cancer Cells by Titanium Dioxide Enrichment and Mass Spectrometry**; Li-Rong Yu[1]; Zhongyu Zhu[2]; King C. Chan[1]; Thomas P. Conrads[1]; Haleem J. Issaq[1]; Dimiter S. Dimitrov[2]; Timothy D. Veenstra[1]; [1]*SAIC-Frederick, Inc., Frederick, MD;* [2]*National Cancer Institute at Frederick, Frederick, MD*

TP 459 **Selective Zirconium Dioxide-Based Enrichment of Phosphorylated Peptides for Mass Spectrometric Analysis**; Hye Kyong Kweon[1]; Kristina Hakansson[1]; [1]*University of Michigan, Ann Arbor, MI*

TP 460 **Phosphoproteome analysis of Human Stem Cell Plasma Membranes using TiO2 Columns and Mass Spectrometry**; Tine E. Thingholm[1]; Martin R. Larsen[1]; Leonard J. Foster[2]; Moustapha Kassem[3]; Ole N. Jensen[1]; [1]*Biochemistry and Molecular Biology, Odense, Denmark;* [2]*Biochemistry and Molecular Biology, BC, Vancouver, Canada;* [3]*Clinic of Endocrinology Treatment, Odense, Denmark*

TP 461 **Evaluation of the Titanium Oxide-Based Phosphopeptide Enrichment in Phosphoproteomics**; Clementine Klemm[1]; Sebastian Otto[1]; Constanze Wolf[1]; Michael Beyermann[1]; Eberhard Krause[1]; [1]*Institute of Molecular Pharmacology, Berlin, Germany*

TP 462 **Profiling the Phosphoproteome of Endometrial Carcinoma**; Adrian M. Taylor[1]; Leroi DeSouza[1]; K.W. Michael Siu[1]; [1]*York University, Toronto, ON, Canada*

TP 463 **Phosphorylation Site Mapping of an Arabidopsis Di19 Protein by a Calcium-Dependent Kinase with TiO_2 Column Enrichment;** Ing-Feng Chang[1]; David R. Quilici[1]; [1]*University of Nevada, Reno, Reno, NV*

TP 464 **Comparison Between the Behavior of Different Sorbents Commonly Used for the Selective Isolation of Phosphopeptides from Complex Peptide Mixtures**; Stefano Gotta[1]; Georg C. Terstappen[1]; Roberto Raggiaschi[1]; [1]*Sienabiotech S.p.A. Discovery Research, Siena, Italy*

TP 465 **A Novel Mixed Mode Chromatography Method for the Isolation and Separation of Phosphopeptides**; Ying Qing Yu[1]; Jennifer Fournier[1]; Petra Olivova[1]; Martin Gilar[1]; John Gebler[1]; [1]*Waters Corporation, Milford, MA*

TP 466 **Analysis of Phosphopeptides using Off-line TiO2 Microcolumns Followed by Nano-HPLC Coupled to ESI Ion Trap**; JUAN CASADO-VELA[1]; Antonio Núñez[1]; Jose Ignacio CASAL[1]; [1]*CNIO. Spanish National Cancer Centre, MADRID, SPAIN*

TP 467 **Phosphopeptide Enrichment for Mass Spectrometry Analysis Using Micro Scale Titanium Dioxide Solid Phase Extraction**; Jennifer Fournier[1]; Ying Qing Yu[1]; Martin Gilar[1]; Grace M. Credo[1]; Weibin Chen[1]; John C. Gebler[1]; [1]*Life Science R&D, Waters Corporation, Milford, MA*

TP 468 **Optimization of IMAC and TiO2 Chromatography for Phosphoproteomics**; Susumu Imanishi[1]; Hanna-Mari Pallari[1]; Vitaly Kochin[1]; John E. Eriksson[1]; [1]*Turku Centre for Biotechnology, Turku, Finland*

TP 469 **Unraveling the Phosphoproteome by Combinations of SCX, TiO2 Phosphopeptide Enrichment, Chip Based LC and Electron Transfer Induced Dissociation;** Shabaz Mohammed[1]; Martijn Pinkse[1]; Joris Benschop [1]; Albert JR Heck[1]; [1]*Utrecht University, Utrecht, The Netherlands*

TP 470 **Metal Affinity Capture Tandem Mass Spectrometry for the Selective Detection of Phosphopeptides**; Grady R. Blacken[1]; Michael H. Gelb[1]; František Turecek[1]; [1]*University of Washington, Seattle, WA*

TP 471 **Using Titanium Dioxide to Selective Enrich and Fractionate Phosphorylated Peptides from Complex Mixtures**; David R. Craft[1]; Kenneth A. Chisholm[1]; Devanand M. Pinto[1]; [1]*National Research Council - IMB, Halifax, Canada*

TP 472 **Comparison of IMAC and TiO2 Methodologies for Phosphopeptide Enrichment before MALDI-TOF Analysis**; Eliandre Oliveira[1]; Oscar Blanco[2]; Maria Antonia Odena[1]; *[1]Barcelona Science Park - University of Barcelona, Barcelona, Spain; [2]IRB_Biomedical Research Institute, Barcelona Scien, Barcelona, Spain*

TP 473 **Label-free Comparative Study of Phosphatase Inhibitor Induced Phosphoproteomics Using Data-directed Analysis**; feng yang[1]; Navdeep Jaitly[1]; Hemalatha Jayachandran[2]; quanzhou luo[1]; Marina Gristenko[1]; David J. Anderson[1]; rui zhang[1]; Samuel O. Purvine[1]; Ronald J. Moore[1]; Heather M. Mottaz[1]; Mary S. Lipton[1]; David G. Camp, II[1]; Harold R. Udseth[1]; Sandra Rossie[2]; Richard D. Smith[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]Department of Biochemistry, Purdue University, West Lafayette, IN*

TP 474 **Global Phosphoproteome Analysis by Combining Highly Selective TiO2 Enrichment and EDTA-Enhanced Detection by LC-MS**; Cunjie Zhang[1]; Suya Liu[1]; John Lenehan[1]; David W. Litchfield[1]; Gilles A. Lajoie [1]; *[1]The University of Western Ontario, London, Canada*

PROTEOMICS: FUNDAMENTAL STUDIES

TP 475 **Analysis of the Extracellular Matrix and Vesicle Proteomes in Osteoblasts**; Zhen Xiao[1]; Corinne E. Camalier[2]; Kunio Nagashima[1]; King C. Chan[1]; David A. Lucas[1]; Stephen Lockett[1]; Haleem J. Issaq[1]; Timothy D. Veenstra[1]; George R. Beck, Jr. [2]; Thomas P. Conrads[2]; *[1]SAIC-Frederick, Inc., Frederick, MD; [2]Emory University, Atlanta, GA*

TP 476 **Enzymes Screening with Enzymatic Proteomics**; Chao-Lin Liu[1]; Yu-Sheng Chen[1]; Jeen-Kuan Chen[3]; Long-Chung Wu[1]; Chia-Rui Shen*[2]; *[1]MingChi University of Technology, Taishan, Taiwan; [2]Chang Gung University, Kweishan, Taiwan; [3]Chinese Petroleum Company, Chiayi, Taiwan*

TP 477 **Evaluation of Methionine Oxidation State on the Efficacy of MS/MS based Database Search Analysis Strategies**; Jennifer M. Froelich[1]; Gavin E. Reid[1]; *[1]Michigan State University, East Lansing, MI*

TP 478 **Efficient detection of fragment ions and its utilization for protein identification using Curved Field Reflectron-based High Energy CID MS/MS**; Yuzo Yamazaki[1]; Masaki Yamada[1]; Hiroki Nakajima[1]; Hiroyuki Fukuda[1]; *[1]Life Science Laboratory, Shimadzu Corpration, Kyoto, Japan*

TP 479 **Altering Electrospray Responses of Peptides via Zwitterionic Additives**; Tegafaw T. Mekecha[1]; Harsha P. Gunawardena[1]; Scott A. McLuckey[1]; *[1]Purdue University, West Lafayette, IN*

TP 480 **Stable Isotope Labelling Strategies to Measure the Dynamics of Protein Turnover on a Proteome-Wide Scale in Intact Animals**; Ian J Edwards[1]; Mary K Doherty [1]; Rob J Beynon[1]; Dominique Rocha[2]; Heather McCormack[3]; Colin Whitehead[3]; *[1]University of Liverpool, Liverpool, United Kingdom; [2]Genus Plc, Cambridge, United Kingdom; [3]Roslin Institute, Edinburgh, Scotland*

TP 481 **Cooporative Effect of Factors Governing Molecular Ion Yield in Desorption/ionization Mass Spectrometry**; Takashi Nishikaze[1]; Mitsuo Takayama[1]; *[1]Yokohama City Univercity, Yokohama, Japan*

TP 482 **Building Cotyledon Proteome Map in Arabidopsis thaliana using Two Dimensional Gel Electrophoresis and Multi dimensional Protein Identification**; Brahmananda Reddy Chitteti[1]; Zhaohua Peng[1]; *[1]Mississippi State University, Starkville, MS*

TP 483 **Reproducible and Specially Designed Internal Process Performance Standards for in-Gel Protein Identification using LC/MS/MS;** D. Eric Anderson[1]; *[1]PMSF/NIDDK/NIH, Bethesda, Maryland*

TP 484 **Improving Top Down Sequencing of Proteins on a Quadrupole Ion Trap Mass Spectrometer Using Heavy Gases**; Angela M. Fahey[1]; Richard W. Vachet[1]; *[1]University of Massachusetts, Amherst, MA*

TP 485 **Tsg101 Gene Knock Down using siRNA, and its Effect on Protein Expression in 293 Mammalian Cells using SILAC Technology;** Mahbod Hajivandi[1]; Xiquan Liang[1]; Marshall Pope[1]; *[1]Invitrogen, Carlsbad, California*

