

Monday, August 25th

MPS01 - Fourier-Transform MS

Abstract No.	Presenting Author	Affiliation	Abstract Title
MPS01-01	Croce, Annamaria	Università degli Studi de L'Aquila	Hydrothermal liquefaction of biomass model compounds: characterization study by FTICR-MS
MPS01-02	Fujiwara, Makoto	Hiroshima City University	Coulomb-Interaction-Induced Effects on FT-ICR Mass Spectral Peak Shape: A Many-Particle Simulation Using GRAPE
MPS01-03	Mamontov, E. V.	RGRTU	Ion trap with a superposition of linear high frequency and homogeneous static electric fields
MPS01-04	Guigues, Elodie	Aix-Marseille Université	Creation and Injection Device for a 3D RF Ion Trap operated in Fourier Transform Mode applied to Fission Gas Release Analysis
MPS01-05	Tomalová, Iva	Masarykova univerzita	FT-ICR MS for measurement of initial velocities of ions formed in MALDI process
MPS01-06	Kekäläinen, Timo	University of Eastern Finland	Characterization of Fractionated Pinewood Slow Pyrolysis Oils by Ultrahigh-Resolution FT-ICR Mass Spectrometry
MPS01-07	Wang, Xuxiao	Max-Planck-Institut für Kohlenforschung	Rapid and selective analysis of sulfur-containing species in crude oils by electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry
MPS01-08	G. Santos, Vanessa	Thomson Mass Spectrometry Laboratory	Petroleum and Its Fractions: Exploring the Saturated and Aromatic Hydrocarbon Composition by APCI(+)-FT-ICR-MS
MPS01-09	Su, Hung	National Sun-Yat Sen University	Laser Ablation for Introducing Internal Calibrant for High Performance Liquid Chromatography/Fourier Transform-Ion Cyclotron Resonance (HPLC/FT-ICR)
MPS01-10	Mistrik, Robert	HighChem	TreeRobot: A new software for automated acquisition of MS ⁿ spectral trees on Orbitrap hybrid mass spectrometers
MPS01-11	Santos Júnior, Júlio César	Department of Clinical Pathology, School of Medical Sciences, University of Campinas — UNICAMP	Vitreomics by ESI (+) FT-ICR-MS
MPS01-12	Mejía-Ospino, Enrique	Universidad Industrial de Santander	Comparing LDI-FT-ICR and LDI-TOF/TOF Mass Spectrometry to Characterize Vacuum Residue of Colombian Crude Oils
MPS01-13	Tsybin, Oleg Yu.	Saint-Petersburg State Polytechnical University	Instantaneous frequency theory and applications in FTMS
MPS01-14	Nagornov, Konstantin	Ecole polytechnique fédérale de Lausanne	High-performance FT-ICR MS at unperturbed cyclotron frequency
MPS01-15	Ding, Chuan-Fan	Fudan University	Design of a Permanent Magnetic Orbital Trap Mass Analyzer
MPS01-16	Lang, Johannes	2nd Physics Department, JLU Giessen	A Mobile Multiple-Reflection Time-of-Flight Mass Spectrometer with Ultra-High Resolution MS ⁿ Capabilities

MPS02 - Polymers

Abstract No.	Presenting Author	Affiliation	Abstract Title
MPS02-01	Yuping, Tian	Shanghai Institute of Measurement and Testing Technology	Analysis of PFOS in Plastic Products by LC-MS/MS and the Assessment of Uncertainty

MPS02-02	De Winter, Julien	University of Mons	One step further in the folding of multiply charged sodium cationized polylactides : ion mobility mass spectrometry and molecular modelling
MPS02-03	Feilden, Andrew	Smithers Rapra	Comprehensive Analysis of Extractables from Rubber Stoppers used in Medical Devices and Pharmaceutical Container Closure Systems
MPS02-04	Zannoni, Carla	ENI Corporate University SPA	Direct probe mass spectrometry (DIP-MS) for characterisation of asphaltenes
MPS02-05	Okamoto, Mami	YAZAKI Corporation	Characterization of thermal degradation products of polymer material by reactive pyrolysis-GC/MS using EI ionization method and PI ionization method
MPS02-06	Crotty, Sarah	Friderich Schiller University FSU	Sequencing of Copolymers using Mass Spectrometry
MPS02-07	Kitada, Yukio	YAZAKI corporation	Evaluation of the thermal degradation of poly (butylene terephthalate) by high-resolution MALDI-TOFMS combined with Kendrick mass defect analysis
MPS02-08	Wang, Meng-Jiy	National Taiwan University of Science and Technology	Electrospun Nanofiber Surface Assisted Laser Desorption/ Ionization Mass Spectrometry
MPS02-09	Chendo, Christophe	Aix-Marseille University	Production of doubly charged species during solvent-free MALDI of small synthetic polymers
MPS02-10	Buchmann, William	University of Evry	ETD as an alternative fragmentation technique to CID for the characterization of polytetrahydrofuran and polycaprolactone
MPS02-11	Fouquet, Thierry	Public Research Centre Henri Tudor	TOF-SIMS / MALDI-TOF combination for the molecular weight depth profiling of a polymeric bilayer
MPS02-12	Absalon, Christelle	ISM - University of Bordeaux	Copolymer characterization by combination of MALDI and pyrolysis GC-MS
MPS02-13	Hermannova, Martina	Contipro Pharma a.s.	Detailed insight into tyramine cross-linking in hyaluronan-based hydrogels
MPS02-14	Altuntas, Esra	Aix Marseille University	Ion mobility spectrometry-mass spectrometry (IMS-MS) analysis of polyamidoamine (PAMAM) dendrimers
MPS02-15	Jordens, Jan	DSM Resolve	Resolving ionization processes of polyamides in ESI-MS by ESI-IMS-MS
MPS02-16	Frache, Gilles	Centre de Recherche Public - Gabriel Lippmann	Plasma-Enhanced Chemical Vapour Deposition investigated by Atmospheric-Pressure MALDI High-Resolution Mass Spectrometry using matrix pre-coated substrates
MPS02-17	Garbaras, Andrius	Center for Physical Sciences and Technology	Application of stable isotope method for the nanocomposites investigation
MPS02-18	Sun, Shuqi	SINOPEC Beijing Research Institute of Chemical Industry	Determination Method of VOCs in Accelerated Aging Polypropylene by Thermal Desorption-Gas Chromatography/Mass Spectrometry
MPS02-19	Shiea, Jentaie	National Sun-Yat Sen University	Real-time Characterization of Polymers by Using Thermogravimetry Coupled with An Ambient Mass Spectrometry
MPS02-20	Aldawsari, Abdullah	King Saud University	Investigation on asphaltene composition in crude oil in Saudi Arabia using mass spectrometry

MPS03 - MS Instrumentation

Abstract No.	Presenting Author	Affiliation	Abstract Title
MPS03-01	Hashimoto, Yuichiro	Hitachi, Ltd.	Simultaneous FAIMS detection without scanning compensation voltage
MPS03-02	Douglas, Donald	University of British Columbia	The Effective Potential of a Radio Frequency Linear Quadrupole Ion Trap
MPS03-03	Konenkov, Nikolai	University of British Columbia	Mass Selectivity with Dipole Excitation of Ions in a Linear Quadrupole Ion Trap with Round Rods
MPS03-04	Chen, Evan	Duke University	Greater than 10X signal gain in magnetic sector mass spectrometry via aperture coding
MPS03-05	Zhuravlev, V.V.	RGRTU	Planar Discrete Electrode Systems for a Creation superposition of DC and RF Electric Fields
MPS03-06	Lindinger, Christian	IONICON Analytik GmbH.	Separation of Isomers with Proton-Transfer-Reaction Mass Spectrometry: Selective Reagent Ionization and FastGC Inlet
MPS03-07	Dojahn, Joerg	AB Sciex	Exploring Impact of Dynamic Accumulation for Improving MS/MS Quality of QqTOF Data
MPS03-08	Lai, Szu-Hsueh	Genomics Research Center, Academia Sinica, Taipei, Taiwan	Advanced bioparticle accelerator

MPS03-09	Yoshinari, Kiyomi	Hitachi, Ltd., Hitachi Research Laboratory	Mechanism of Loss Occurrence of Ions Injected into Ion Guide Electrodes and Quadrupole Mass Spectrometer based on the Simulation of Transmission Efficiencies
MPS03-10	Strupat, Kerstin	Thermo Fisher Scientific	Improvements in Shotgun Proteomics Using a Benchtop Quadrupole High-Field Orbitrap.
MPS03-11	Giannakopoulos, Anastassios	ThermoFisher Scientific	Experimental and numerical study of a two-mirror multireflectron
MPS03-13	Breuer, Matthew	Photonis USA	CHARACTERIZATION OF A NEW HIGH RESOLUTION ION BEAM IMAGER TO IMPROVE ION BEAM ANALYSIS IN MASS SPECTROMETERS
MPS03-14	Chen, Evan	Duke University	multi Resonant Frequency Excitation (mRFE) Ejection Mass Analysis on Quadrupole Ion Trap Systems
MPS03-15	Lai, Yin-Hung	Genomics Research Center, Academia Sinica	Manipulating Alkali Metal Ion Distribution in MALDI with Sample Preparation Protocols as Revealed by Dual-Polarity Time-of-Flight Imaging Mass Spectrometry
MPS03-16	Gurov, Victor	Ryazan State Radio Engineering University	High-aperture energy and mass spectrometer of ion fluxes
MPS03-17	Guo, Meiru	Science and Technology on Vacuum & Cryogenics Technology and Physics Laboratory, Lanzhou Institute of Physics	The exploration of space atmosphere composition by a miniature magnetic sector spectrometer
MPS03-18	Lange, Kathrin	Technical University Munich	Experimental setup for the recognition of chiral metal clusters
MPS03-19	Hebert, Yann	Bruker Daltonics Inc.	Advances in signal dependent detector optimization for coeluting peaks in triple quad MS
MPS03-20	Martens, Jonathan	FELIX Facility - Radboud University Nijmegen	Development of a Quadrupole Ion Trap Mass Spectrometer for Spectroscopic Characterization of ETD/CID Generated Peptide Fragments using FELIX

MPS06 - Clinical Applications and Screening

Abstract No.	Presenting Author	Affiliation	Abstract Title
MPS06-01	Dabbish, Eslam		Carnosine and its Complexes with Pt-based Anti-Cancer Drugs: A Mass Spectrometry, Computational Modelling and In Vitro Cell Bioassay Study
MPS06-02	Ekström, Simon	Department of Biomedical Engineering, Lund University,	ACOUSTIC TRAPPING FOR BACTERIA TYPING IN BLOOD CULTURE WITH MALDI-MS
MPS06-03	Huang, Ren-Yeong	School of Dentistry, Tri-Service General Hospital, National Defense Medical Center	The Role of Plasminogen Activation System in Periodontal Tissue Destruction: Differential Proteomic and bioinformatic analysis in Two Experimental Periodontitis
MPS06-04	Surindar Singh, Gurmeet Kaur	ANZAC Research Institute, University of Sydney and Faculty of Pharmacy, Universiti Teknologi MARA (UiTM)	Pharmacokinetic-Pharmacodynamic Study of Subcutaneous Injection of Nandrolone Decanoate Using Dried Blood Spots (DBS) Blood Sampling coupled with LC-MS/MS
MPS06-05	Shimada, Takashi	SHIMADZU Corporation	Selective detection and quantitation of complementarity-determining regions of monoclonal antibodies for the development of therapeutic drug monitoring by MS
MPS06-06	Teramoto, Kanae	JEOL Ltd.	Characterization of Bacterial Fatty Acids by MALDI spiral-TOFMS Combined with Kendrick Mass Defect Plot Analysis
MPS06-07	Shirangi, Mehrnoosh	Utrecht University	Assessment and Identification of Acylated Peptides from Poly(alpha-hydroxyl ester) Microspheres by LC-MS-MS
MPS06-08	Ray, Andrew	AstraZeneca	Use of on-line mass spectrometry for understanding dissolution processes of oral dosage forms
MPS06-09	Michelsen, Vibeke Barman	University of Bergen, Faculty of Medicine and Dentistry	Comparison of EI and CI based GC-MS analysis of leachables from Dental Polymer-Based Restorative Materials
MPS06-10	Takeda, Sen	University of Yamanashi	Developing a human cancer diagnostic system: Overview of the system construction
MPS06-11	Elnaggar, Mariam	Prosolia	Extractive Analysis and Tissue Profiling using Flowprobe Mass Spectrometry