TP 486 **Global Survey of Organ and Organelle Protein Expression in Mouse through Combined Proteomic and Transcriptomic Profiling**; Thomas Kislinger[1]; Brian Cox[2]; Anitha Kannan[1]; Clement Chung[1]; Pingzhao Hu[1]; Alexandr Ignatchenko[1]; Michelle S. Scott[3]; Anthony O. Gramolini[1]; Quaid Morris[1]; Michael T. Hallett[3]; Janet Rossant[2]; Timothy R. Hughes[1]; Brendan Frey[1]; Andrew Emili[1]; *[1]University of Toronto, Toronto, ONT Canada; [2]Hospital for Sick Children, Toronto, ONT Canada; [3]McGill University, Montreal, QC Canada*

TP 487 **New strategies for a "Peptide Mass Fingerprint" Database Search using Less Specific Proteolytic Enzymes**; Björn Meyer[1]; Bernd Ludwig[1]; Michael Karas[1]; *[1]J.W. Goethe University, Frankfurt am Main, Germany*

TP 488 **Bath Gas Pressure Effects on Protein Charge State Distribution and Intensity**; Brittany L. Butler[1]; Gary L. Glish[1]; *[1]The University of North Carolina at Chapel Hill, Chapel Hill, NC*

TP 489 **Bioinformatic Analysis of Body Fluid Proteomes**; Søren Schandorff[1]; Jun Adachi[2]; Bartosz Pilch[2]; Gustavo De Souza[2]; Matthias Mann[2]; Alexandre Podtelejnikov[1]; *[1]Proxeon, Odense, Denmark; [2]Max Planck Institute of Biochemistry, Martinsried, Germany*

TP 490 **The Study of the Effect of MicroRNA on Protein Expression in Cultured Cells**; Haibo Qiu[1]; Yinsheng Wang[1]; *[1]University of California, Riverside, Riverside, CA*

PROTEOMICS: NEW METHODS II

TP 491 **Automated Ultra-high Pressure Multidimensional Protein Identification Technology (MudPIT) for Improved Peptide Identification of Proteomic Samples**; Akira Motoyama[1]; John D. Venable[1]; Cristian I. Ruse[1]; John R. Yates, III[1]; *[1]The Scripps Research Institute, La Jolla, CA*

TP 492 **Proteomic Analysis of Ubiquitinated Proteins from Human MCF-7 Cells Using a Novel Gel-Free Approach**; Julian Vasilescu[1]; Nicholas Denis[1]; Martin Ethier[1]; Daniel Figeys[1]; *[1]Ottawa Institute of Systems Biology, Ottawa, Canada*

TP 493 **Low Pressure Liquid Chromatographic (LPLC) Peptide Separation Allows for Fast and Accurate Protein Identification by Online ESI MS/MS;** Ole Hørning[1]; Ole Nørregaard Jensen[1]; Ole Vorm[2]; *[1]University of Southern Denmark, Odense, Denmark; [2]Proxeon Biosystems A/S, Odense, Denmark*

TP 494 **Comprehensive Characterization of Post-Translational Modifications In Vivo Using NanoLC-ESI-q-TOF Tandem Mass Spectrometry: Selectively Excluded Mass Screening Analysis (SEMSA)**; Jawon Seo[1]; Jaeho Jeong[1]; Kong-Joo Lee[1]; *[1]Center for Cell Signaling Research, SEOUL, Korea*

TP 495 **Processing ESI-MS1 Data Obtained on a Q-TOF Mass Spectrometer to Improve the Results of Protein Analysis**; Nadezhda A Galeva[1]; Lei Jiang[1]; Asma Zaidi[1]; Mary L Michaelis[1]; Todd D Williams[1]; *[1]University of Kansas, Lawrence, KS*

TP 496 **Proteomic Approach for Characterization of Lipid Modified Proteins**; Chie Murata[1]; Yoshiya Oda[1]; Moonjin Ra[1]; Kazutaka Ikeda[1]; Takao Shimizu[1]; Ryo Taguchi[1]; *[1]The University of Tokyo, Tokyo, Japan*

TP 497 **Fast LC-MS strategies for protein identification and modification characterization of a gel-free Ash1 immunoprecipitation;** David M Cox[1]; Brett Larsen[2]; Chris

Lock[1]; Nic Bloomfield[1]; QuinQuan Liu[2]; Marcia Roy[2]; Mike Tyers[2]; [1]*Applied Biosystems / MDS Sciex, Concord, Canada;* [2]*Samuel Lunenfeld Research Institute, Toronto, Canada*

TP 498 **ppTime-of-Flight Mass Spectrometry for the Identification of c-type Cytochromes from Geobacter Species**; Angela J. Ahrendt[1]; Carl Lindberg[1]; Gyorgy Babnigg[1]; Kelly P. Nevin[2]; Derek R. Lovley[2]; Carol S. Giometti[1]; [1]*Argonne National Laboratory, Argonne, IL;* [2]*University of Massachusetts, Amherst, MA*

TP 499 **Digitized Nanobore LC-MS Control System with Integrated Emitter Divert and Rinse for Improved Nanospray Performance**; James L. Stephenson[1]; Jonathan L. Bundy[1]; Gary A. Valaskovic[2]; Mike S. Lee[3]; [1]*RTI International, Research Triangle ParK, NC;* [2]*New Objective Inc., Woburn, MA;* [3]*Milestone Development Services Inc., New Town, PA*

TP 500 **Miniaturized Multi-dimensional LC-MS Platform Using 20 µm ID Monolithic Columns and Novel Microfluidic Connectors for Enhancing Proteomic Dynamic Range**; Eileen Yue[1]; Shiaw-Lin Wu[1]; Gary Valaskovic[2]; Barry Karger[1]; [1]*Northeastern University, Boston, MA;* [2]*New Objective, Woburn, MA*

TP 501 **The Impact of High Efficiency Peptide Separations on Dissecting the Human Serum Proteome**; Koen Sandra[1]; Christine Labeur[1]; Gregoire Thomas[1]; Lies Vanneste[1]; Filip D'Hondt[1]; Koen De Cremer[1]; Koen Kas[1]; Pat Sandra[2]; Katleen Verleysen[1]; [1]*Peakadilly N.V., Zwijnaarde, Belgium;* [2]*Research Institute for Chromatography (RIC), Kortrijk, Belgium*

TP 502 **Protein Identification in Human Plasma by Integrated Multidimensional Liquid Chromatography (IMDL) Coupled with Mass Spectrometry**; Jie Dai[1]; Chia-Hui Shieh[1]; Rong Zeng[1]; [1]*Shanghai Institutes for Biological Scineces, Shanghai, China*

TP 503 **High Dynamic Range Protein Mapping by Automated Nanoelectrospray Combined with an Orbitrap**; Ai-Ping Lu[1]; Reinaldo Almeida[2]; Jesper V. Olsen[1]; Guoqing Li[1]; Matthias Mann[1]; [1]*Max-Planck Institute for Biochemistry, Munich, Germany;* [2]*Advion Biosciences Limited, Norfolk, UK*

TP 504 **Increased Sequence Coverage in Protein Analysis using Automated Nanofraction Collection in Combination with Nanospray MS/MS Infusion**; Maria Eugenia Soria-Diaz[1]; Emmanuel Varesio[1]; Gerard Hopfgartner[1]; [1]*LSMS, EPGL-University of Geneva, Geneva, Switzerland*

TP 505 **Effect of Guanidination-Dimethylation Labeling for Membrane Proteome Analysis Using Nano-LC-ESI QTOF**; Chengjie Ji[1]; Andy Lo[1]; Sandra L. Marcus[1]; Liang Li[1]; [1]*University of Alberta, Edmonton, Canada*

TP 506 **Fully Automated Top-Down Protein Identification using µLC-MSn on a Linear Ion Trap Mass Spectrometer**; Jesse D. Canterbury[1]; Peter Brzovic[1]; Rachel E. Klevitt[1]; Michael J. MacCoss[1]; [1]*University of Washington, Seattle, WA*

TP 507 **Effects of LC-ESI QTOF MS/MS Data Acquisition Methods on Proteome Analysis of Tissue Samples**; Nan Wang[1]; Jing Zheng[1]; Randy Whittal[1]; Liang Li[1]; [1]*University of Alberta, Edmonton, Canada*

TP 508 **HPLC Elution Shifts Reflecting Protein-Protein Interactions and Post-Translational Modifications detected by Mass Spectrometry**; Samuel L. Perkins[1]; Lili Niu[2]; William K. Russell[1]; Neil Sharma[3]; Issa Isaac[3]; Matthew M. Champion[4]; Deborah A. Siegele[5]; James C. Hu[2]; David H. Russell[1]; [1]*Chemistry Department, Texas A&M University, College Station, TX;* [2]*Biochemistry Department, Texas A&M University, College Station, TX;* [3]*Genomic Solutions, Ann Arbor, MI;* [4]*Applied Biosystems, Foster City, CA;* [5]*Biology Department, Texas A&M University, College Station, TX*

TP 509 **Improved Hydrophobic Peptide Recovery during Online 2D Nano LC/MS/MS for Proteomic Analysis**; Hongji Liu[1]; Jeffrey W. Finch[1]; John C. Gebler[1]; [1]*Waters Corporation, Milford, MA*

TP 510 **Automated capillary HPLC Systems for Mass Spectrometric Analyses of Proteomic and Metabolomic Samples**; Eric A. Livesay[1]; Rui Zhao[1]; Keqi Tang[1]; Yufeng Shen[1]; Daniel J. Orton[1]; Tom O. Metz[1]; Michael A. Buschbach[1]; Beverley K. Taylor[1]; Ronald J. Moore[1]; Gordon A. Anderson[1]; Harold R. Udseth[1]; Richard D. Smith[1]; [1]*Pacific Northwest National Laboratory, Richland, WA*

TP 511 **Improved Protein Separation and Identification from Mass Spectrometry-Based Proteomics Experiments by use of 2D Liquid Protein Fractionation**; Konstantinos Thalassinos[1]; Susan E. Slade[1]; Martha M. Clokie[1]; Nicholas H. Mann[1]; James H. Scrivens[1]; [1]*University of Warwick, Coventry, United Kingdom*

TP 512 **Utilization of Temperature to Improve LC/MS Preformance in Proteomics**; Kerry Nugent[1]; Peter Kent[1]; Eric Kemp[1]; Lori Ann Upton[1]; [1]*Michrom Bioresources, Inc., Auburn, CA*