MPS06-12	Nováková, Lucie	Univerzita Karlova v Praze, Farmaceutická fakulta v Hradci Kralove	Optimization and application of UHPSFC-MS/MS method for screening of doping agents
MPS06-13	Hee, Daryl Kim Hor	National University of Singapore	Development and validation of LC-MS/MS method for quantification of first line tuberculosis drugs and metabolites in plasma and application in clinical study
MPS06-14	Eigenmann, Daniela Elisabeth	Pharmaceutical Biology, Department of Pharmaceutical Sciences, University of Basel, Klingelbergstrasse 50, 4056 Basel, Switzerland	Full Validation of a UPLC-MS/MS Method for Determination of an Anti-Allergic Indolinone Derivative and Application to Brain Drug Permeability Studies
MPS06-15	Bártl, Josef	Institute of Inherited Metabolic Disorders, General University Hospital and 1st Faculty of Medicine, Charles University, Prague, Czech Republic	Optimization of laboratory MS/MS newborn screening of inherited metabolic diseases
MPS06-16	Schoumacker, Rachel	INRA - SFC	Real time monitoring of the metabolic capacity of ex-vivo rat olfactory mucosa by PTR-MS
MPS06-17	Lozan, Ecaterina	Université de Bordeaux	High Performance Liquid Chromatography-Tandem Mass Spectrometry method for quantification of 17- β -Estradiol in mouse plasma and brain
MPS06-18	Hoshi, Tomoomi	Shimadzu Corporation	Developing a human cancer diagnostic system: Validation of the system robustness
MPS06-19	Skeene, Kirsty	Department of chemistry, University of York	Development of a mass spectrometric approach to study disorders of protein O-glycosylation
MPS06-20	Gonzalez Antuña, Ana	University of Oviedo	MINIMAL LABELLING AND LOW RESOLUTION SELECTED REACTION MONITORING FOR ACCURATE IDMS DETERMINATIONS BY LC-ESI-MS/MS
MPS06-21	Anders, Ulrike	ETH Zurich	Interaction Analysis using SPRI-MALDI MS
MPS06-22	Moradi-Afrapoli, Fahimeh	Pharmaceutical Biology, Department of Pharmaceutical Sciences, University of Basel	Full validation of UHPLC-MS/MS methods for the determination of kaempferol and 4-HPAA, and application to in vitro BBB and intestinal drug permeability studies
MPS06-23	Asperger, Arndt	Bruker Daltonik GmbH	A SISCAPA Immuno-MS Assay for Quantification of Soluble Transferrin Receptor in Human Serum
MPS06-24	Balog, Julia	Imperial College London	The novel iEndoscope for the rapid identification of gastrointestinal polyps and tumours in-vivo using rapid evaporative ionization mass spectrometry
MPS06-25	Kiehne, Andrea	Bruker Daltonik GmbH	New Workflows for Identification and Profiling of Disulfide Bonds in Biopharmaceuticals
MPS06-26	Chervet, Jean-Pierre	Antec	Mimicking Drug Metabolism by EC/MS
MPS06-27	Ferreirós, Nerea	Institute of Clinical Pharmacology, Goethe-University, Frankfurt am Main, Germany	Quantitation of nucleosides and nucleoside triphosphates using LC-MS/MS in bioanalysis
MPS06-28	Pilařová, Veronika	Charles University in Prague, Faculty of Pharmacy in Hradec Králové, Department of Analytical Chemistry	DETERMINATION OF QUERCETIN AND ITS METABOLITES IN RAT PLASMA BY ULTRA HIGH PERFORMANCE LIQUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY
MPS06-29	Enjalbal, Christine	Institut des Biomolécules Max Mousseron	STRUCTURAL CHARACTERIZATION OF IN VITRO METABOLITES OF THE NEW ANTICANCER AGENT, EAPB0503, BY LIQUID CHROMATOGRAPHY-TANDEM MASS SPECTROMETRY
MPS06-30	Eberl, Anita	Joanneum Research HEALTH	Determination of 2H-labeling of water in the interstitial fluid of rat brain using gas chromatography - quadrupole mass spectrometry
MPS06-31	Heller, Manfred	University of Bern	Quantitative Protein Measurement of Circulating Plasma Microparticles by Data-Independent nanoLC-MS2

MPS06-32	Challal, Soura	University of Geneva	Combining miniaturized Zebrafish bioactivity-guided fractionation with UHPLC-Orbitrap-MS and NMR dereplication for the early stage anticonvulsant's discovery
MPS06-33	Steinhoff, Robert	ETH Zurich	Metabolite monitoring in fed batch cell cultures using MALDI-TOF-MS
MPS06-34	Lacoursière, Jean	Phytronix Technologies Inc	Fast and simple sample preparation for ultra-fast screening of drugs in urine by LDTD-MS/MS
MPS06-35	Pabst, Martin	ETH Zurich	Micro-Arrays for Mass Spectrometry (MAMS): Microarray Targets for Rapid Quantitative MALDI-MS
MPS06-36	Peng, Wen-Ping	National Dong Hwa University	Screening Mycobacterium Tuberculosis Complex with Detonation Nanodiamond
MPS06-37	Senior, Adam	Biotage GB Ltd	Evaluation of a Novel 96-well Filter Plate for the Effective Removal of Serum Protein and Phospholipids prior to LC-MS/MS Analysis
MPS06-38	Raml, Reingard	Joanneum Research, Institute Health	An analytical method (UHPLC-MS/MS) to determine the pharmacodynamic behaviour of the topically applied antiviral drug acyclovir
MPS06-39	Lafitte, Daniel	Aix Marseille Université	On tissue characterization of amyloidosis using MALDI mass spectrometry
MPS06-40	Vlčková, Hana	Department of Analytical Chemistry, Faculty of Pharmacy in Hradec Králové, Charles University in Prague	An alternative approach for the analysis in clinical practice: determination of amphetamine and methadone in human urine by direct MEPS-MS/MS analysis
MPS06-41	Dillen, Lieve	Janssen R&D	Strategies for development of high sensitive quantitative analysis
MPS06-42	Friedecký, David	Palacky University Olomouc	Biotransformation of tyrosine kinase inhibitor - imatinib by high resolution mass spectrometry
MPS06-43	Nye, Leanne C.	Imperial College, London	Identification of a Novel Metabolite for The HIV treatment Tenofovir Disoproxil with LC-MS/MS
MPS06-44	De Nardi, Claudio	ThermoFisher	Benefits of High Resolution and Accurate Mass Instrument for therapeutic monitoring of baclofen and its metabolites in plasma and urine.
MPS06-45	Nye, Leanne	Imperial College, London	A Validated High-throughput Assay for the Quantification of Amino Acids in Metabolic Phenotyping Studies
MPS06-46	El-Aneed, Anas	University of Saskatchewan	The Establishment of a General ESI-MS/MS Behavior of a Series of Antineoplastic Curcumin Analogues & The Formation of Unique [M-H] ⁺ Ions During Photoionization
MPS06-47	Piestansky, Juraj	Faculty of Pharmacy, Comenius University Bratislava	Two dimensional capillary electrophoresis coupled with tandem mass spectrometry for determination of varenicline in urine matrices
MPS06-48	Kuhtinskaja, Maria	Institute of Chemistry, Tallinn University of Technology	STUDY OF UPF PEPTIDE-POLYPHENOL CONJUGATION BY MASS SPECTROMETRY
MPS06-49	Ji, Injung	1.AGRS, Chungnam National University, Daejeon, Korea 2.GRAST, Chungnam National University, Daejeon, Korea	Abberant Glyosylation in Skin Tissue of Atopic Syndrome Patients
MPS06-50	Veizerová, Lucia	Faculty of Pharmacy, Comenius University	Characterization of phenolic compounds in <i>Lycopus europaeus</i> L. by HPLC-DAD-ESI-QTOF
MPS06-51	Thorn, Jim	SCIEX SEPARATIONS	MULTILEVEL CHARACTERIZATION OF THERAPEUTIC ANTIBODIES BY CESI-MS
MPS06-52	Pánczél, József	sanofi R&D, DSAR Frankfurt Operational Center	Comparison of fragmentation patterns of Q-TOF and Orbitrap accurate mass spectrometers for drug metabolism studies
MPS06-53	Galba, Jaroslav	Faculty of Pharmacy, Comenius University Bratislava	DETERMINATION OF BLEOMYCIN A2 AND B2 IN PLASMA BY HPLC-ESI-QTOF METHOD
MPS06-54	Steiner, Carine	Geneva University Hospitals / F. Hoffmann-La Roche	Mass spectrometry quantification of HER2 peptides in FFPE breast cancer tissues
MPS06-55	Longuespée, Rémi	Mass Spectrometry Laboratory	Down-scaling tissues proteomics, toward precious FFPE tissue samples preparation

MPS06-56	Rybicka, Magda	University of Gdansk	MALDI-TOF MS for Monitoring Drug Resistance in Hepatitis B Virus-Infected Patients during Antiviral Therapy
MPS06-57	Mueller, Patrick	University of Sydney	Antiviral Potential of Catechins to Arrest Influenza Virus Infections with Confocal Microscopy, Molecular Docking and Mass Spectrometry
MPS06-58	Downard, Kevin	University of Sydney	Anthocyanidin Inhibitors Against the Influenza Virus by Mass Spectrometry
MPS06-59	Aros-Calt, Sandrine	CEA Saclay - LEMM	Development of an LC-HRMS-based metabolomic approach to study methicillin-resistant Staphylococcus aureus
MPS06-60	Dewaele, Debbie	University of Antwerp	Analysing covalent protein-drug adducts: protein-melphalan adducts
MPS06-61	Capka, Vladimir	Novartis Institutes for Biomedical Research, Inc.	Catabolite Identification of Antibody Drug Conjugates Using High Resolution Mass Spectrometry with Segmented Window Data Independent Acquisition
MPS06-62	Paskins, Aimee	Sheffield Hallam University	Investigating Metal Binding and the Resulting Conformational Changes of Monomeric Alpha-Synuclein
MPS06-63	Hari, Yvonne	University of Bern	Tandem mass spectrometric characterization of a sugar-modified antisense oligonucleotide
MPS06-64	El Aribi, Houssain	ABSCIEX Switzerland	Ultra-Sensitive Quantitation of Exenatide with Micro-Flow LC Trap-and-Elute and High Resolution and Triple Quadrupole Mass Spectrometry Workflow