TP 513 **Reversed-Phase Separation, on-Line Digestion, and Automated MS Identification of Proteins at Picogram Levels**; Gordon W. Slysz[1]; David C. Schriemer[1]; [1]*University of Calgary, Calgary, Canada*

TP 514 **Rapid Determination of Disulfide Bonds in Large Proteins by Top Down Liquid Chromatography Mass Spectrometry**; Ying Ge[1]; Dong S. Zhao[1]; Andy S. Lemoff[1]; Xuelin Gu[1]; Derek M. Wood[1]; Xiaoya Ding[1]; [1]*PPD, Inc., Madison, WI*

TP 515 **Improved Matching of Methionine Oxide-containing Peptides by Including Neutral Loss from Methionine Oxide Residues**; Andrew J Thompson[1]; Ritchie Williamson[1]; Helen L Byers[2]; James Campbell[2]; Malcolm Ward[2]; Brian Anderton[1]; [1]*MRC Centre for Neurodegeneration Research KCL, IOP, London, UK;* [2]*Proteome Sciences plc, London, UK*

TP 516 **Protein Sequence Coverage Optimization by HPLC Separation and Consecutive Enzymatic Digestion**; Pavel Metalnikov[1]; Andrei Starostine[1]; Vivian Nguyen[1]; [1]*Samuel Lunenfeld Research Institute, Toronto, Canada*

TP 517 **Rapid Determination of a Protein's Optimal MRM Transition for Sensitive Detection in Complex mixtures**; Michael A. Kuzyk[1]; S.-W. Grace Cheng[1]; Gregg B. Morin[1]; [1]*Genome Sciences Centre, B.C. Cancer Agency, Vancouver, Canada*

TP 518 **Novel Strategies for Expression Profiling of Low Abundance Proteins in Human Serum**; Lining Qi[1]; Lifang Yang[1]; Rebecca Pitts[2]; Xiangming Fang[3]; O. John Semmes[1]; [1]*Eastern Virginia Medical School, Norfolk, VA;* [2]*Bruker Daltonics Inc., Billerica, MA;* [3]*GenWay Biotech, Inc., San Diego, CA*

TP 519 **Investigation of Atypical Peptides Found via Thorough Database Search**; Alpesh A Patel[1]; Wilfred H Tang[1]; Sean L Seymour[1]; Ignat V Shilov[1]; Daniel A Schaeffer[1]; [1]*Applied Biosystems|MDS Sciex, Foster City, CA*

TP 520 **Intact Protein Separation and Identification by non-Porous Reversed Phase Liquid Chromatography and Mass Spectrometry;** Claire Dauly[1]; David H. Perlman[1]; Hua Huang[1]; Mark E. McComb[1]; Catherine E. Costello[1]; [1]*Boston University School of Medicine, Boston, MA*

TP 521 **Digging Deeper into the Plant Proteome with Monolithic LC-MS/MS**; David P Sumpton[1]; Emma Edwards[1]; James Ault[1]; João Rodrigues[1]; Clara Diaz[2]; Herman P Spaink[2]; Jerry R Thomas[1]; Jane Thomas-Oates[1]; [1]*University of York, York, UK;* [2]*Leiden University, Leiden , Netherlands*

TP 522 **Highly Specific Enrichment of Phosphorylated Peptides from Peptides Mixtures utilizing Magnetic Nanoparticles**; He-Hsuan Hsiao[1]; Hsin-Yu Hsieh[1]; Shu-Yu Lin[1]; Chi-Chi Chou[1]; Andrew H.-J. Wang[2]; Kay-Hooi Khoo[2]; [1]*Core*

Facilities for Proteomic Research, Academia Sinica, Taipei, Taiwan; [2]Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan

TP 523 **Purification and Characterization of the Human 26S Proteasome using a New Tandem Affinity Purification Strategy and Quantitative Mass Spectrometry**; Xiaorong Wang[1]; Chi-Fen Chen [2]; Cortnie Guerrero[1]; Peter Baker [3]; Phang-lang Chen[2]; Peter Kaiser[2]; Lan Huang[1]; *[1]Dept of Physiology & Biophysics, UC Irvine, Irvine, CA; [2]Dept of Biological Chemistry, UC-irvine, Irvine, CA; [3]3Dept of Pharmaceutical Chemistry, UCSF, San Francisco, CA*

TP 524 **Comparison of an Affinity MALDI Plate and Magnetic beads Conjugated with Phenylboronic acid for Direct Detection of Glycoproteins**; Jeong Heon Lee[1]; Moonkwon Lee[2]; Jungsuk Park[3]; Hyoung Soon Park[4]; Yangsun Kim[1]; *[1]Proteonik, INC, Ansan, Korea; [2]Microbiochip Ct., Ansan, Korea; [3]Korea Polytechnic University, Siheung, Korea; [4]ProBiond,co,ltd, Seoul, Korea*

TP 525 **Analysis of BCL2 Proteins Interactions by Tandem Mass Spectrometry**; David K. Crockett[1]; Amit R. Phansalkar[1]; Megan S. Lim[2]; Kojo S.J. Elenitoba-Johnson[2]; *[1]ARUP Laboratories, Salt Lake City, UT; [2]University of Utah School of Medicine, Salt Lake City, UT*

TP 526 **Use of Ethylenediaminetetraacetic Acid (EDTA) - Magnetic Bead Complex in Protein Isolation and Detection by MALDI-TOF Mass Spectrometry**; Mohammad Abul Farah[1]; Jeong Heon Lee[1]; Yangsun Kim[1]; *[1]Proteonik Inc., Ansan City, South Korea*

TP 527 **Proteomic Mapping of the Vascular Endothelium Luminal Surface for Tissue Specific Target Identification**; Eric Sousa[1]; Xiang-Yang Tan[1]; Wei Liu[1]; Vasu Maganti[1]; Yongchang Qiu[1]; Debra Pittman[1]; Jeffrey Feldman[1]; Robert Schaub[1]; James Keith[1]; Davinder Gill[1]; Steve Herrmann[1]; Jiang Wu[1]; *[1]Wyeth Research, Cambridge, MA*

TP 528 **Analysis of cGMP/cAMP Signaling Pathways Using a Chemical Proteomics Approach in Heart Tissue**; Arjen Scholten[1]; Mee Kian-Poh[1]; Toon van Veen[1]; Marc Vos[1]; Albert J R Heck[1]; *[1]Utrecht University, Utrecht, Netherlands*

TP 529 **A New Tandem Affinity Tag to Study Proteome-Wide Ubiquitination and ULP modification Profiles;** Christian Tagwerker[1]; *[1]UC Irvine, Irvine, CA*

TP 530 **Proteomic Analysis of Human Blood Serum using Peptide Library Beads**; Lau Sennels[1]; Mogjiborahman Salek[2]; Lee Lomas[3]; Egisto Boschetti[3]; Pier G. Righetti[4]; Juri Rappsilber[1]; *[1]The Wellcome Trust Center, University of Edinburgh, Edinburgh, United Kingdom; [2]FIRC Institute for Molecular Oncology Foundation, Milan, Italy; [3]Ciphergen Biosystems Inc, Fremont, CA; [4]Polytechnic of Milano, MIlan, Italy*

TP 531 **Pathogen derived MHC-Binding Peptides – A Proteomics Approach to their Identification**; Karin M Green[1]; Iwona Strug[1]; Jinal Patel[1]; Shibani Mitra-Kaushik[1]; Lawrence J Stern[1]; James E Evans[1]; *[1]University of Massachusetts Medical School, Worcester, MA*

TP 532 **Peptide and Protein Analysis by MALDI-TOF MS using Magnetic Bead Based Metal Ion Affinity Chromatography**; Katja Blaesing[1]; Thomas Elssner[2]; Markus Kostrzewa[2]; *[1]Hochschule Anhalt, Köthen, Germany; [2]Bruker Daltonik GmbH, Leipzig, Germany*

TP 533 **High Throughput Mass Spectrometric Immunoassays in Human Plasma Profiling and Targeted Protein Analysis**; Randall W Nelson[1]; Urban A Kiernan[1]; Dobrin Nedelkov[1]; Kemmons Tubbs[1]; Eric E Niederkofler[1]; *[1]Intrinsic Bioprobes, Inc., Tempe, AZ*

TP 534 **Targeted Proteomic Analysis of Active Transcription Factor Complexes using Oligoprecipitation**; Zhaojing Meng[1]; Corinne E. Camalier[2]; David A. Lucas[1]; Timothy D. Veenstra[1]; George R. Beck, Jr. [2]; Thomas P. Conrads[1]; *[1]SAIC-Frederick, Inc., Frederick, MD; [2]Emory University School of Medicine, Atlanta, GA*

PROTEOMICS: SAMPLE PREPARATION AND FRACTIONATION II

TP 535 **Temporal Separation of Endocytotic Pathway Vesicles by Magnetic Fractionation and Subsequent Proteomic Analysis**; Gregg A Czerwieniec[1]; Georgia Dolios[1]; Fannie W Chen[1]; Yiannis A Ioannou[1]; Rong Wang[1]; *[1]Mount Sinai School of Medicine, New York, NY*

TP 536 **Multi dimensional Chromatography Coupled with MALDI-TOF/TOF for Proteomic Analysis of Complex Samples**; Stephanie Hahner[1]; Urs Lewandrowski[2]; Albert Sickmann[2]; Sven Brand[1]; Jörg Glandorf[1]; Wolfgang Jabs[1]; Sergei Dikler[3]; Detlev Suckau[1]; *[1]Bruker Daltonik GmbH, Bremen, D; [2]Rudolf-Virchow-Zentrum, University Würzburg, Würzburg, D; [3]Bruker Daltonics, Billerica, MA*

TP 537 **Negative-Pressure Liquid Chromatography (nPLC): Design and Performance of a Novel Off-Line Separation-Deposition Interface for MALDI-Mass Spectrometry;** Vincent C. Chen[1]; Vlad-Andre Ionescu[1]; James I. Nagy[1]; Helene Perreault[1]; *[1]University of Manitoba, Winnipeg, Canada*