MPS07 - Imaging MS – Instrumentation

Abstract No.	Presenting Author	Affiliation	Abstract Title
MPS07-01	Nielen, Michel	RIKILT, Wageningen University and Research Centre	Macroscopic and microscopic spatially-resolved analysis of food contaminants using Laser Ablation Electrospray Ionization Imaging Mass Spectrometry
MPS07-02	Hollebrands, Boudewijn	Unilever R&D	Molecular mapping of skin and biofilms by MALDI MS imaging
MPS07-03	Jirasko, Robert	University of Pardubice	Application of New Nanostructured Materials in the LDI-MS Analysis of Small Molecules
MPS07-04	Vens-Cappell, Simeon	University Münster	Dithranol is an Efficient Matrix for MALDI-MS Imaging of Glyco- and Phospholipids with High Lateral Resolution
MPS07-05	Spivak-Lavrov, Igor	Aktobe Regional State University named after K. Zhubanov, Aktobe	Line ion accelerator on the basis of the Wedge-shaped Mirror with Two-dimensional Field as Time-of-Flight Mass Spectrometer
MPS07-06	Janfelt, Christian	Dept. of Pharmacy, University of Copenhagen	Studies of an insect model for drug metabolism by Desorption Electrospray Ionization Mass Spectrometry Imaging
MPS07-07	Yan, Cunyu	University of Manchester	High throughput detection of directed evolution driven biotransformation reactions with liquid surface extraction analysis mass spectrometry
MPS07-08	Glascott-Jones, Andrew	e2v	Comparison of Interleaved and Single Core Analog to Digital Converters and their Applications to TOF Mass Spectrometry
MPS07-09	Xu, Fuxing	Fudan University	A linear ion trap constructed with ladder shape electrodes
MPS07-10	Staab, Dieter	Novartis	iMatrixSpray - Open Source Sample Prep Solution for MS Imaging
MPS07-11	Zhong, Xiaoqin	EPFL	Electrostatic Spray Ionization (ESTASI) Mass Spectrometry Imaging of Thin-Layer Chromatography
MPS07-12	Witt, Matthias	Bruker Daltonik GmbH	In-depth identification of protein images by combining high mass resolution MALDI FTMS Imaging and high performance qTOF nLC-MS/MS
MPS07-13	Asperger, Arndt	Bruker Daltonik GmbH	3D MALDI Imaging of Mouse Heart after Myocardial Infarction
MPS07-14	Hartmanova, Lucie	RCPTM, Palacky University in Olomouc	Mass spectrometric imaging of plant tissues using desorption nanoelectrospray ionization
MPS07-15	Almazov, Victor	Institute for Analytical Instrumentation RAS. St. Petersburg, Russia	Dependence of mass peak shape on r/r0 ratio in quadrupole mass analyser
MPS07-16	Franceschi, Pietro	Fondazione E. Mach	Self-organizing maps: A versatile tool for the automatic analysis of untargeted imaging datasets

MPS07-17	Franceschi, Pietro	Fondazione E. Mach	Tissue Surface Properties Jeopardize Quantitative DESI Imaging of Organic Acids in Grapevine Stem
MPS07-19	Aoki, Jun	Osaka University	Development of new stigmatic imaging mass spectrometer and its application for surface analysis of high functional organic materials
MPS07-20	Lockyer, Nick	University of Manchester	A new ion beam based on water clusters for ToF-SIMS imaging
MPS07-21	Ogata, Koretsugu	Shimadzu corporation	Identifying the distribution of chlorpromazine and its metabolites in mouse liver samples using a newly developed Imaging Mass Microscope: iMScope
MPS07-22	Janulyte, Aurika	Aix-Marseille University	Effect of elastic collisions on state of an ion cloud confined in an RF quadrupole trap elucidated by the temporal invariance method
MPS07-23	Chan, Dominic	The Chinese University of Hong Kong	Development of a novel Two Channel Off-axis Ion Funnel Trap (TCOAIFT) for use in a FTICR Mass Spectrometer
MPS07-24	Touboul, David	CNRS ICSN	IMPROVEMENTS OF TOF-SIMS MASS SPECTROMETRY IMAGING: HIGH SPATIAL RESOLUTION COMBINED WITH HIGH MASS RESOLUTION AND HIGH SENSITIVITY FOR RELATIVE QUANTIFICATION
MPS07-25	Ellis, Shane	FOM Institute AMOLF	Direct Ion Imaging with Active Pixel Detectors

MPS08 - Carbohydrates

Abstract No.	Presenting Author	Affiliation	Abstract Title
MPS08-01	Clerc, Florent	Leiden University Medical Center (LUMC)	Plasma protein N-glycosylation profiling by LC-MS of glycopeptides after depletion of 14 high abundant proteins
MPS08-02	Oh, Myung Jin	AGRS/Chungnam National University	Characterization of biotherapeutic protein glycosylation with structure-specific LC/MS/MS
MPS08-03	An, Hyun Joo	AGRS/Chungnam National University	A microfluidic chip-based strategy for biopharmaceutical glycome analysis
MPS08-04	ERRA BALSELLS, Rosa	University of Buenos Aires	Searching the interaction of carbohydrates with Z- and E-sinapinic in solid MALDI samples
MPS08-05	Sandeep, Deshmukh	University of Leipzig, Germany	Improving the quantitation of carbohydrates for metabolite profiling of biological extracts by GCMS.
MPS08-06	Kiehne, Andrea	Bruker Daltonik GmbH	Improved glycopeptide analysis using acetonitrile enriched sheath gas and oxonium ion dependent ETD
MPS08-07	Lattova, Erika	Masaryk University	MASS SPECTROMETRIC PROFILING OF PATATIN GLYCOCONJUGATES AND THEIR ALTERATIONS WITH GENOTYPE VARIABILITY
MPS08-08	Zamfir, Alina	West University, Timisoara	A nanoESI-QTOF MS approach for screening and sequencing of underivatized dextran chains containing up to 35 glucose repeats
MPS08-09	Martin Mnatsakanyan, Mariam	University of Geneva	Preparation and Characterisation of Chito - Oligosaccharides by MALDI-TOF MS and Size Exclusion Chromatography (SEC-MALLS) for Biomedical Applications
MPS08-10	Yu, Ying Qing	waters corporation	Automated Glycan Assignment Using Accurate Mass Measurement with a Calibrated Retention Time in Glucose Units
MPS08-11	Mank, Marko	Nutricia Research	Negative Ion Mode ESI-LC-MRM-MS for Differentiation of Native Human Milk Tetra- and Pentaoses & Possible Application in Human-Milk-Typing
MPS08-12	Thorn, Jim	Sciex Separations	Bottom-up characterization of a monoclonal antibody Trastuzumab with sheathless CESI-MS coupled to the Orbitraps mass spectrometers
MPS08-13	Pang, Poh-Choo	Imperial College London	Sulphoglycomics Made Easy: a Simplified for Procedure for N- and O-glycomics

MPS31 - Biomarkers and Diagnostics

Abstract No.	Presenting Author	Affiliation	Abstract Title
MPS31-02	Koal, Therese	BIOCRATES Life Science AG	The influence of different sample collection methodologies on blood metabolomic phenotype LC-MS/MS profiles

MPS31-03	Yoshimura, Kentaro	University of Yamanashi	Developing a cancer diagnostics system: Towards on-site multi purpose gadgetry
MPS31-04	Chen, Chao-Jung	China Medical University	Novel urine assay for predicting acute pancreatitis severity by MALDI-TOF mass spectrometry
MPS31-06	Kinumi, Tomoya	NMIJ, National Institute of Advanced Industrial Science and Technology (AIST)	Toward standardization of C-peptide measurement: Development of reference material and serum C-peptide measurement by isotope-dilution mass spectrometry
MPS31-07	Zabela, Volha	University of Basel	Validation of UHPLC-MS/MS methods for the determination of kaempferol and 4-hydroxyphenylacetic acid in rat plasma, and application to pharmacokinetic studies
MPS31-08	Chen, Sung-Fang	National Taiwan Normal University	Quantitative analysis of prostate specific antigen isoforms using immunoprecipitation and isotope dilution mass spectrometry
MPS31-09	Tonoli, David	University of Geneva	Evaluation of endocrine disruptors in H295R cells culture media with high-resolution mass spectrometry using a qualitative and quantitative steroidomic approach
MPS31-10	Tsuji, Makoto	Daiichisankyo RD Novare Co., Ltd.	A validated quantitative LC-MS/MS method using isotopic MRM transitions to evaluate global ratios of modified cytosines
MPS31-11	Gamoh, Keiji	Kochi University	Biomarkers of autism spectrum disorders (ASD) based on the comparative analysis of the metabolite concentrations in saliva
MPS31-12	Veron, Laurent	BioMérieux	Comparison of three sample preparation methods for identification of bacterial pathogens from urine specimens by MALDI-TOF Mass Spectrometry.
MPS31-13	Jeanneret, Fabienne	University of Geneva	Chemical and biological study of human urinary biomarkers of dioxin exposure previously highlighted by metabolomics with high-resolution mass spectrometry
MPS31-14	Borén, Mats	Denator	Preserve the integrity of tissue sample analytes by heat stabilization
MPS31-15	Ehret-Sabatier, Laurence	IPHC-LSMBO	SRM as a new efficient detection tool for the early diagnosis of the Lyme disease
MPS31-16	Dojahn, Joerg	AB Sciex	Investigating Biological Variation in Human Hepatocytes of Phase I and II drug Metabolism Enzymes
MPS31-17	Rocha, Daniele F. O.	ThoMSon Mass Spectrometry Laboratory - University of Campinas - UNICAMP	Understanding Leishmania Life Cycle by MALDI-MS Profile and Chemometric Analysis
MPS31-18	Shibasaki-Hirano, Hiromi	Tokyo University of Pharmacy and Life Sciences	In vivo cytochrome P450 3A activity in a pregnant woman as measured by endogenous cortisol 6 β -hydroxylation clearance
MPS31-20	Sato, Hiroaki	National Institute of Advanced Industrial Science and Technology (AIST)	Rapid identification of fungi of the genus Aspergillus using ribosomal protein biomarkers as observed by MALDI-MS
MPS31-21	Yokokawa, Akitomo	Tokyo University of Pharmacy and Life Sciences	A novel index for assessing 3 β -hydroxysteroid dehydrogenase activity in humans based on the measurement of dehydroepiandrosterone and androstenedione
MPS31-22	Nilsson, Ralf	Astrazeneca	Ticagrelor effects on the adenosine pathway revealed by stable isotopes and mass spectrometry in a dog heart ischemia study
MPS31-23	Perrot, Nadine	bioMérieux	Detection of LPS modification as a biofilm signature using the VITEK [®] MS system
MPS31-24	Krijt, Jakub	General University Hospital and 1st Faculty of Medicine, Charles University	The utilization of LC-MS/MS methods in diagnosis of cystathionin- β -synthase deficiency.
MPS31-25	Aurand, Craig	Sigma-Aldrich	Improved Sample Preparation and HPLC/MS Analysis of Vitamin D Metabolites from Human Plasma
MPS31-26	Ganief, Tariq	IIDMM, UCT	A proteomic investigation into the molecular mechanism of HIV tat induced neuronal apoptosis
MPS31-27	Blackler, Adele	OncoPlexDx	Quantification of HER2 from FFPE Tumor Tissue using Targeted Mass Spectrometry (MS)
MPS31-28	Guray, Melda Zeynep	Izmir Institute of Technology	Proteomic Analysis of Bence Jones Proteins Isolated from Urine Sample
MPS31-29	Donzeli Pereira, Caroline	Osaka University	A Method for Isolating Free Thiol-Containing Proteins from Plasma

MPS31-30	Iguchi, Kohta	Japan	Plasma proteomic biomarker strategy in a porcine hepatectomy model
MPS31-31	Abdel-Khalik, Jonas	Swansea University	Analysis of vitamins D metabolites by isotope-dilution liquid chromatography – tandem mass spectrometry using enzyme-assisted derivatisation
MPS31-32	Cole, Laura	BMRC, Sheffield Hallam University	Lipidomic and Proteomic Profiling and Imaging of Uveal Melanoma using MALDI-IMS-MS
MPS31-33	Pailleux, Floriane	University of Geneva	Mass Spectrometry-Based Biomarker Discovery: Quantification of Targeted Neuropeptides in Neuropathic Pain
MPS31-34	Kasama, Takeshi	Tokyo Medical and Dental University	Micro-heterogeneity of pyrrole-imidazole polyamides (PIPs) which are the novel diagnostic agent and/or drug candidates using mass spectrometry
MPS31-35	Bovet, Cédric	Institute of Clinical Chemistry, Inselspital, Bern University Hospital, Bern, Switzerland	The Clinical Metabolomics Facility (CMF) – accelerating translational research
MPS31-36	Spiller, Sandro	Institute of Bioanalytical Chemistry, Faculty of Chemistry and Mineralogy, Universität Leipzig	MS based quantification of individual glycation sites in plasma proteins as potential type 2 diabetes biomarkers
MPS31-37	Gillet, Sylvie	Université Paris Descartes, Sorbonne Paris Cité, Faculté des Sciences Pharmaceutiques et Biologiques de Paris, CNRS UMR 8638	Epigenetic effects of Benzo[a]Pyrene on placental histones: a new global MS-based profiling approach
MPS31-38	Iden, Charles	Stony Brook University	Nanoflow LC/MS for the Quantitation of Aristolochic Acid DNA Adducts
MPS31-39	Nye, Leanne C.	Imperial College, London	A Systems Biology / Multi-Omics Approach for the Study of Heart Regeneration in Zebrafish
MPS31-40	Buchmann, William	University of Evry	BIOMARKERS PROBED IN BIOLOGICAL FLUIDS BY SURFACE PLASMON RESONANCE IMAGING COUPLED TO MALDI MASS SPECTROMETRY IN ARRAY FORMAT
MPS31-41	Barkovits, Katalin	Ruhr-University Bochum	Analysis of Cerebrospinal Fluid using High Resolution Mass Spectrometry
MPS31-42	Kacer, Petr	ICT - Prague	UHPLC-MS/MS Method for Monitoring of Neurotransmitters and Their Metabolites in Brain Microdialysates
MPS31-43	Kacer, Petr	ICT - Prague	Molecularly Imprinted Polymers Separation Combined with UHPLC-MS/MS: A Tool for Experimental and Clinical Diagnostics
MPS31-44	dela Rosa, Mira Anne C.	Department of Chemistry, National Taiwan University	Nanoprobe-based affinity mass spectrometry for quantification and glycosylation profiling of liver cancer biomarkers
MPS31-45	Karu, Naama	ACROSS, University of Tasmania	TARGETED AND NON-TARGETED METABOLOMICS IN THE RESEARCH OF CHRONIC KIDNEY DISEASE
MPS31-46	Söderling, Ann-Sofi	astrazeneca	Plasma levels of Tβ4 in cardiac patients and matched controls analyzed by LC-MS and ligand binding assay
MPS31-47	Siroka, Jitka	Institute of Molecular and Translational Medicine, Faculty of Medicine and Dentistry, Palacký University in Olomouc	Plasma metabolite profiling of chronic myeloid leukemia patients
MPS31-48	Dostler, Martin	metanomics GmbH	Application of an improved LC-MS/MS method for the measurement of steroid levels in supernatant of H295R cells to meet the criteria of OECD TG 456
MPS31-49	Gethings, Lee	Waters Corporation	PERFORMANCE INVESTIGATION OF A NOVEL INTEGRATED MICROFLUIDICS PLATFORM IN HIGH-THROUGHPUT LC-MS MRM DISEASE PROTEIN MARKER VERIFICATION
MPS31-50	Bloch, Robert	Helmholtz Centre for Environmental Research GmbH - UFZ	Non-target screening of mercapturic acids in human urine – comparison of different LC-MS approaches
MPS31-51	Barupal, Dinesh	International Agency for Research on Cancer	UHPLC-QTOF Based Metabolomics for discovering Etiological Biomarkers of Liver Cancers Using Serum Samples from a Large Multinational Prospective Cohort

MPS31-52	Lorey, Martina	University of Helsinki	Applications of Mass Tags for Diagnostic Immuno Mass Spectrometry
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Tuesday, August 26th

TPS11 - Targeted and Quantitative Proteomics

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS11-01	Becker, René	Humboldt-Universität zu Berlin	Substrate screening with MeCAT – A comparison of strategies for relative protein quantification
TPS11-02	Budnik, Bogdan	FAS Center for Systems Biology, Harvard University	Multiplexing TMT and SILAC for accurate quantification of mammalian proteomes in MS2 mode
TPS11-03	Sui, Ping	Analytical Chemistry, Department of Chemistry – BMC and SciLifeLab, Uppsala University, Sweden	Global proteome changes in rat spinal cord associated with neuropathic pain
TPS11-04	Chiu, Chih-Wei	National Taiwan Normal University	Differential Proteomics of Monosodium Urate Crystal Induced Inflammatory Response in Dissected Murine Air Pouch Membranes by iTRAQ Technology
TPS11-05	Macur, Katarzyna	Intercollegiate Faculty of Biotechnology University of Gdansk & Medical University of Gdansk, Gdansk, Poland	Optimization of workflow for targeted MS-based proteomic quantification of osteopontin in healthy and cancerous human breast tissues
TPS11-06	Fridström, Anders	Sigma-Aldrich	Characterization of SIL Universal Antibody and SIL Human Proteins for Quantitative Mass Spectrometry
TPS11-07	Ickert, Stefanie	Humboldt-Universität zu Berlin	Metal labelling for quantification of post translational sugar modifications of proteins
TPS11-08	Patel, Ekta	Biomedical Research Centre, Sheffield Hallam University	The investigation of detergent addition to tryptic digests for improving in-situ proteomic experiments.
TPS11-09	Mitchell, Christopher	Biomedical Research Centre, Sheffield Hallam University	Protein expression changes within the epidermis of living skin equivalent tissue observed across a time-course by MALDI-MSI using on-tissue digestion protocols.
TPS11-10	Pepaj, Milaim	Oslo University Hospital	Unraveling the effects of Vitamin D on global protein expression in insulin producing cells by using SILAC in combination with 2D LC MS/MS
TPS11-11	Charretier, Yannick	Genomic Research Laboratory, Service of Infectious Diseases, Geneva University Hospitals	Label free SRM-based relative quantification of antibiotic resistance in Pseudomonas aeruginosa isolates
TPS11-12	Miladinovic, Sasa	Biognosys AG, Zurich, Switzerland	Comparison of data-independent and data-dependent proteomic analysis of human cells on a Thermo Scientific Q Exactive Plus instrument
TPS11-13	Hentschel, Andreas	Leibniz-Institut für Analytische Wissenschaften – ISAS – e.V.	A targeted proteomics study of lipid synthesis pathways in stromal stem cells
TPS11-14	Annette, Michalski	Bruker Daltonik GmbH	Characterization of an Improved Ultra-High Resolution QTOF for Proteomics Applications
TPS11-15	Michalski, Annette	Bruker Daltonik GmbH	High quantification efficiency in plasma targeted proteomics with a Q-TOF platform
TPS11-16	Kuropka, Benno	Forschungsverbund Berlin e.V.	Sortase A-mediated site-specific immobilization of peptides and proteins for interactome analysis by LC-MS/MS
TPS11-17	Stejskal, Karel	RG Proteomics, Central-European Institute of Technology (CEITEC)	Monitoring of H3K56ac level in cancer cell lines during cell cycle by SRM
TPS11-18	Dojahn, Joerg	AB Sciex	Increasing Depth of Coverage in Data Independent Acquisition

TPS11-19	Güler, Ülkü	Hacettepe University, Department of Chemistry	HIGHLY SELECTIVE PROTEIN PROTEOLYSIS USING APTAMER IMMOBILIZED POLYMER SUPPORTS FOR MASS SPECTROMETRY BASED PROTEOMICS
TPS11-20	Galozzi, Sara	Ruhr-Universität Bochum	Amyloid beta peptide quantification via Direct Infusion - Mass Spectrometry
TPS11-21	Neffling, Milla	AB Sciex	The Optimization of Host-cell Protein Detection using data-independent SWATH-MS
TPS11-22	Rodriguez-Gonzalez, Pablo	University of Oviedo	DETERMINATION OF CYSTATIN C IN HUMAN SERUM BY ISOTOPE DILUTION MASS SPECTROMETRY USING MASS OVERLAPPING PEPTIDES
TPS11-23	Doneanu, Catalin	Waters	Identification and Quantification of Low Abundance Host Cell Proteins in a High Purity Monoclonal Antibody
TPS11-24	Taylor, Lester	Agilent Technologies Inc.	Enhanced Performance and Robustness in Peptide Quantitation Using a Newly Developed Triple Quadrupole Instrument
TPS11-25	Alghanem, Bandar	Life Sciences Mass Spectrometry, University of Geneva	The Automated Optimization of Selected Reaction Monitoring Methods for Higher Sensitive Measurements of Peptides
TPS11-26	Chang, Po-Chih	Department of Chemistry, National Dong Hwa University, Hualien, Taiwan	Investigating the effect of protein degradation on the quantification of genetically modified soya using stable isotope labeling and mass spectrometry
TPS11-27	Liao, Wei-Li	OncoPlex Diagnostics	Quantitation of MET using Mass Spectrometry for Clinical Application: Correlation with IHC and MET Gene Amplification in FFPE Tumor Tissue
TPS11-28	Fabritz, Sebastian	AB Sciex, Darmstadt, GERMANY	Automated High Throughput Peptide and Protein MRM Optimization for Pharmaceutical Method Development
TPS11-29	Kumar, Mukesh	Max Planck Institute of Molecular Cell Biology and Genetics (MPI-CBG)	Flexible and Multiplexed Targeted Quantification of Proteins by GeLC MS/MS
TPS11-30	Szrentic, Kristina	Ecole Polytechnique Federale de Lausanne	Chemical hydrolysis-based middle-down proteomics
TPS11-31	Boehm, Guenter	CTC Analytics AG	Automated sample preparation workflows for MS-based proteomics applications
TPS11-32	Glatzer, Timo	Biozentrum Basel	Comparison of different sample preparation strategies reveals quantification biases in gram-negative bacteria and human cells
TPS11-33	Ahrné, Erik	Proteomics Core Facility, Biozentrum, University of Basel	A new method to control ratio distortion for isobaric labeling approaches
TPS11-34	Singh, Kapil Dev	Institute of Molecular Life Sciences, University of Zurich	Studying the effect of natural genetic variation on protein abundance in C. elegans
TPS11-35	Colgrave, Michelle	CSIRO	There's a hole in my assay, dear ELISA, dear ELISA! Using targeted MS to detect gluten in beer that is invisible to ELISA.
TPS11-36	Tsiatsiani, Liana	Utrecht University	Evaluation of candidate proteases for middle-down proteomics
TPS11-37	Hidasi, Anita O	Eawag/EPFL	Targeted proteomics approach to develop a bioassay detecting environmental glucocorticoids with zebrafish embryos
TPS11-38	Navakauskiene, Ruta	Vilnius University Institute of Biochemistry	Mass spectrometry-based proteomics of amniotic fluid incident to normal, preeclampsia and polyhydramnion pregnancies