TP 538 **Sequential Extraction of *E. coli* Outer Membrane Proteins for Bottom-up Proteomic Analysis of Low Abundance Proteins at Different Growth Phases**; Leon H.Y. Lau[1]; Andy Lo[1]; Chengjie Ji[1]; Monica M. Palcic[2]; Liang Li[1]; *[1]University of Alberta, Edmonton, Canada; [2]Carlsberg Research Center, Copenhagen, Denmark*

TP 539 **Removal of High Abundance Proteins for Proteomic Analysis of Cerebrospinal Fluid (CSF) using Molecular Weight Cutoff Filters;** Kevin S. Shores[1]; Daniel R. Knapp[1]; *[1]Medical University of South Carolina, Charleston, South Carolina*

TP 540 **WAX-RPLC/FTICR-MS for Profiling Intact Proteins**; Seema Sharma[1]; David C. Simpson[1]; Nikola Tolic[1]; Natacha Lourette[1]; Richard D. Smith[1]; Ljiljana Pasa-Tolic[1]; *[1]Pacific Northwest National Laboratory, Richland, WA*

TP 541 **Protein pre-Fractionation to Enhance Differential Expression Analysis with LC-MS**; Johan Axelman[1]; Caroline Berg[1]; Daniel Haid[1]; Daniel Ivansson[1]; Staffan Renlund[1]; *[1]GE Healthcare, Uppsala, Sweden*

TP 542 **Divide and Conquer: Fractionating Salivary Proteins**; Pinmanee Boontheung[1]; Prasanna Ramachandran[1]; Yongming Xie[1]; Shen Hu[1]; David T. Wong[1]; Joseph A. Loo[1]; *[1]University of California-Los Angeles, Los Angeles, CA*

TP 543 **Fractionation of Complex Proteomic Samples for Low Abundant Biomarker Discovery by MS**; Tony J. Tegeler[1]; Dariusz J. Janecki[1]; *[1]Indiana Centers for Applied Protein Sciences, Indianapolis, IN*

TP 544 **Application of Micro-scale Solution Isoelectrofocusing for Proteomic Analysis of Urines from Sodium Fluoride Treated Rats**; Charlotte C. Yu Ip[1]; Raymond J. Gonzalez[1]; Frank D. Sistare[1]; William H. Schaefer[1]; *[1]Merck Research Laboratories, West Point, PA*

TP 545 **Development of a Proteomic Reactor for Efficient Protein Digestion and Mass Spectrometric Preparation**; Martin Ethier[1]; Weimin Hou[1]; Daniel Figeys[1]; *[1]Ottawa Institute of Systems Biology, Ottawa, Canada*

TP 546 **Characterizing an Albumin Enriched Fraction of Human Serum via Chromatography, MALDI-TOF MS and LC-MS/MS**; Rebekah L Gundry[1]; Christine A Jelinek[1]; Qin Fu[1]; Jennifer E Van Eyk[1]; Robert J Cotter[1]; *[1]Johns Hopkins University School of Medicine, Baltimore, MD*

TP 547 **Off-Gel Electrophoretic Fractionation of Proteins and Peptides to Improve Protein Identification in Complex Samples**; Patric Hoerth[1]; Christine A. Miller[2]; Christian

Wenz[1]; [1]*Agilent Technologies GmbH, Waldbronn, Germany;* [2]*Agilent Technologies, Santa Clara, CA*

TP 548 **Reversed-phase LC/LC Separation of Immunodepleted Human Blood Serum, with Subsequent Characterization by MALDI TOF/TOF/MS and ESI/MS**; William R. Alley[1]; Milan Madera[1]; Iveta Klouckova[1]; Yehia Mechref[2]; Milos V. Novotny[1]; [1]*Indiana University, Bloomington, IN;* [2]*METACyt Biochemical Analysis Center, Bloomington, IN*

TP 549 **Feasibility of Multi-lectin Glycoprotein Capture Combined with Free-Flow Electrophoreses (FFE) Separation prior to LC-MS/MS Bottom-Up Identification of Plasma Glycoproteins**; Daniel Eikel[1]; Sonja Hess[1]; [1]*National Institutes of Health - NIDDK, Bethesda, MD*

TP 550 **Investigation of Non-Specific Protein:Protein Interactions Following Removal of Twenty High Abundance Proteins From Human Plasma;** Graham B.I. Scott[1]; Chris D. Melm[1]; Angela S. Crawford[1]; Holly A. Chapman[1]; Justin Wildsmith[1]; Kevin B. Ray[1]; Dian Er Chen[1]; Mark D. Schuchard[1]; [1]*Sigma-Aldrich, Life Science and Technology Center, St. Louis, MO*

TP 551 **Comparison of Multiple Liquid Partition Chromatography to Fractionationate Human Serum for LC-MALDI Mass Spectrometry and LC-ESI Tandem Mass Spectrometry;** Monika Tucholska[1]; Peihong Zhu[1]; Catherine Stacey[2]; John Marshall[1]; [1]*Ryerson University, Toronto, Canada;* [2]*Bruker Daltonics, Ballerica, MA*

PROTEOMICS: QUANTITATIVE TECHNIQUES II

TP 552 **Quantification and Identification in Protein Biomarker Discovery Using Hybrid Ion Trap and TOF Mass Spectrometer Combining with Stable Isotope Coding**; Fan Xiang[1]; Joseph Fox[1]; Jia Zhao[2]; Willard Bankert[1]; David M Lubman[2]; [1]*Shimadzu Biotech, Pleasanton, CA;* [2]*The University of Michigan, Ann Arbor, MI*

TP 553 **Quantitative Proteomics of Fruit Fly Development by Metabolic Labeling**; Joost W. Gouw[1]; Martijn W.H. Pinkse[1]; Tokameh Mahmoudi[2]; Maria Monti[1]; C. Peter Verrijzer[2]; Albert J.R. Heck[1]; Jeroen Krijgsveld[1]; [1]*Utrecht University, Utrecht, The Netherlands;* [2]*Erasmus Medical Center, Rotterdam, The Netherlands*

TP 554 **Absolute Quantification of Multiple Proteins in Biological Systems using Artificial QconCAT Proteins as Internal Standards for Mass Spectrometry**; Jenny Rivers[1]; Mary K Doherty[1]; Deborah M Simpson[1]; Simon J Gaskell[2]; Dominique Rocha[3]; Robert J Beynon[1]; [1]*University of Liverpool, Liverpool, U.K;* [2]*University of Manchester, Manchester, U.K;* [3]*Genus Cambridge Research Laboratory, Cambridge, U.K.*

TP 555 **Quantification of Cell Surface Proteins and Plasma Proteins between Normal and Malignant Breast Cells**; Xiquan Liang[1]; Mahbod Hajivandi[1]; Erlend Ragnhildstveit[2]; Geir Fonnum[2]; Marie Bosnes[2]; David Gillooly[2]; Marshall Pope[1]; [1]*Invitrogen, Carlsbad, California;* [2]*Dynal Biotech ASA, Oslo, Norway*

TP 556 **Identification and Quantification of Different Protein Species by using the ICPL (isotope-coded protein labelling) Technology**; Thomas M. Halder[1]; Conny Ciosto[2]; Josef Kellermann[2]; Friedrich Lottspeich[2]; [1]*TopLab, Martinsried, Germany;* [2]*Max-Planck-Institute for Biochemistry, Martinsried, Germany*

TP 557 **Novel Approach to Identify Peroxin Interacting Proteins using Metabolic Labeling and Quantitative Mass Spectrometry**; Silke Oeljeklaus[1]; Christine David[2]; Ralf Erdmann[2]; Helmut E. Meyer[1]; Bettina Warscheid[1]; [1]*Medical Proteom-Center, Ruhr-University, Bochum, Germany;* [2]*Department for Systems Biochemistry, Bochum, Germany*

TP 558 **Quantitative Proteomic Identification of &Alpha-Synuclein- and DJ-1-Associated Proteins using Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC)**; Jinghua Jin[1]; Yan Wang[1]; Catherine Pan[1]; Jing Zhang[1]; [1]*University of Washington School of Medicine, Seattle, WA*

TP 559 **Non-Isobaric Triplex-Labeling Strategies for Proteome Analyses are Compatible with Protein Pre-fractionation**; Josef Kellermann[1]; Friedrich Lottspeich[1]; Eva Keidel[1]; W Jabs[2]; S Hahner[2]; S Brand[2]; Detlef Suckau[2]; [1]*Max-Planck-Institute for Biochemistry, Martinsried, Germany;* [2]*Bruker Daltonik GmbH, Bremen, Germany*

TP 560 **Stable Isotopic Labeling of Amino Acids in Cultured Primary Neurons for the Study of Protein Turnover and Neuronal Signal Transduction**; Daniel S. Spellman[1]; Rithwick Rajagopal[1]; Moses V. Chao[1]; Thomas A. Neubert[1]; [1]*Skirball Institute, NYU School of Medicine, New York, NY*

TP 561 **Use of N-15 Metabolic Labeling for Biomarker Discovery in the *Apc^{min}* Mouse Model for Colorectal Cancer**; Edward L. Huttlin[1]; Adrian D. Hegeman[1]; Xiaodi Chen[1]; Greg Barret-Wilt[1]; Amy C. Harms[1]; William F. Dove[1]; Michael R. Sussman[1]; [1]*University of Wisconsin, Madison, WI*

TP 562 **Quantitative Proteomics Analysis using Stable Isotope Dilution Nanospray LC/MS after Inhibition of Endothelial Cell Dihydrofolate Reductase**; Colin G. Barry[1]; Alexander S. Whitehead[1]; Anastasia K. Yocum[1]; Ian A. Blair[1]; [1]*University of Pennsylvania, Philadelphia, PA*

TP 563 **Quantitative Profiling of Tumor Cell Lines Using Isotope Coded Protein Labeling (ICPL) and Liquid Chromatography-Tandem Mass Spectrometry**; Yang Shi[1]; Chun-Ming Huang[2]; Gongyi Shi[3]; Wenhong Zhu[1]; Jeffrey Smith[1]; Yuliang Ma[1]; [1]*The Burnham Institute for Medical Research, La Jolla, CA;* [2]*La Jolla Institute for Molecular Medicine, San Diego, CA;* [3]*Bruker Daltonics Inc., Fremont, CA*