TPS12 - Lipidomics

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS12-01	Jagadeesan, Kishore Kumar	Dept. of Biomedical Engineering, Lund University	Solid phase extraction materials for the extraction of Phosphatidylethanol

TPS12-02	Chagovets, Vitaliy	University of Pardubice	Effects of fatty acyl chain lengths, unsaturation degree, concentration and used matrix on phosphatidylcholine responses in MALDI-MS
TPS12-03	Šala, Martin	National Institute of Chemistry	Separation of Triacylglycerol Regioisomers by Differential Mobility Spectrometry
TPS12-04	Kim, Young Hwan	Korea Basic Science Institute	Determination of compositions and regioselectivity of two fatty acyl groups in phospholipids by using MALDI-TOF/TOF
TPS12-05	Mi, Jia	Department of Chemistry, Uppsala University	GLP-1's effects on palmitate-induced islet lipotoxicity investigated by targeted lipidomics
TPS12-06	Vrkoslav, Vladimír	Institute of Organic Chemistry and Biochemistry v.v.i., Academy of Sciences of the Czech	Off-line 2D HPLC of aliphatic hydrocarbons
TPS12-07	Bure, Corinne	CBMN/CNRS	A Single Run LC/MS/MS Method for Phospholipidomics: application to <i>S. cerevisiae</i> lipidome and marine lecithin
TPS12-08	Vincendet, JEAN-BAPTISTE	AB SCIEX	Improving Lipid Profiling Performance using Micro Flow Liquid Chromatography and High Resolution Mass Spectrometry
TPS12-09	Papan, Cyrus	AB SCIEX	Qualitative and Quantitative Analysis of Oxidized Fatty Acids by Information Dependent and Data Independent Strategies on a Quadrupole Time-of-Flight Hybrid Ins
TPS12-10	Cvačka, Josef	Institute of Organic Chemistry and Biochemistry AS CR, v.v.i.	HPLC/APCI-MS3 OF 1,2-DIOL DIESTERS IN VERNIX CASEOSA
TPS12-11	Belaz, Katia Roberta Anacleto	ThOMSon Mass Spectrometry Laboratory	THE LIPID PROFILE OF FOLLICULAR FLUID UNDERGOING OVARY SUPERESTIMULATION BY HIGH THROUGHPUT MALDI-MS
TPS12-12	Cífková, Eva	University of Pardubice	Lipidomic Characterization of Kidney Cancer Tissues using HILIC-HPLC/ESI-MS
TPS12-13	Lísa, Miroslav	University of Pardubice	Lipidomics: Supercritical fluid chromatography/ion mobility – mass spectrometry as a tool for fast nontargeted analysis of lipids
TPS12-14	Kania, Magdalena	Institute of Organic Chemistry Polish Academy of Sciences	Mass spectrometry technique coupled with isotopic labeling as an useful tool in metabolism studies of lipid compounds
TPS12-15	Wit, Matthias	Bruker Daltonik GmbH	MALDI Imaging of Rat Testis at 10µm Pixel Size and 470k Mass Resolution
TPS12-16	Thomas, Dominique	Institute of Clinical Pharmacology, Goethe-University Frankfurt	Nano-LC-MS/MS for the Quantitation of Prostanoids in Immune Cells
TPS12-17	Cunha, Ildenize Barbosa da Silva	Universidade Estadual de Campinas (UNICAMP)	Evaluation of oxidation products in fatty acid esters by easy ambient sonic-spray ionization mass spectrometry
TPS12-18	Lanzini, Justine	UMR 8638	MUTATION OF FOXN1 GENE AND CHANGING IN SKIN LIPID PROFILE: A LIPIDOMIC ANALYSIS IN NUDE MICE
TPS12-19	Shaffer, Scott A.	University of Massachusetts Medical School	Robust LC-MS/MS Analysis of CNS-derived GM1 and GM2 Gangliosides
TPS12-20	Nielsen, Mette Marie Bruun	University of Copenhagen	Imaging mass spectrometry for analysing changes in the brain lipidome during cerebral ischemia in mice
TPS12-21	Cha, Sangwon	Hankuk University of Foreign Studies	The Effective MALDI MS Matrixes and Additives for Ganglioside Analysis
TPS12-22	Crick, Peter	Swansea University	Isotopically Labelled Girard Reagents for Multiplexed Analysis of Oxysterols and Cholestenic Acids in Plasma and CSF
TPS12-23	Towers, Mark	Waters Corporation	Lipid visualisation and identification through collision cross section aided correlation of MALDI imaging and MS/MS fragmentation data sets.
TPS12-24	Huang, Yingying	Thermo Fisher Scientific	Higher resolution LC-MS and MS-MS analysis of lipid extracts using benchtop Orbitrap-based mass spectrometers and LipidSearch software

TPS12-25	Hsu, Fong-Fu	Washington University School of Medicine	Structural studies on sphingolipids –a revisit with LIT MSn with high resolution mass spectrometry
TPS12-26	Smith, Rachel	Department of Chemistry, University of York	Application of MALDI-MS for rapid screening of lipid residues in archaeological pottery
TPS12-27	Seyer, Alexandre	Profilomic SA	Lipidomic analysis of spinocerebellar ataxia plasma samples

TPS17 - Protein Phosphorylation and other Post-translational Modifications

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS17-01	Iliuk, Anton	Tymora Analytical Operations	Complementation of Ti-, Zr- and Fe-based PolyMAC for in-depth phosphoproteome analysis of B cell signaling
TPS17-02	Tsai, Chia-Feng	Department of Chemistry, National Taiwan University, Taipei, Taiwan	Motif-Targeting Quantitative Proteomics for Absolute Phosphorylation Stoichiometry Measurement
TPS17-03	Enjalbal, Christine	Institut des Biomolécules Max Mousseron	N- and O-acetylation of threonine residues in the context of proteomics
TPS17-04	Asperger, Arndt	Bruker Daltonik GmbH	Unexpected N-glycosylation occurring in hen eggwhite lysozyme at a non-consensus sequon analyzed by complementary LC-MS/MS based methods
TPS17-05	Shigeri, Yasushi	National Institute of Advanced Industrial Science and Technology (AIST)	Peptide structure analyses using topological mass spectrometry
TPS17-06	Finamore, Francesco	Translational Biomarker Group (TBG), Department of Human Protein Sciences, University Medical Centre, University of Geneva, 1211 Geneva 4, Switzerland.	Effects of glycation on aspirin-mediated acetylation of human blood proteins.
TPS17-07	Trinh, Hung	Retrovirus lab, School of Medicine, Johns Hopkins University	Identification of viral phosphorylation in human immunodeficiency viruses
TPS17-08	Chikaoka, Yoko	The University of Tokyo	Discrimination between symmetry/asymmetry dimethylation on histone H4R3: their cell cycle dependent dynamics
TPS17-09	R. Jersie-Christensen, Rosa	The Novo Nordisk Foundation Center for Protein Research, University of Copenhagen	Simple and reproducible sample preparation for single-shot phosphoproteomics with high sensitivity
TPS17-10	Pabst, Martin	ETH Zurich	Micro-Arrays for Mass Spectrometry (MAMS): Self-Aliquoting Micro-Array Targets for nLC-MALDI-MS
TPS17-11	Tajiri, Michiko	Osaka Medical Center and Research Institute for Maternal and Child Health	Ion mobility mass spectrometry and MM conformational search of glycopeptides
TPS17-12	Quan, Quan	The University of Hong Kong	Fully Automatable Multi-Dimensional Liquid Chromatography with Online Tandem Mass Spectrometry for Proteomics and Selected PTMs
TPS17-13	Chen, Hauh-Jyun Candy	National Chung Cheng University	Identification and Semiquantification of Human Hemoglobin Methylation and Ethylation
TPS17-14	Nielsen, Lennart B.	BMB, SDU	Determining linkages in a heavily disulfide bonded protein using an in-line electrochemical reduction cell
TPS17-15	Heissel, Søren	BMB, SDU	A fast and efficient 3-level method for characterization of N- and O-linked glycosylations
TPS17-17	Hao, Zhiqi	Thermo Fisher Scientific	Structure characterization and differentiation of biosimilar and reference products using unique combination of complementary fragmentation mechanisms

TPS17-18	Wu, Wan-Ling	Institute of Biological Chemistry, Academia Sinica. Taipei 11529, Taiwan	Phosphoproteomic analysis of methanoarchaeon Methanohalophilus portucalensis FDF1T reveals diverse functions in methanogenesis and osmoadaptation
TPS17-19	Gallardo, Karem	Max Planck Institute of Molecular Cell Biology and Genetics	Quantification of post-translational modifications of Histones in a single LC-MS/MS Analysis
TPS17-20	Li, Fu-An	INSTITUTE OF BIOMEDICAL SCIENCES	Screening Method for SUMOylation Sites Using HCD on Orbitrap Mass spectrometer
TPS17-21	Colzani, Mara	Università degli Studi di Milano	High-resolution mass spectrometry for the screening and characterization of protein carbonyl-quenching activities
TPS17-22	Chen, Yu-Ju	Institute of Chemistry, Academia Sinica	Sequential Phosphoproteomic Enrichment through Complementary Metal-Directed Immobilized Metal Ion Affinity Chromatography
TPS17-23	Signor, Luca	Institute of Structural Biology	Combining bottom-up and top-down mass spectrometry to characterise the differential phosphorylation of human RIP2 kinase
TPS17-24	Malosse, Christian	Institut Pasteur	Complete Post-Translational Modification Mapping of Pathogenic N. meningitidis Pilins Requires Top-Down Mass Spectrometry

TPS18 - Ion-Molecule and Ion-Ion Reactions in the Gas-Phase

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS18-01	Koch, Annika	University of Münster	Efficient gas phase dehydrogenation reactions in MALDI mass spectrometry with novel nitroarene matrices or -additives
TPS18-02	Herber, Ina	Institut für Ionenphysik und Angewandte Physik, Universität Innsbruck	Reactivity of Hydrated Monovalent First Row Transition Metal Ions $M+(H_2O)_n$, $M = Cu$ and Zn toward C_6H_5Cl , C_6H_5Br , C_6H_5I and C_3H_7I
TPS18-03	Mayeux, Charly	University of Tartu	Revised and expanded scale of the Lithium cation basicities.
TPS18-04	Newsome, G. Asher	Nova Research	Characterization of Ammonium Nitrate Vapor with Flowing Atmospheric-Pressure Afterglow Mass Spectrometry
TPS18-05	Dubey, Girjesh	Max-Planck-Institute for Solid State Research	Chemical Modification of Graphene via Reactive Landing of Hyper-thermal Molecular Ion Beams
TPS18-06	Dunaev, Anatolii	Ivanovo State University of Chemistry and Technology	The molecular and ionic vapor components over the LaI_3 and the $La-LaI_3$ system
TPS18-07	Lorenz, Yvonne	University of Bonn Kekulé-Institute for Organic Chemistry and Biochemistry	Spin-isomers in the gas-phase: reactivity of ferracyclobutadienes
TPS18-08	Mistarz, Ulrik H	Department of Pharmacy, University of Copenhagen	Improving Usability of Gas-Phase Hydrogen/Deuterium Exchange Mass Spectrometry to Study Conformational Changes of Biomolecules
TPS18-09	Lu, I-Chung	IAMS, Academia Sinica	Ion Intensity and Thermal Proton Transfer Reactions in Matrix-Assisted Laser Desorption/Ionization
TPS18-10	Blanksby, Stephen	Queensland University of Technology	Manipulating radical reactivity by charge polarity switching in gas phase distonic ions
TPS18-11	Schweikhard, Lutz	University of Greifswald	Poly-Anion Production in Penning and RFQ Ion Traps
TPS18-12	Bier, Mark	Carnegie Mellon University	A Relative Comparison of Proton Affinities of MALDI Matrices Using Bacteriophage HK97 Head II Capsid
TPS18-13	Gerbaux, Pascal	University of Mons	Supramolecular mass spectrometry: association of MS methods to computational chemistry to access, at a molecular level, systems relevant to host-guest chemistry
TPS18-14	Poad, Berwyck	University of Wollongong	Dianions as strong gas-phase bases

TPS18-15	Guarcini, Laura	Sapienza-University of Rome	Spectroscopic evidence for a gas-phase librating G-quartet/Sodium ion complex
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TPS20 - Imaging MS - Applications

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS20-01	Jean-Nicolas, Audinot	CRP-GL	STUDY OF INTERACTIONS BETWEEN REACTIVE GAZ SPECIES AND MICROORGANISMS BY NANO-RESOLUTION MASS SPECTROMETRY IMAGING
TPS20-02	Giampà, Marco	Proteome and Metabolome Research, Center for Biotechnology, Bielefeld University	The important role of the matrix (application) in the MALDI MS Imaging procedure.
TPS20-04	Powell, Matthew	Protea Biosciences	Direct Analysis of Animal and Plant Tissues by LAESI-MSI and Ion Mobility for Mapping of Metabolites and Small Proteins
TPS20-05	Takahashi, Katsutoshi	National Institute of Advanced Industrial Science and Technology	MALDI/LDI-FTMS imaging of intact plant tissues
TPS20-06	Hanrieder, Jörg	Chalmers Univiersity of Technology	Multimodal Imaging Mass Spectrometry for Probing A β -Plaque Pathology in Transgenic Alzheimer's Disease Mice
TPS20-07	Hou, Keyong	Key Laboratory of Separation Science for Analytical Chemistry, Dalian Institute of Chemical Physics, Chinese Academy of Sciences	Development of Quasi-trapping Chemical Ionization Source with VUV Lamp for Online Mass Spectrometry
TPS20-08	Sugiura, Yuki	Keio University	Visualization and quantification of brain metabolic fluxes of glucose in the awake mice by mass spectrometry
TPS20-09	Apuy, Julius	Celgene Corporation	BRAIN DISTRIBUTION OF SELECTIVE SEROTONIN REUPTAKE INHIBITORS IN MALE CD-1GS RATS USING MALDI-TOF MASS SPECTROMETRIC IMAGING.
TPS20-10	Ueda, Yoshihisa	JEOL Ltd.	2D and 3D analyses for the organic thin film using laser desorption ionization.
TPS20-11	Shimma, Shuichi	National Cancer Center Research Institute	Methodology for precise understanding of drug imaging mass spectrometry using Mass Microscope
TPS20-12	Creceius, Anna C.	Laboratory of Organic and Macromolecular Chemistry	Exploring the head and neck tumor in situ metabolome by MALDI FT-ICR MSI
TPS20-13	Koide, Tatsuo	National Institute of Health Sciences	Evaluation of Distribution of Ingredients in Pharmaceutical Solid Dosage Forms using Time of Flight Secondary Ion Mass Spectrometry

TPS41 - Gas-phase Ion Fragmentation Mechanisms

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS41-01	Consta, Styliani	Department of Chemistry, University of Western Ontario	Unraveling the role of solvent-macromolecule interactions in determining the conformations of macromolecules in bulk, droplet and vacuum environments
TPS41-02	Consta, Styliani	Department of Chemistry, University of Western Ontario	Classification of the ejection mechanisms of charged macromolecules from liquid droplets
TPS41-03	Gernert, Claus	Christian Albrechts Universität zu Kiel	Propane loss from diethylamines, investigation of the fragmentation mechanism using FT-ICR and sector-field experiments in combination with DFT calculations
TPS41-04	Clemen, Martin	Christian-Albrechts-Universität zu Kiel	Fragmentation Reaction of Azo Dyes using High Resolution Fourier Transform Ion Cyclotron Resonance Mass Spectrometry
TPS41-05	Cartoni, Antonella	university of rome sapienza	Photofragmentation spectra of halogenated methanes in the VUV photon energy range: the role of the halogen atom

TPS41-06	Seulen, Sarah	Christian-Albrechts-Universität Kiel	Kinetic energy release and fragmentation pathways of substituted benzeneamines
TPS41-07	Rijs, Nicole	Technical University Berlin	Exploring the structure and reactivity of metal complexes with ion mobility mass spectrometry and ion/molecule reactions.
TPS41-08	Mikaia, Anzor	National Institute of Standards and Technology	Surprising fragmentation of N-substituted N-perfluoroacyl-amino acids
TPS41-09	Miyashita, Masahiro	Graduate School of Agriculture, Kyoto University	N-terminal Charge Derivatization for Discrimination between Leu and Ile in Peptides by High-Energy CID MS/MS Analysis
TPS41-10	Kellner, Ina D.	Friedrich-Alexander-University Erlangen-Nuremberg	Crown ether/fullerene conjugates: ionisation, alkali metal ion affinities and dimerisation
TPS41-11	Kirschbaum, Rolf W.	Friedrich-Alexander-University Erlangen-Nuremberg	Ligand-Sphere Chemistry and Sphere-Sphere Interactions of Negatively Charged Alkoxyated Fullerenes
TPS41-12	Hitzenberger, Jakob	Friedrich-Alexander-University Erlangen-Nuremberg	The sodium ion affinity sequences of ligated fullerenes, PCBM fullerenes and trimetallic nitride endohedral metallofullerenes
TPS41-13	Kjeldsen, Frank	University of Southern Denmark	Protection of Labile Phosphate Ester Groups by Metal Complexes Reveal Dependence on Charge and Size of Interacting Metals
TPS41-14	Zampieri, Davila	ThoMSon Mass Spectrometry Laboratory	Probing the Mechanism of One-pot Synthesis of the Benzopyranopyrimidines by ESI-MS
TPS41-15	Chu, Ivan	THE UNIVERSITY OF HONG KONG	Isomerization and Dissociation of Radical Peptide Ions: Sigma- and Alpha-Carbon-Centered Radical Cations
TPS41-16	Yalcin, Talat	Izmir Institute of Technology	Effect of Tyrosine Position on the Fragmentation Reactions of b3 Ions from Model Tripeptides
TPS41-17	Ceraulo, Leopoldo	University of Palermo	Collision induced decomposition of AOT5Yb2+: an unexpected intracluster rearrangement
TPS41-18	Schmidt, Melanie	University of Bonn Kekulé-Institute for Organic Chemistry and Biochemistry	Synthesis and characterization of silver(I)-NHC complexes. Mass spectrometrical studies of relative bond dissociation energies.
TPS41-19	Görgün, Özge	Izmir Institute of Technology	Effect of Basic Amino Acid Residues on the Charged Separation Reactions of Doubly-Protonated Model Heptapeptides
TPS41-20	Ferreira, Bruno	University of Campinas - UNICAMP	Probing the Mechanism of Brønsted Acid Catalyzed Azlactone Ring Opening by ESI-MS
TPS41-21	Yamagaki, Tohru	Suntory Institute for Bioorganic Research	Laser-Induced Hydrogen Radical Removal in UV MALDI-MS Allows for the Differentiation of Polyphenol Isomers
TPS41-22	Hongo, Yayoi	RIKEN	Structure and energy dependent ion isomerizations of folates detected using ER-IMS/MSn
TPS41-23	Marshall, David	Queensland University of Technology	Probing the effect of charge location and polarity on energetics of gas phase distonic ions
TPS41-24	Zhurov, Konstantin O.	Ecole Polytechnique Fédérale de Lausanne	Heterolytic N-C α Cleavage to the N-terminal Side of the Aminoketyl Radical in ECD/ETD
TPS41-25	Takayama, Mitsuo	Yokohama City University	Formation of benzyl carbanion in collision-induced dissociation of deprotonated phenylalanine homologues
TPS41-26	Koshino, Hiroyuki	RIKEN	Study of small neutral losses and ion rearrangements on protonated bunodosine 391 and IAA(indole-3-acetic acid)-amino acid conjugates
TPS41-27	Guaratini, Thais	FCFRP-USP	Collision induced dissociation of Erythrinian Alkaloids in ESI-MS/MS: experimental and computational studies
TPS41-28	Babaev, Vasily	A.E. Arbuzov Institute of Organic and Physical Chemistry of the Russian Academy of Sciences	Gas-phase behavior of novel binuclear nickel(II) and cobalt(II) complexes with bridging phosphinato ligands under MALDI and ESI conditions

TPS41-29	Czerwenka, Christoph	AGES	The use of fragmentation und retention patterns of BADGE , BFDGE and their derivatives for detecting related substances without reference compounds
TPS41-30	Vendramini, Pedro Henrique	UNICAMP	Monitoring the Oxidative Desulfurization Process of Organic Compounds by FT-ICR
TPS41-31	Danikiewicz, Witold	Institute of Organic Chemistry PAS	A MASS SPECTROMETRY AND COMPUTATIONAL STUDY OF THE COMPETITION BETWEEN INTRAMOLECULAR SNAr AND SUBSTITUTION OF HYDROGEN REACTIONS IN THE GAS PHASE
TPS41-32	Oomens, Jos	Radboud University	Identification of diketopiperazine b2-ions from deprotonated peptides