TP 564 **Determination of Quantitative Proteomics Changes in Mixed Lineage Leukemia By Stable Isotope Dilution Nanospray LC/MS**; Anastasia K. Yocum[1]; Carolyn A. Felix[2]; Ian A. Blair[1]; [1]*University of Pennsylvania, Philadelphia, PA;* [2]*The Children's Hospital of Philadelphia, Philadelphia, PA*

TP 565 **Quantification of Secreted Proteins between Normal and Malignant Breast Cells**; Xiquan Liang[1]; Jarkko Huuskonen[1]; Mahbod Hajivandi[1]; Marshall Pope[1]; [1]*Invitrogen, Carlsbad, California*

TP 566 **Comparison of Three Methods of Quantitative Proteomics by Mass Spectrometry**; Qiangwei Xia[1]; Tiansong Wang[1]; Fred Taub[1]; Erik L. Hendrickson[1]; John A. Leigh[1]; Murray Hackett[1]; [1]*University of Washington, Seattle, WA*

TP 567 **Quantitative Proteomic Comparison of Wild-type and Adenylyl Cyclase VII Transgenic Mouse Synaptic Membranes Utilizing ^{15}N Metabolic Labeling and MudPIT**; Kathleen J. Grant[1]; Boris Tabakoff[1]; Christine C. Wu[1]; [1]*University of Colorado Health Sciences Center, Aurora, CO*

TP 568 **Comprehensive Identification of Proteome Changes Associated With Metastatic Melanoma By Combining SILAC and 3-D Protein Profiling**; Huan Wang[1]; Logan J Everett[2]; Mee-Jung Han[1]; David Speicher[1]; [1]*The Wistar Institute, Philadelphia, PA;* [2]*University of Pennsylvania, Philadelphia, PA*

TP 569 **Mass Spectrometric analysis of Associated Proteins of rab11a in the Endocytosis Process of a-Synuclein Into Microglia**; Jun Liu[1]; Jing Zhang[1]; [1]*University of Washington School of Medicine, seattle, USA*

TP 570 **Quantifying Proteomic ICPL Samples by ESI Ion Trap MS**; Ulrike Schweiger-Hufnagel[1]; Marina Behrens[1]; Ali Kettani[1]; Carsten Baessmann[1]; [1]*Bruker Daltonik GmbH, Bremen, Germany*

TP 571 **Comparing ^{15}N-Metabolic Labeling Relative Quantification Strategies with Light or Dark Grown**

Arabidopsis: As Clear as Night and Day?; Adrian D. Hegeman[1]; Edward L. Huttlin[1]; Amy C. Harms[1]; Michael R. Sussman[1]; [1]*University of Wisconsin, Madison, WI*

TP 572 **Use of QconCAT Multiplexed Quantification for Polymorphism Mapping by Stable Isotope Dilution Mass Spectrometry**; Stuart D. Armstrong[1]; Deborah M. Simpson[1]; Jane L. Hurst[1]; Simon J. Gaskell[2]; Robert J. Beynon[1]; [1]*University of Liverpool, Liverpool, UK;* [2]*University of Manchester, Manchester, UK*

TP 573 **Study of Stable Isotope Labeling with Amino Acids in cell culture (SILAC) in combination with 1DE and 2DE**; Annika Dahl[1]; Erik Portelius[1]; Kristina Hedberg-Fogel[1]; Kaj Blennow[1]; Ann Westman-Brinkmalm[1]; [1]*Inst of Neuroscience and physiology, Mölndal, Sweden*

TP 574 **Evaluation of a Stable Isotope Labeled Whole Protein for Absolute Protein Quantitation Using LC/MS/MS and Multiple Reaction Monitoring;** Zhaoyan Jin[1]; [1]*Eli Lilly and Company, Greenfield, IN;* [2]*Roche Protein Expression Group, Indianapolis, IN*

TP 575 **Subtle Modification of Isotope-Ratio Proteomics (SMIRP) in Multicellular Organisms: $^{15}N/^{14}N$ Alteration in Plants;** Andrew J. Norris[1]; Arthur Laganowsky[2]; John Nishio[2]; Sara Bassilian[1]; Frederic Halgand[1]; Puneet Souda[1]; Kym F. Faull[1]; Jonathan Katz[1]; Julian P. Whitelegge[1]; [1]*University of California, Los Angeles, CA;* [2]*California State University, Chico, CA*

TP 576 **Comparative Secretomics in RPE Cells from Normal and Age Related Macular Degeneration Donors;** Eunkyung An[1]; Xiaoning Lu[1]; Jessica Flippin[1]; Joe Devaney[1]; Brian Halligan[2]; Karl Csaky[3]; Yetrib Hathout[1]; [1]*Children's National Medical Center, Washington, DC;* [2]*Medical College of Wisconsin, Milwaukee, WI;* [3]*NEI/NIH, Bethesda, MD*

TP 577 **Identification of Endogenous Protein-Protein Interactions by RNAi and Quantitative Proteomics**; Matthias Selbach[1]; Matthias Mann[1]; [1]*Max Planck Institute of Biochemistry, Munich, Germany*

TP 578 **Double Stable Isotope Labeling with Amino Acids in Cell Culture: Quantitation and Dynamics of Acetylation and Methylation In Cancer Cells**; Chen Ren[1]; Shujun Liu[1]; Guido Marcucci[1]; Kalpana Ghoshal[1]; Samson T. Jacob[1]; Michael A. Freitas[1]; [1]*The Ohio State University, Columbus, OH*

TP 579 **A Mass Spectrometry-Based Approach to Absolute Quantitation of mRNA Capping Enzyme in Mammalian Total Cell Lysate**; Haiyan Zheng[1]; Chun Chu[1]; Aaron J Shatkin[1]; [1]*University of Medicine and Dentistry of New Jersey, Piscataway, NJ*

PROTEOMICS: BIOCHEMISTRY: NON-MAMMALIAN

TP 580 **Characterization of Polyglutamine aggregates by Mass Spectrometry**; Yan Wang[1]; Anatoli B. Meriin[1]; Michael Y. Sherman[1]; Catherine E. Costello[1]; [1]*Boston University, Boston, MA*

TP 581 **Identification and Molecular Characterisation of Centrosomal Proteins in Drosophila Melanogaster**; Johan Gobom[1]; Hanna Mueller[1]; Verena Lehmann[1]; Gustavsson Niklas[2]; Lehrach Hans[1]; Lange Bodo[1]; Mirgorodskaya Ekaterina[1]; [1]*Max Planck Institute for Molecular Genetics, Berlin, Germany;* [2]*Lund University, Lund, Sweden*

TP 582 **Hemagglutinating Activity and Protein Characterization of Curcuma Plants in Thailand**; Polkit Sangvanich[1]; Sophon Kaeothip[1]; Chantragan Phiphobmongkol[2]; Jisnuson Svasti[2]; Pornpimon Thiptara[1]; Amorn Petsom[1]; [1]*Faculty of Science, Chulalongkorn University, Bangkok, Thailand;* [2]*Chulabhorn Research Institute, Bangkok, Thailand*

TP 583 **Mass Spectrometry Based Proteomic Analysis of Bacterial Cold Adaptation in Exiguobacterium sp. Strain 255-15**; Yinghua Qiu[1]; Sophia Kathariou [2]; Fan Xiang[3]; David M. Lubman[1]; [1]*University of Michigan, Ann Arbor, MI;* [2]*North Carolina State University, Raleigh, NC;* [3]*Shimadzu Biotech, Pleasanton, CA*

TP 584 **Mapping the 26S Proteasome Interaction Network in Saccharomyces Cerevisiae using QTAX**; Cortnie M. Guerrero[1]; Christian Tagwerker[1]; Peter Kaiser[1]; Lan Huang[1]; [1]*University of California, Irvine, Irvine, CA*

TP 585 **Post-Translational Modifications of Caulobacter Crescentus Ribosomal Proteins**; William E. Running[1]; James P. Reilly[1]; [1]*Indiana University, Bloomington, IN*

TP 586 **Examining Aspergillus Niger Morphology Control by Global Proteome Analysis**; Ellen A. Panisko[1]; Laura J Hubbard[1]; Linda L. Lasure[1]; [1]*Pacific Northwest National Laboratory, Richland, WA*

TP 587 **Differential Protein Expression Analysis of *Drosophila melanogaster* Embryogenesis using Liquid Chromatography with Ion-Mobility and Ion-Trap Mass Spectrometry**; Ruwan T. Kurulugama[1]; Stephen J. Valentine[1]; Thomas C. Kaufman[1]; David E. Clemmer[1]; [1]*Indiana University, Bloomington, IN*

TP 588 **Identification of Immune Induced Peptides in the Hemolymph of the Fruitfly;** Geert Baggerman[1]; Peter Verleyen[1]; Wannes D'Hertog[1]; Evy Vierstraete[1]; Steven Husson[1]; Liliane Schoofs[1]; [1]*K.U.Leuven, Leuven, Belgium*

TP 589 **Iron-Regulated Protein Expression Profiling in B. Anthracis using Amine Specific Labeling and LC MS/MS analysis**; Andrew Koppisch[2]; Sanjeev Bhardwaj[1]; Christy Ruggiero[2]; Srinivas Iyer[2]; [1]*Applied Biosystems, Framingham, MA;* [2]*Los Alamos National Laboratory, Los Alamos, NM*

TP 590 **Tandem LC-MS/MS Comparison of COP9/Signalosome Interactions Across Various Species**; Marcia M Roy[1]; Lionel Pintard[1]; Danielle Dewar[1]; Brett Larsen[1]; Mike Tyers[1]; [1]*Samuel Lunenfeld Research Institute, Toronto, Ontario, CANADA*

TP 591 **Automated High Throughput Microfluidics nano-LC/MS/MS of Transient Protein Assemblies in Bacteria**; William R. Wikoff[1]; Sunia Trauger[1]; Junefredo Apon[1]; Angeli Menon[2]; Michael Adams[2]; Gary Siuzdak[1]; [1]*The Scripps Research Insitute, La Jolla, CA;* [2]*University of Georgia, Athens, GA*