TPS42 - Forensics and Doping

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS42-01	Minohata, Toshikazu	Shimadzu Corporation	Simultaneous analysis for forensic drugs in human blood and urine using ultra-high speed LC-MS/MS
TPS42-02	Furtos Matei, Alexandra	University of Montreal, Department of Chemistry	Rapid Screening of Adulterated & Counterfeit Products using a Bench-Top High Resolution Mass Spectrometer and mzCloud Database Search
TPS42-03	Kuwayama, Kenji	National Research Institute of Police Science	Highly sensitive analysis of 11-nor-9-carboxy- Δ^9 -tetrahydrocannabinol in hair by micro-pulverized extraction and liquid chromatography/tandem mass spectrometry
TPS42-04	Enderle, Yeliz	University Hospital Heidelberg	Validation of dried-blood-spot analysis for the quantification of drug concentrations in capillary whole blood samples within targeted PAH therapies
TPS42-05	Hashimoto, Yuichiro	Hitachi, Ltd.	Evaluation of high-throughput automatic explosives trace detection systems using the dry transfer method
TPS42-06	Naito, Yasuhide	The Graduate School for the Creation of New Photonics Industries	Development of a Novel Apparatus for Analyzing Minerals in a Single Strand of Hair
TPS42-07	Thevis, Mario	German Sport University Cologne	Investigations on storage-induced changes of the red blood cell lipidome
TPS42-08	Bradshaw, Robert	Biomedical Research Centre	MALDI MS Profiling and Imaging of Illicit Drugs in Fingermarks in tandem with Conventional Enhancement Techniques
TPS42-09	Tretyakov, Kirill	National Institute of Standards and Technology	Mass spectra of some benzodiazepine series drugs and their trimethylsilyl derivatives
TPS42-10	Flinders, Bryn	FOM Institute AMOLF	Monitoring the distribution of drugs of abuse in longitudinal sectioned hair samples by multi-modal mass spectrometry imaging
TPS42-11	Fabregat, Andreu	Fundació IMIM	SEMI-UNTARGETED METABOLOMIC APPROACH BASED ON PRECURSOR ION SCAN FOR METABOLIC STUDIES: STEROID METABOLISM AS A PROOF OF CONCEPT
TPS42-12	Szensy, Matthias	Bruker Daltonik GmbH	Enhanced Confirmation Criteria for Reducing False Positive Rates (FPR) in Toxicology Screening using High Resolution, LC-QToF, Accurate Mass Analysis
TPS42-13	Kiehne, Andrea	Bruker Daltonik GmbH	A fast, reliable automated LC-MSn drug screening solution for clinical research and forensic toxicology
TPS42-14	Musselman, Brian	IonSense	Novel sorbent coated samplers for Trace Chemical Detection by Solid Phase Microextraction Direct Analysis in Real Time (DART) Mass Spectrometry
TPS42-15	Grüning, Anja	Shimadzu Europa GmbH	Analysis of doping agents using ultrafast LCMS/MS with scheduled MRM
TPS42-16	Liscio, Camilla	LGC	Atmospheric Solid Analysis Probe-Mass Spectrometry (ASAP-MS) for rapid screening of drugs of abuse in biological fluids
TPS42-17	Zvereva, Irina	Moscow Antidoping center	Development of method for GHRPs determination in urine with solid-phase extraction microplates
TPS42-18	Queiroz, Marcos	Université de Genève	HPLC-ESI-MS/MS for the determination the alkaloid content of the stem bark of Tetrapteryx mucronata, a Malpighiaceae occasionally used to prepare the ayahuasca
TPS42-19	Müller, Lars	Bundeskriminalamt	Solid-Phase Micro Extraction Atmospheric Pressure Chemical Ionization Mass Spectrometry (SPME-APCI/MSn) and its Application in Forensic Toxicology
TPS42-20	Ho, Emmie Ngai Man	The Hong Kong Jockey Club	Controlling the abuse of cobalt in horses

TPS42-21	Pütz, Michael	Bundeskriminalamt	Rapid analysis of active ingredients in different dosage forms of pharmaceutical products by Desorption Electrospray Ionization Mass Spectrometry (DESI-MS)
TPS42-22	Lisa, Stork	Universität Münster	Use of dynamic bilayer polymer coatings in the trace analysis of controlled substances by capillary electrophoresis-mass spectrometry
TPS42-23	Münster-Müller, Sascha	Fresenius University of Applied Sciences	Isolation and mass spectrometric identification of new cannabimimetic designer drugs and related synthesis impurities in 'Spice' products
TPS42-24	Garrido, Bruno	Inmetro	Detection of methasterone metabolites in human urine, elucidation of their glucuconjugates and excretion kinetics
TPS42-25	Cheng, CHAO-HSIN	Forensic Science Division, Investigation Bureau, Ministry of Justice, Taiwan, R.O.C.	Quantitation of 23 designer Cathinones in Urine by GC-MS-MS
TPS42-26	Nováková, Lucie	Univerzita Karlova v Praze, Farmaceuticka fakulta v Hradci Kralove	Optimization and application of UHPSFC-MS/MS method in screening of doping agents

TPS43 - Environmental Analysis

Abstract No.	Presenting Author	Affiliation	Abstract Title
TPS43-01	Lamoree, Marja	Institute for Environmental Studies, VU University	Effluent, surface, ground and drinking water analysis of classical and novel drugs used in cancer treatment: 5-fluorouracil and protein kinase inhibitors
TPS43-02	Leroy, Eric	Université Paul Sabatier-Service commun de spectrométrie de masse	Development of new materials for passive samplers based on porous organogels followed by GC-MS analysis
TPS43-03	Chou, Pei-Hsin	National Cheng Kung University	Occurrence of endocrine active substances in wastewater and river water collected from the aquatic environment of Taiwan
TPS43-04	Yamamoto, Atsushi	Osaka City Institute of Public Health and Environmental Sciences	Identification of chemical structures of polyfluoroalkyl substances in fire extinguishing chemicals by using ultra high resolution mass spectrometry
TPS43-05	Cheong, Nam-Yong	Korea	Determination of alkylphenol ethoxylate in textiles and leathers by NPLC and quadrupole orbitrap MS
TPS43-07	Rodriguez Cea, Andres	University of Oviedo	Quantification of TBT by GC-MS/MS in water samples at levels required by the WFD and stability studies of butyltin compounds by using a triple spike approach.
TPS43-08	Somoano Blanco, Lourdes	University of Oviedo	COMPARISON OF DIFFERENT MASS SPECTROMETRIC TECHNIQUES FOR THE DETERMINATION OF POLYCHLORINATED BYPHENYLS BY ISOTOPE DILUTION USING ³⁷ Cl-LABELLED ANALOGUES
TPS43-09	Grüning, Anja	Shimadzu Europa GmbH	Multi-component quantitative analysis of pharmaceuticals in the environment by UHPLC-MS/MS with on-line SPE
TPS43-10	Kosjek, Tina	Jozef Stefan Institute	Aerobic activated sludge transformation of methotrexate: identification of biotransformation products
TPS43-11	Fabregat-Cabello, Neus	Universitat Jaume I. IUPA	DETERMINATION OF ENDOCRINE DISRUPTING COMPOUNDS IN WATER SAMPLES BY ISOTOPE DILUTION MASS SPECTROMETRY
TPS43-12	Boertz, Jens	Sigma-Aldrich	Ease of Use and Low Detection Limits of a New Dry Sampler for Determination of Vapor Phase and Particulate Isocyanate Derivatives
TPS43-13	Otto, Johanna	Department of Environmental Chemistry, Eawag: The Swiss Federal Institute of Aquatic Science and Technology, 8600 Dübendorf, Switzerland	Evaluating the performance of advanced waste water treatment steps via quantitative screening of 483 micropollutants using SPE-LC-HRMS
TPS43-14	Stahl-Zeng, Jianru	AB SCIEX	Screening and Quantitation of Targeted and Non-targeted Environmental Pollutants in Water Samples

TPS43-15	Chou, Jo-Han	National Sun-Yat Sen University	Multiple Solid Phase Microextraction (m-SPME) Coupled with Ambient Mass Spectrometry (AMS) for Rapidly and Accurately Quantifying Trace Emerging Pollutants in p
TPS43-16	Raber, Georg	University of Graz	Quantification of Arsenolipids in the Certified Reference Material NMII 7405-a (Hijiki) Using RP-HPLC-ICPMS and High-Resolution-ESMS
TPS43-17	Moldovan, Zaharie	National Institute of Research and Development for Isotopic and Molecular Technology, INCDTIM	Determination of organic pollutants families in environmental samples based on characteristic ions obtained by Electron Impact
TPS43-18	Rothardt, Judith	EAWAG, Swiss Federal Institute of Aquatic Science and Technology Department of Environmental Chemistry	Quantification of micropollutant degradation in the riverbank using a LC-HR MS screening method
TPS43-19	Cody, Robert	JEOL USA, Inc.	Analysis of electronics waste by GC x GC combined with high-resolution mass spectrometry: using exact mass information to explore the data.
TPS43-20	Williams, Renee	University of California San Diego	Marine Microorganisms as a Source of Volatile Organic Carbons and Reactive Aldehydes
TPS43-21	Tölgyesi, László	Agilent Technologies Sales & Services GmbH & Co. K	Determination of Endocrine Disrupting Chemicals in Drinking Water at Sub ng/L Levels using Direct Injection and Triple Quadrupole Mass Spectrometry
TPS43-22	Kay, Lorraine	LECO Instruments UK Ltd.	Non-target and post-target analysis of organic environmental contaminants in river sediments
TPS43-23	Moreau, Stephane	SHIMADZU Europa GmbH	DETERMINATION OF PCB AND SCREENING OF ENVIRONMENTAL POLLUTANTS USING SIMULTANEOUS SCAN AND MRM MEASURING OF GC-MS/MS
TPS43-24	Moreau, Stephane	SHIMADZU Europa GmbH	AN ANALYTICAL METHOD FOR ENVIRONMENTAL POLLUTANTS USING GCxGC-MS/MS WITH ULTRA FAST MRM SWITCHING MODE
TPS43-25	Jimenez Villarin, Javier	Hidroquimia Tractaments i Quimica Industrial, S.L.	Characterisation of ofloxacin's transformation products by UHPLC-HRMS after a photocatalytic treatment based on TiO ₂ nanofibers.
TPS43-26	Rohwer, Prof. Egmont R.	University of Pretoria	Simultaneous determination of tri-hepta brominated diphenyl ethers and thermally-labile deca-BDE with 60 m capillary column using gradient pressure programming
TPS43-27	Zelenov, Vladislav	Talrose Institute for Energy Problems of Chemical Physics of Russian Academy of Sciences	Kinetic Parameters of the NO ₂ / Methane Soot Uptake for Tropospheric Modeling
TPS43-28	Pisarčíková, Jana	Slovak Academy of Sciences, Institute of Animal Physiology	Monitoring of glufosinate degradation in rumen fluid using liquid chromatography coupled with tandem-mass spectrometry
TPS43-29	Amantonico, Andrea	Firmenich SA	Microfluidic electrochemical cell with MS detection as tool for the study of the biotransformation of perfumery compounds
TPS43-30	Pati, Sarah	Eawag	Compound-Specific Isotope Analysis of Dioxygenation Products by LC-IRMS
TPS43-31	Mueller, Laarnie	Helmholtz Zentrum München Deutsches Forschungszentrum für Gesundheit und Umwelt (GmbH)	Investigation of the effect of air-fuel-equivalence ratio on soot emission from a flame source
TPS43-32	Heringa, Maarten	Paul Scherrer Institut	Comparison of electron ionization and vacuum ultraviolet photoionization of atmospherically relevant aerosol components using an aerosol mass spectrometer
TPS43-33	Franco, Caroline	Fluminense Federal University	Development and application of analytical method by GC/MS for urban dust analysis
TPS43-34	Akutsu, Hiroaki	Asahikawa Medical University	Determination of monoterpene concentrations in the blood and urine using HS-SPME/GC/MS
TPS43-35	Waridel, Patrice	Protein Analysis Facility, University of Lausanne	Shotgun ecotoxicoproteomics of Daphnia pulex: biochemical effects of the anticancer drug tamoxifen at environmentally relevant concentrations

TPS43-36	Kostyukevich, Yury	Institute for Energy Problems of Chemical Physics Russian Academy of Sciences	Isotopic exchange mass spectrometry reveals molecular structure of Natural Organic Matter
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Wednesday, August 27th