TP 592 **Mapping The Stimulus-specific Signaling Pathways Involved in THP-1 Cells Exposed to Porphyromonas gingivalis LPS vs. Fimbria vs. Live P.g;** Julian A. Saba[1]; David H. Perlman[2]; Hua Huang[2]; Mark E. McComb[2]; Catherine E. Costello[2]; Salomon Amar[1]; [1]*BU Goldman School of Dental Medicine, Boston, MA;* [2]*Boston University School of Medicine, Boston, MA*

TP 593 **Characterization of Novel Ubiquitin-Specific Protease Interacting Proteins by Mass Spectrometry and Genetic Experiments**; Jeroen A.A. Demmers[1]; B.R. Prashanth Kumar[1]; Jan A. van der Knaap[1]; Karel Bezstarosti[1]; C. Peter Verrijzer[1]; [1]*Erasmus University Medical Center, Rotterdam, The Netherlands*

TP 594 **Time-Resolved Proteomic Characterization of Distinct States of the Eukaryotic Pre-Initiation Complex of the DNA Replication Cycle**; Matthew D Sekedat[1]; Alan J Tackett[1]; Brian T Chait[1]; [1]*The Rockefeller University, New York, New York*

TP 595 **Studies on the Mitochondrial Proteome of Tetrahymena thermophila using LC/LC-MS/MS**; Daryl G.S. Smith[1]; David F. Spencer[2]; Michael W. Gray[2]; Ronald E. Pearlman[1]; K.W. Michael Siu[1]; [1]*York University, Toronto, Canada;* [2]*Dalhousie University, Halifax, Canada*

TP 596 **Shotgun Proteomic Analysis of Lrp regulated Proteins of *Methanococcus maripaludis* Using Accurate Mass Measurement and ^{15}N-Metabolic Labeling**; Li Jing[1];

Yuchen Liu[1]; William B. Whitman[1]; I. Jonathan Amster[1]; *[1]University of Georgia, Athens, GA*

TP 597 **Serum proteomics of honeybee castes**; Queenie WT Chan[1]; Leonard J Foster[1]; *[1]University of British Columbia, Vancouver, Canada*

TP 598 **Quantitative Protein Profiling and Genetic Analysis of TOR-inhibition in Yeast Reveal Novel Insights into Connections Between Cellular Growth and Stress**; Sricharan Bandhakavi[1]; Hongwei Xie[1]; DoHyung Kim[1]; Timothy J Griffin[1]; *[1]University of Minnesota, Minneapolis, MN*

TP 599 **Mass Spectrometric Identifiation of Cellular Proteins Targeting the N-termini of KSHV-LANA Homologs**; Donna L Potts[1]; Brenna K Kelley-Clarke[2]; Andrew Barbera[2]; Kenneth M Kaye[2]; Catherine E Costello[1]; *[1]Boston University School of Medicine, Boston, MA; [2]Brigham and Women's Hospital, Boston, MA*

TP 600 **Characterization of Aromatic Compound Degradation Pathways and Their Regulation in *Rhodopseudomonas palustris* Using Stable Isotope Labeling Quantitative Proteomics**; Chongle Pan[1]; Patricia K. Lankford[1]; Bing Zhang[1]; Yasuhiro Oda[2]; Nagiza F. Samatova[1]; Caroline S. Harwood[2]; Dale A. Pelletier[1]; Robert L. Hettich[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN; [2]University of Washington, Seattle, WA*

PROTEOMICS: BIOMARKERS IN TISSUE AND SERUM

TP 601 **Serum Glycan Profiling as a Diagnostic Aid in Breast Cancer**; Suzanne Miyamoto[1]; Crystal Kirmiz[2]; Bensheng Li[2]; Hyun Joo An[2]; Robert Alecio[3]; Anthony Ferrige[3]; Carlito Lebrilla[2]; *[1]UC Davis Cancer Center, Sacramento, CA; [2]UC Davis, Davis, CA; [3]Positive Probability Limited, Isleham, UK, CB7 5RX*

TP 602 **Using IMS-MS for Human Plasma Proteome Profiling**; Xiaoyun Liu[1]; Manolo Plasencia[1]; Stephen Valentine[2]; David Clemmer[1]; *[1]Department of Chemistry, Indiana University, Bloomington, IN; [2]Predictive Physiology and Medicine(PPM), Bloomington, IN*

TP 603 **Proteomic Analysis of Rat's Cerebrospinal Fluid Changes Following Lipopolysaccharide-induced CNS Inflammation by Liquid Chromatography Tandem Mass Spectrometry**; Yun-Han Wang[1]; Yu-Chang Tyan[1]; Pao-Chi Liao[1]; *[1]National Cheng Kung University, Tainan, Taiwan*

TP 604 **A Comparison of the Protein Expression Lists from Mass Spectrometry of Human Blood Fluids Using Peptide Sequences and BLAST**; Peihong Zhu[1]; Peter Bowden[1]; Voitek Pendrak[1]; Ken Kupfer[1]; Ken Evans[2]; Terry Sills[2]; Herbert Thiele[1]; KW Siu[2]; Eleftherios P Diamandis[2]; Marshall John[1]; *[1]Ryerson University, Toronto, Canada; [2]Ontario Cancer Biomarker Network, Toronto, Canada; [3]Bruker Daltonics, Bremen, Germany*

TP 605 **The Proteomic Responses in Mouse Plasma to Sepsis Generated from CLP Model**; Yan Ren[1]; Jiandong Wang[2]; Ji Xia[1]; Ning Ning[2]; Kang Zhao[1]; Ningzhi Xu[1]; Yingxin Xu[2]; Siqi Liu[1]; *[1]Beijing Genomics Institute,CAS, Beijng, China; [2]The General Hospital of Military, Beijing, China*

TP 606 **Quantitative Proteomic Analysis of Fibrosis Progression in Human Liver Biopsies from Hepatitis C Virus (HCV)-Infected Patients**; Deborah L. Diamond[1]; Jon M. Jacobs[2]; Zachary Caldwell[1]; Marina A. Gritsenko[2]; David G. Camp II[2]; Anne M. Larson[3]; Richard D. Smith[2]; Michael G. Katze[1]; *[1]University of Washington, Seattle, WA; [2]Pacific Northwest National Laboratory, Richland, WA ; [3]Hepatology Section, University of Washington, Seattle, WA*

TP 607 **New Serum Biomarkers for Gastric Cancer Discovered using SELDI Protein Chip Technology**; Wenjing Wang[1]; Liang Zhu[2]; Zhiwen Luo[2]; Ping Liao[1]; Weifen Xie[2]; Wei Lu[1]; *[1]Shanghai Center for Disease Control and Prevention, Shanghai, CHINA; [2]Chang-zheng Hospital, Shanghai, CHINA*

TP 608 **Large-Scale Identification of Protein in Human Urine Proteome by Gel-Free Proteomic Approach**; Yu-Chang Tyan[1]; How-Ran Guo[1]; Chia-Yuan Liu[1]; Pao-Chi Liao[1]; *[1]National Cheng Kung University, Tainan, Taiwan*

TP 609 **A Proteomic Approach to the Discovery of Biomarkers in the Urine of Cachectic Cancer Patients;** Andrew, David Cronshaw[1]; Alan R. Millar[1]; Robert Wakefield[1]; Alastair Aitken[1]; Christopher Deans[1]; Alastair Lowrie[1]; Kenneth C.H. Fearon[1]; James A. Ross[1]; *[1]University of Edinburgh, Edinburgh, Scotland*

TP 610 **An Integrated Approach for Profiling Potential Biomarkers in Human Plasma for Detection of Non-small Cell Lung Cancer**; Valeriy E. Shevchenko[1]; Irina B. Zborovskaya[1]; Natalia E. Arnotskaya[1]; Oxana P. Trifonova[1]; Valentina A. Yurchenko[1]; Maria E. Kochetkova[1]; David G. Zaridze[1]; *[1]N. N. Blokhin Russian Cancer Research Center, Moscow, Russia*

TP 611 **Mass Spectrometric Assay for Specific Subtypes of Low Abundance Cytokine in Human Serum**; Anita Izrael-Tomasevic[1]; Qui Phung[1]; David Arnott[1]; *[1]Genentech, Inc., South San Francisco, California*

TP 612 **Fast LC/MS Separations: Improved Platform for Discovery and Identification of Plasma Protein Biomarkers**; Michael Schirm[1]; Kevin Eng[1]; Kossi Lekpor[1]; Sylvain Tessier[1]; Greg Opiteck[1]; Paul Kearney[1]; Joanna Hunter[1]; *[1]Caprion Pharmaceuticals, Montreal, Canada*

TP 613 **Developing a Procedure for Specific and Efficient Isolation of N-linked Glycopeptides for Serum Profiling**; Yong Zhou[1]; Ruedi Aebersold[1]; Hui Zhang[1]; *[1]Institute for Systems Biology, Seattle, WA*

TP 614 **A Protein Identification Strategy by Combining Accurate MS and MS/MS Data and Plasma Proteome Analysis**; Jin Young Kim[1]; Kyung-Hoon Kwon[1]; Gun Wook Park[1]; Jeong Hwa Lee[1]; Ju Yeon Lee[1]; Kun Cho[1]; Young Ki Paik[2]; Jong Shin Yoo[1]; *[1]Korea Basic Science Institute, Daejeon, South Korea; [2]Yonsei University, Seoul, South Korea*

TP 615 **Applying Protein Microarrays and Mass Spectrometry to the Study of Pancreatic Cancer Signatures in Patient Serum;** Tasneem H. Patwa[1]; Diane Simeone[1]; David M. Lubman[1]; *[1]Univeristy of Michigan, Ann Arbor, MI*

TP 616 **A Global Proteome Investigation of Inter and Intra Variability of Human Serum Samples**; Nicolas A. Stewart[1]; DaRue A. Prieto[1]; David A. Lucas[1]; Louis M. Cosentino[1]; Thomas P. Conrads[1]; Timothy D. Veenstra[1]; *[1]SAIC-Frederick, Inc., Frederick, MD*

TP 617 **Histone Deacetylase Inhibitor SAHA Arrests Cancer Cell Growth – A Proteomics Based Study for Screening Posttranslational Modifications by Acetylation**; Christian Scharf[1]; Le Thi Thu Hong[1]; Jürgen Sonnemann[1]; Elke Hammer[1]; Karanam Narasimha Kumar[1]; James F. Beck[1]; Uwe Völker[1]; *[1]Ernst-Moritz-Arndt-University, Medical School, Greifswald, Germany*

TP 618 **LC-MS-based Proteomic Analysis of Plasma from Sled Dogs for Potential Biomarkers of Exertion-Induced Muscle Injury**; Fanyu Meng[1]; Xuemei Zhao[1]; J. Greg Slatter[2]; Nathan Yates[1]; Kenneth Hinchcliff[3]; Roger G. Ulrich[2]; Ronald Hendrickson[1]; *[1]Merck & Co., Inc., Rahway, NJ; [2]Rosetta Inpharmatics LLC, Merck & Co., Inc., Seattle, WA; [3]Ohio State University, Columbus, OH*

TP 619 **Development of Nanoprobe-Based Affinity Mass Spectrometry for Plasma Protein Profiling**; Po-Hung Chou[2]; Shu-Hua Chen[2]; Hsin-Kai Laio[1]; Po-Chaio Lin[1]; Gour-Rong Her[2]; Chun-Chen Lin[1]; Yu-Ju Chen[1]; *[1]Institute of Chemistry and Genomic Research Center, Taipei, TAIWAN;*

[2]*Department of Chemistry, National Taiwan Universit, Taipei, TAIWAN*

TP 620 **Proteome-Wide Analysis of Formalin-Fixed Paraffin Embedded Head and Neck Cancer Tissues Using Laser Capture Microdissection and Mass Spectrometry**; Brian L. Hood[1]; Vyomesh Patel[2]; David A. Lucas[1]; Thomas P. Conrads[1]; Alfredo Molinolo[2]; J. Silvio Gutkind[2]; Timothy D. Veenstra[1]; [1]*SAIC-Frederick, Inc., Frederick, MD;* [2]*National Institutes of Health, Bethesda, MD*

TP 621 **Quantitative Proteomic Research on Different Stage of HCC**; Heyi Yang[1]; Yezhou Sun[1]; Gregg Czerwieniec[1]; Weijia zhang[1]; Rong Wang[1]; [1]*Mount Sinai School of Medicine, New York, NY*

TP 622 **Proteomic Analysis of Serum for the Discovery of Biomarkers for Head and Neck Carcinomas**; Lisa J. Zimmerman[1]; Robbert J. Slebos[1]; Amy N. Evjen[1]; David L. Tabb[1]; Daniel C. Liebler[1]; Wendell G. Yarbrough[1]; [1]*Vanderbilt University, Nashville, TN*

TP 623 **Searching for Proteomic Predictors of Disease Progression in a Subpopulation of African American Subjects with Kidney Disease Using SELDI/TOF/MS**; Victor Anbalagan[1]; John Roboz[1]; Michael S. Lipkowitz[1]; [1]*Mount Sinai School of Medicine, New York, NY*

TP 624 **Detection of Oxidatively-Modified Proteins in Human Cerebrospinal Fluid (CSF) using an Aldehyde Reactive Probe**; Woon-Gye Chung[1]; Cristobal L. Miranda[1]; Claudia S. Maier[1]; [1]*Oregon State University, Corvallis, OR*

TP 625 **Plasma Protein Profile Changes from Adolescence to Adulthood**; Yan Zhang[1]; Alan Sinaiko[1]; Gary Lee Nelsestuen[1]; [1]*University of Minnesota, Minneapolis, Minnesota*

TP 626 **Identification of Expression Changes and Biomarkers in Mucinous and Serous Pancreatic Cystic Neoplasms;** Babak Hassanzadeh[1]; Puneet Souda[1]; James Farrell[1]; Julian P Whitelegge[1]; Kym F Faull[1]; [1]*University of California Los Angeles, Los Angeles, CA*

TP 627 **A Two-Step Proteomic Strategy for Rapid Identification of Potential Plasma Biomarkers**; Tatiana Plavina[1]; Marina Hincapie[1]; Eric Wakshull[2]; William S. Hancock[1]; [1]*Barnett Institute, Northeastern University, Boston, MA;* [2]*Biogen Idec, Inc., Cambridge, MA*

TP 628 **Annexin-I as a Target Protein for Green Tea Extract (GTE) Induced Actin Remodeling**; Gary Guishan Xiao[1]; Yu-Sheng Jin[2]; Zuo-Feng Zhang[2]; Arie Belldegrun[2]; Robert Figlin[2]; Qing-Yi Lu[2]; Allan Pantuck[2]; Yun Yen[3]; JianYu Rao[2]; [1]*University of California Irvine, Irvine, CA;* [2]*UCLA, Los Angeles, CA;* [3]*City of Hope National Medical Center, Duarte, CA*

TP 629 **Proteomic Analysis of Modified ApoB100 Formed by Lipid Peroxidation of LDL in Human Blood Plasma**; Hye-Young H. Kim[1]; Keri A. Tallman[1]; Jianxin Ji[1]; Daniel C. Liebler[1]; Ned A. Porter[1]; [1]*Vanderbilt University, Nashville, TN*

TP 630 **Development of a Reference Method for the Quantitation of B-type Natriuretic Peptide in Serum by Liquid Chromatography-Mass Spectrometry**; Johanna E Camara[1]; David M Bunk[1]; Michael J Welch[1]; [1]*NIST, Gaithersburg, MD*

TP 631 **Serum Protein Profiling for Detection of Pancreatic Cancer**; Jianzhong Chen[1]; Diane M Simeone[1]; David M Lubman[1]; [1]*University of Michigan-Ann Arbor, Ann Arbor, MI*

TP 632 **Pancreatic Cancer Biomarker Discovery - Comparative Analysis of the Low Molecular Fraction from Case/Control Plasma Samples Analyzed by LC/MS TOF;** Michael W. Holmes[1]; Kenneth L. Johnson[1]; H. Robert Bergen III[1]; Douglas W. Mahoney[1]; Ann L. Oberg[1]; David A. Weil[2]; David C. Muddiman[3]; [1]*Mayo Clinic College of Medicine, Rochester, MN;* [2]*Agilent Technologies, Schaumburg, IL;* [3]*North Carolina State University, Raleigh, NC*

TP 633 **Determination of Beta-Amyloid Peptide Signatures in Cerebrospinal Fluid using Immunoprecipitation-Mass Spectrometry**; Erik Portelius[1]; Henrik Zetterberg[1]; Kaj Blennow[1]; Ann Westman-Brinkmalm[1]; [1]*Institute of Clinical Neuroscience and Physiology, Göteborg, Sweden*

TP 634 **Multidimensional Separations for Improved Protein Identification for Proteomes of Human Serum and Rat Liver Tissues**; Iveta Klouckova[1]; Yehia Mechref[2]; Milan Madera[1]; Milos V Novotny[3]; [1]*Indiana University, Bloomington, IN;* [2]*National Center of Glycomics and Glycoproteomic, Bloomington, IN;* [3]*METACyt Biochemical Analysis Center, Bloomington, IN*

TP 635 **Identification of Glycoproteins from Human Cerebrospinal Fluid Using Mass Spectrometry Based Proteomics**; Yan Wang[1]; Jinghua Jin[1]; Catherine Pan[1]; Jane Li[1]; Jing Zhang[1]; [1]*University of Washington School of Medicine, Seattle, WA*

TP 636 **Differentiating Various Anti-Hypertensives Based on Clinical Response and Plasma Profiling**; Sylvain Tessier[1]; Heather Butler[1]; Nathan Currier[1]; Joanna Hunter[1]; Paul Kearney[1]; Gregory J. Opiteck[1]; [1]*Caprion Pharmaceuticals, Montreal, Canada*

TP 637 **Expression Profiling in Rat Serum after Carcinogen Administration for Liver Cancer Biomarker Discovery**; Jihyeon Lim[1]; Anuradha Menthena[1]; Linda Siconolfi-Baez[1]; Peicheng Du[1]; Phyllis M. Novikoff[1]; Ruth H. Angeletti[1]; [1]*Albert Einstein College of Medicine, Bronx, NY*

BIOINFORMATICS II

TP 638 **Reducing False Positive Rates in MS/MS Sequence Searching and Incorporating Intensity into Match Based Statistics**; Lewis Y. Geer[1]; Dina L. Bai[2]; Jeffrey Kowalak[3]; An Chi[2]; Ming Xu[1]; Jeffrey Shabanowitz[2]; Sanford P. Markey[3]; Donald F. Hunt[2]; Stephen H. Bryant[1]; [1]*National Library of Medicine, Bethesda, MD;* [2]*University of Virginia, Charlottesville, VA;* [3]*National Institute for Mental Health, Bethesda, MD*

TP 639 **Human Plasma PeptideAtlas**; Eric Deutsch[1]; Nichole King[1]; Jimmy Eng[2]; Alexey Nesvizhskii[3]; Olga Vitek[1]; Ruedi Aebersold[4]; [1]*Institute for Systems Biology, Seattle, WA;* [2]*Fred Hutchinson Cancer Research Center, Seattle, WA;* [3]*University of Michigan Medical School, Ann Arbor, MI;* [4]*Institute for Molecular Systems Biology,ETH Zurich, Zurich, Switzerland*

TP 640 **DTASelect 2.0: Improving the Confidence of Peptide and Protein Identifications**; Daniel Cociorva[1]; John R Yates[1]; [1]*The Scripps Research Institute, La Jolla, CA*

TP 641 **Processing Raw Mass Spectral Data for High Mass Accuracy**; Yongdong Wang[1]; Ming Gu[1]; [1]*Cerno Bioscience, Danbury, CT*

TP 642 **Improved Fragment Assignment by Visual Assistance (FAVA) program**; Shenheng Guan[1]; Alma L. Burlingame[1]; [1]*University of California, San Francisco, CA*

TP 643 **Protein Extractor – from Peptide ID to Protein ID**; Martin Blueggel[1]; Gerhard Koerting[1]; Katrin Marcus[3]; Daniel Chamrad[1]; Ulrike Schweiger-Hufnagel[2]; Jörg Glandorf[2]; Meyer Helmut E. [3]; Herbert Thiele[2]; [1]*Protagen AG, Dortmund, Germany;* [2]*Bruker Daltonics GmbH, Bremen, Germany;* [3]*Medizinisches Proteom Center, Bochum, Germany*

TP 644 **Seeking Effiective Combinations of Library Search Methods for Peptide Identifications: A study Using Two Enzymes, Three Concentrations and Five Methods;** Gelio Alves[1]; Wells Wu[2]; Guanghui Wang[2]; Rong-Fong Shen[2]; Yi-Kuo Yu[1]; [1]*NCBI/NLM/NIH, Bethesda, Maryland;* [2]*NHLBI/NIH, Bethesda, Maryland*

TP 645 **Clustering Precursors and Associated Products Data Across Multiple Samples**; Guo-Zhong Li[1]; Marc V Gorenstein[1]; Dan Golick[1]; Richard Denny[1]; Craig A.

Dorschel[1]; Jeffrey C. Silva[1]; Scott J. Geromanos[1]; [1]*Waters Corporation, Milford, MA*

TP 646 **Models Utilizing Randomized Databases and Peptide Frequency Information from MS/MS for Protein Identification and Relative Expression**; Roger S. Higdon[1]; Jason M. Hogan[1]; Eugene Kolker[1]; [1]*The BIATECH Institute, Bothell, WA*

TP 647 **False positive assessment in database search**; Wilfred H. Tang[1]; Sean L. Seymour[1]; [1]*Applied Biosystems|MDS Sciex, Foster City, CA*

TP 648 **A Next Generation Search Engine that Substantially Improves Peptide Identification by Using Sequence Temperatures and Feature Probabilities**; Sean L. Seymour[1]; Ignat V. Shilov[1]; Alpesh A. Patel[1]; Alex Loboda[1]; Wilfred H. Tang[1]; Sean P. Keating[1]; Daniel A. Schaeffer[1]; [1]*Applied Biosystems|MDS Sciex, Foster City, CA*

TP 649 **Strategies for achieving high confidence peptide identifications from tandem MS data without losing low abundance components in complex proteomes**; Glenn C. Tan[1]; Hsin-Yao Tang[1]; David W. Speicher[1]; [1]*The Wistar Institute, Philadelphia, PA*

TP 650 **Integrated Top-Down and Bottom-Up Protein Identification Software - PTMSearch Plus**; Heather M. Connelly[1]; Vilmos Kertesz[2]; Robert L. Hettich[2]; [1]*UT-ORNL Graduate School of Genome Science, Oak Ridge, TN;* [2]*Oak Ridge National Laboratory, Oak Ridge, TN*

TP 651 **A Support Vector Machine Classifier to Reduce False Positive Peptide Spectrum Matches by Identifying Poor Quality Spectra**; Barbara E Frewen[1]; Aaron A Klammer[1]; William Stafford Noble[1]; Michael J MacCoss[1]; [1]*University of Washington, Seattle, WA*

TP 652 **Protein Panorama: Probability and Parsimony-based Software for Assessing Proteins Assembled from Peptides Inferred from MS/MS Data**; Jian Feng[2]; Bret Cooper[1]; Daniel Q. Naiman[2]; [1]*Soybean Genomics and Improvement Laboratory, USDA, Beltsville, MD;* [2]*The Johns Hopkins University, Baltimore, MD*

TP 653 **Genome Annotation via Mass Spectrometry**; Stephen Tanner[1]; Francisco Camara[3]; Liliana Florea[2]; Roderic Guigo[3]; Pavel Pevzner[1]; Vineet Bafna[1]; [1]*Univ. Cal. San Diego, San Diego, CA;* [2]*George Washington Univ, Washington, D.C;* [3]*Univ. Barcelona, Barcelona, Spain*

TP 654 **Comparing Methods of Associating Precursor and Fragment Ions using Chromatographic Elution Profiles from Data Independent Tandem Mass Spectrometry**; Gregory K. Taylor[1]; Catalin E. Doneanu[1]; David R. Goodlett[1]; [1]*University of Washington, Seattle, WA*

TP 655 **An Open-Source Framework for Evaluating MS/MS Score Functions: "Pluggable Scoring" in X! Tandem**; Brendan MacLean[1]; Jimmy Eng[2]; Martin McIntosh[2]; [1]*LabKey Software, Seattle, WA;* [2]*Fred Hutchinson Cancer Research Center, Seattle, WA*

TP 656 **Cross Correlation Algorithm for Calculation of Peptide Molecular Weight from Tandem Mass Spectra**; John Venable[1]; Tao Xu[1]; Daniel Cociorva[1]; John R. Yates III[1]; [1]*The Scripps Research Institute, La Jolla, CA*

TP 657 **Contribution of Proteomics Data to the Analysis of the Genome of Francisella tularensis Ssp. Novicida Strain U112**; Laurence Rohmer[1]; Mitch Brittnacher[1]; Jinzhi Chen[1]; Tina Guina[1]; Mike Wasnick[1]; Christie Fong[1]; Ted Larson Freeman[1]; Rajinder Kaul[1]; Scott Shaffer[1]; Byron Gallis[1]; Greg Taylor[1]; David R. Goodlett[1]; Samuel I. Miller[1]; [1]*University of Washington, Seattle, WA*

TP 658 **Incorporating Predicted Peptide Fragmentation Patterns into MASPIC Scoring Scheme**; Chandra Narasimhan[1]; Robert, L. Hettich[3]; Edward, C. Uberbacher[2]; [1]*UT-ORNL Genome Science & Tech., Oak Ridge, TN;* [2]*Life Science Division, Oak Ridge National Lab, Oak Ridge, TN;* [3]*Chemical Science Division, Oak Ridge National Lab, Oak Ridge, TN*

TP 659 **Principle and Applications of a new Algorithm for Monoisotopic Mass Determination**; Jens Decker[1]; Michael Easterling[2]; Christian B. Berg[2]; [1]*Bruker Daltonik, Bremen, Germany;* [2]*Bruker Daltonics, Billerica, MA*

TP 660 **Intensity-Based Scoring for Peptide Identification using Tandem Mass Spectra**; Randy J. Arnold[1]; Divya Aggarwal[1]; David E. Clemmer[1]; Narmada Jayasankar[1]; Predrag Radivojac[1]; Zhiyin Xun[1]; Haixu Tang[1]; [1]*Indiana University, Bloomington, IN*

TP 661 **Automated Reprocessing Pipeline for Analysing Heterogenic Data of the HUPO Brain Proteome Project Pilot Phase;** Christian Stephan[1]; Martin Blüggel[4]; Kai A. Reidegeld[1]; Gerhard Körting[4]; Daniel Chamrad[4]; Michael Hamacher[1]; Katrin Marcus[1]; Rolf Apweiler[2]; Henning Hermjakob[2]; Michael Müller[2]; Lennart Martens[3]; Herbert Thiele[5]; David Parkinson[6]; Andre Dowsey[7]; Michael Dunn[8]; Helmut E. Meyer[1]; [1]*Medical Proteom-Center, Bochum, Germany;* [2]*European Bioinformatics Institute, Hinxton, United Kingdom;* [3]*Department of Medical Protein Research, Ghent, Belgium;* [4]*Protagen AG, Dortmund, Germany;* [5]*Bruker Daltonics GmbH, Bremen, Germany;* [6]*Biomedical Research Centre, Sheffield, United Kingdom;* [7]*Imperial College, London, United Kingdom;* [8]*Proteomics Department, Conway Institute, Dublin, Ireland*

TP 662 ***De novo* Algorithm Significantly Outperform Database Search in Coverage of "Normal" Proteins**; Andrey Gorin[1]; Robert M. Day[1]; Nikita D. Arnold[1]; Tema Fridman[1]; [1]*Oak Ridge National Laboratory, Oak Ridge, TN*

RECOMBINANT PROTEINS

TP 663 **Characterization of Monoclonal Antibody Degradants**; Qing (Mike) Tang[1]; Maggie Huang[1]; Weijun Ren[1]; Michael J. Lewis[1]; Michael D. Bond[1]; [1]*Centocor, Inc., Radnor, PA*

TP 664 **Evaluating the Disulfide Map of A Recombinant Membrane Protein by LC/MS/MS**; Marc Wenger[1]; Peter A. DePhillips[1]; Lorenzo H. Chen[1]; [1]*Merck & Co., Inc., West Point, PA*

TP 665 **High-Throughput Identification of Recombinant Protein Phosphorylation Sites using ESI Q-TOF Mass Spectrometry**; Matthew R. Stump[1]; Mark T. Cancilla[1]; [1]*Sunesis Pharmaceuticals, South San Francisco, CA*

TP 666 **Rapid Removal of Non-ionic Detergents From Monoclonal Antibodies and Other Proteins for Mass Spectrometry Analysis Using Centrifugal Ultrafiltration**; Gary W Lange[1]; Joseph W Leone[1]; Barrett R Thiele[1]; Megan A Danielewicz[2]; Stone D-H Shi[2]; [1]*Pfizer Inc, St. Louis, MO;* [2]*Pfizer Inc, La Jolla, CA*

TP 667 **Characterization of Antibody-Drug Conjugates by ESI/LC/MS**; Galahad U Deperalta[1]; [1]*Genentech, South San Francisco, CA*

TP 668 **Characterization and Investigation of N-terminal Cyclization of Monoclonal Antibodies in the Formulation Products**; Bryan L. Yu[1]; Alona Vizel[1]; Richard L. Remmmele Jr.[1] Bing He[1]; [1]*Amgen, Thousand Oaks, CA*

TP 669 **Rapid Identification of Therapeutic Proteins by Peptide Mass Fingerprinting**; Mary Zhu[1]; William E. Haskins[1]; Viswanatham Katta[1]; [1]*Genentech, Inc., South San Francisco, CA*

TP 670 **Characterization of Inter-Capsomeric Disulfide Bonding in Human Papillomavirus Recombinant Virus-Like Particles Using LC/MS**; Colleen E. Price[1]; Marc Wenger[1]; Pete DePhillips[1]; Lorenzo Chen[1]; [1]*Merck and Co., Inc., West Point, PA*

TP 671 **Determination of Minor Variants in Recombinant Proteins by Hydrophobic Interaction Chromatography Combined with High Resolution Mass Spectrometry;** Terry D. Cyr[1];