WPS21 - New Ionization Techniques			
Abstract No.	Presenting Author	Affiliation	Abstract Title
WPS21-01	Lebeau, Diane	CEA	Direct Analysis in Real Time Mass Spectrometry (DART-MS) of irradiated magnesium stearate
WPS21-02	Kumano, Shun	Hitachi, Ltd.	Low-Pressure Dielectric Barrier Discharge Ionization Source for High Sensitive Analysis of Explosives
WPS21-03	Zeegers, Guido	ETH Zürich	Influence of the target plate material and sample layer thickness on LDI ionization efficiency for C60
WPS21-04	Burger, Udo	Institut of Organic Chemistry / University Basel	Direct Analysis in Real Time (DART) Mass Spectrometry - Benefits in Organic Synthesis
WPS21-05	Burk, Piia	University of Tartu	Ionization efficiency model for multiple charged ions in negative mode ESI-MS
WPS21-06	Kim, Seung Yong	Korea Basic Science Institute	Cold Electron for Pulsed Ionization Mass Spectrometers
WPS21-07	Wiegelmann, Marcel	Institute for Hygiene, Biomedical Mass Spectrometry, University of Münster, Germany	Wavelength and Fluence Dependence of UV-MALDI-MS with 2,4,6-Trihydroxyacetophenone and Dithranol Matrices for the Analysis of Lipids
WPS21-08	Chen, Lee Chuin	University of Yamanashi	Super-Heated Electrospray Ionization Mass Spectrometry for Sub-Critical Aqueous Solution
WPS21-09	Picard, Pierre	Phytronix Technologies Inc	A New Tool to Predict Thermal Desorption Efficiency Based on Molecular Functional Groups and the Chemistry behind it for High-Throughput LDTD-MS/MS Analysis
WPS21-10	Linden, Mathias H.	Linden CMS GmbH	Orbitrap mass spectrometer with LIFDI and ESI ion sources simultaneously installed on axis
WPS21-11	Ni, Chi-Kung	Institute of Atomic and Molecular Sciences, Academia Sinica	Ion-to-Neutral Ratios and Thermal Proton Transfer Reactions in Matrix-Assisted Laser Desorption/Ionization
WPS21-12	Kawahata, Masatoshi	Faculty of Pharmaceutical Sciences at Kagawa Campus, Tokushima Bunri University	Nanoporous Complex Assisted Laser Desorption Ionization
WPS21-13	Wolf, Jan-Christoph	Department of Chemistry and Applied Biosciences, ETH Zürich	Active Capillary Dielectric Barrier Discharge Ionization: Investigation of the Ionization Mechanism(s)
WPS21-14	Pollack, Leonhard	Markes International	Enhanced screening of environmental pollutants in complex matrices by GCxGC-TOF MS with variable-energy electron ionisation
WPS21-15	Moritani, Kousuke	University of Hyogo	Sputtering and ionization of biomolecules induced by molecular cluster and noble gas cluster ion beams
WPS21-16	Foley, Casey	Wayne State University	Characterization of Architectural Differences of Synthetic Polymers using Vacuum Ionization-Ion Mobility Spectrometry-Mass Spectrometry
WPS21-17	Desbenoit, Nicolas	Centre de Recherche Public - Gabriel Lippmann	Improvement of ionization yields in TOFSIMS using Optimized Charge Compensation and Matrix enhanced ionization
WPS21-18	Bierstedt, Andreas	Federal Institute for Materials Research and Testing	Combination of Raman/LIF spectroscopy and laser ablation mass spectrometry
WPS21-19	Michalik, Aleksandra	BAM Federal Institute for Materials Research and Testing	The effect of the laser pulse duration in infrared free-liquid MALDI
WPS21-20	Warschat, Carsten	BAM Federal Institute for Materials Research and Testing	Improving the performance of an ultrasonic levitator coupled to API-TOF MS

WPS21-21	Knochenmuss, Richard	Tofwerk	Possible Triplet Ionization Mechanisms in the UV MALDI Matrix 2,4,6 Trihydroxyacetophenone
WPS21-22	Qiao, Liang	EPFL	Electrostatic Spray Ionization: a New Versatile Ambient Ionization Technique

WPS22 - Cell Biology and Cellular Pathways

Abstract No.	Presenting Author	Affiliation	Abstract Title
WPS22-01	Lee, Shin Jung C.	POSTECH	Conformational Analysis of alpha-Synuclein in Membrane Systems Using Traveling Wave Ion Mobility Mass Spectrometry
WPS22-02	Clavier, Séverine	Laboratoire des Biomolécules UMR 7203 Université Pierre and Marie Curie	Understanding the molecular basis of (R/W)9 cell penetrating peptide (CPP) effect on the phenotype of EF cells, a model cell line for Ewing sarcoma.
WPS22-03	Kokesch-Himmelreich, Julia	Institute of Physical Chemistry, Justus Liebig University of Giessen	ToF-SIMS analysis of osteoblast-like cells and their mineralized extracellular matrix on strontium enriched bone cements
WPS22-04	Häkkinen, Merja	University of Eastern Finland	LC-MS/MS as a tool to study polyamine flux
WPS22-05	Jufvas, Åsa	Linköping University	Proteomic analysis of scaffolding protein interaction network by IP- GeLCMS/MS
WPS22-06	Kotz, Sandra	University of Cologne	Identification of intracellular platin-protein complexes and their effect towards development of cisplatin resistance
WPS22-07	Habjan, Matthias	Max Planck Institute of Biochemistry	Sequestration by IFIT1 impairs translation of non-2'O-methylated capped RNA
WPS22-08	Tsuji, Yudai	Doshisha University	Characterizing Mouse Thymus using Imaging Mass Microscope
WPS22-09	Agrèsta, Anna Maria	Institute for Biomedical Technologies, Proteomics and Metabolomics Unit - CNR, Via Fratelli Cervi, 93-20090 Segrate (MI), Italy	MudPIT analysis of Cucumis sativus roots, from plants growth under Fe and/or Mo deficiencies
WPS22-10	Botting, Catherine	University of St Andrews	Breaking the chain and cracking the code: interpreting cyclic peptide fragmentation spectra
WPS22-11	Gentzel, Marc	MPI-CBG	Characterization of beta-Arrestin2 Protein Interactions in the Wnt Signaling Network by Label-free Quantitative Mass Spectrometry
WPS22-12	Muller, Alban	Novartis	Detection of the central carbon metabolism intermediates in immune cells using capillary ion chromatography coupled to tandem mass spectrometry
WPS22-13	Suter, Marc	Eawag	Toxicity and adaptive responses of the green algae Chlamydomonas reinhardtii exposed to silver as manifested on the transcriptome, proteome and phenotype
WPS22-14	Suter, Marc	Eawag, Utox	Stressor-induced proteome alterations in zebrafish: a meta-analysis of response patterns characterized by gel-based and gel-free proteomics
WPS22-15	Polat Koken, Ayse	koc university	Revealing the mystery behind the Epithelial-mesenchymal transition (EMT)
WPS22-16	Ben-Nissan, Gili	Weizmann Institute of Science	Revealing the structural and spatio-temporal plasticity of the COP9-Signalsome complex using a combination of mass-spectrometry and cell biology approaches
WPS22-17	Kast, Juergen	University of British Columbia	Blood Cell Interactions in Atherosclerosis involves the Coordinated Regulation of Multiple Protein Modifications
WPS22-18	Ibanez, Alfredo	ETH Zurich	Calculating cell-to-cell metabolic variability using single-cell mass spectrometry

WPS24 - Trace Gas Analysis of Breath and Food Flavours

Abstract No.	Presenting Author	Affiliation	Abstract Title
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WPS24-01	Sánchez López, José Antonio	Zurich University of Applied Sciences, Institute of Chemistry and Biological Chemistry, 8820 Wädenswil	Online measurement of volatiles from a liquid flow by PTR-ToF-MS: The case of coffee extraction.
WPS24-02	Moniruzzaman, Mohammed	Universiti Sains Malaysia	Identification of volatile and semi-volatile compounds in honey by gas chromatography time-of-flight accurate mass spectrometry
WPS24-03	Dusek, Martin	Research Institute of Brewing and Malting, PLC	Use of High-Resolution Accurate Mass Spectrometry for studying of the changes of the proanthocyanidins during beer brewing process
WPS24-04	Schulte, Hendrik	Shimadzu Europa GmbH	Fast GC-MS/MS Analysis Of Multicomponent Pesticide Residues (360) In Food Matrix
WPS24-05	Wendt, Juergen	LECO Instrumente GmbH	Merits of fast, high resolution time-of-flight mass spectrometry for the aroma profiling of cheese samples at different maturity levels
WPS24-06	Kay, Lorraine	LECO Instruments UK Ltd.	Characterization of Food Products by GCxGC-TOFMS and GC-high resolution TOFMS: A Food "omics" Approach
WPS24-07	Gloess, Alexia N.	ZHAW	On-line analysis with PTR-ToF-MS of coffee roasting reveals different flavour formation for coffee from different origins
WPS24-08	Gosciny, Séverine	Scientific Institute of Public Health	The Combining of an Integrated Microfluidic Device with Collision Cross Section Ion Mobility Screening for the Analysis of Pesticide Residues in Food
WPS24-09	Gosciny, Séverine	Scientific Institute of Public Health	Discovery of Pesticide Protomers Using Routine Ion Mobility Screening
WPS24-10	Hälvin, Kristel	Tallinn University of Technology	Determination of vitamin B3 vitamers in milk and milk products by LC-MS SIDA
WPS24-11	Le, Thao	Aarhus University	Proteomic analysis of protein changes in milk products during processing and storage
WPS24-12	Chipperfield, John	Waters	Application of a Prototype Microfluidic Device with MS for the Screening of Pesticide Residues in Food Analyses
WPS24-13	Španěl, Patrik	J. Heyrovsky Institute of Physical Chemistry of the ASCR	Breath analysis for diagnostics of gastro-esophageal reflux disease
WPS24-14	Romano, Andrea	Fondazione Edmund Mach	Wine analysis by FastGC proton-transfer-reaction time-of-flight mass spectrometry
WPS24-15	Märk, Lukas	IONICON Analytik GmbH.	The Future of Proton-Transfer-Reaction Time-Of-Flight Mass Spectrometry
WPS24-16	Le Quéré, Jean-Luc	INRA - SFC	Modified PTR-MS operating conditions for in vitro and in vivo analysis of wine aroma
WPS24-17	Dryahina, Kseniya	J. Heyrovsky Institute of Physical Chemistry of the ASCR	Analyses of volatile metabolites in breath by a combination of thermal desorption, TD, with selected ion flow tube mass spectrometry, SIFT-MS

WPS26 - Metabolomics

Abstract No.	Presenting Author	Affiliation	Abstract Title
WPS26-01	Koal, Therese	BIOCRATES Life Science AG	Highly Standardised, Fast and Easy Determination of 25-hydroxyvitamin D3/D2 by Supported Liquid Extraction and U/HPLC-MS/MS Analysis
WPS26-02	Schlotterbeck, Götz	FHNW	Identification of unknown metabolites in bamboo leaf extracts by a non-targeted metabolomics approach using UHPLC-QTOF MS/MS driven by chemometrics tools
WPS26-03	Koal, Therese	BIOCRATES Life Sciences AG	Metabolic Phenotyping of Bile Acids - Standardized quantitative bile acids analysis in human plasma/serum and mouse plasma on different (U)HPLC-MS/MS platforms.
WPS26-04	Virgiliou, Christina	Aristotle University of Thessaloniki	Primary metabolites ultra Performance HILIC-MS/MS targeted profiling method in IVF culture medium for the assessment of IVF procedure outcome.
WPS26-05	Virgiliou, Christina	Aristotle University of Thessaloniki	Metabolite profiling study of shikonin's cytotoxic activity in human Huh7 cancer cells.
WPS26-06	Kiehne, Andrea	Bruker Daltonik GmbH	Metabolic pathway driven targeted metabolomics – a "quickstep" from mass spectrometric raw data to biologically relevant conclusions

WPS26-07	Kiehne, Andrea	Bruker Daltonik GmbH	A novel high resolution MS/MS Human Metabolite Spectral Library enabling rapid and accurate metabolite identification in human metabolomics studies
WPS26-08	Iwamoto, Noriko	SHIMADZU Corp.	Metabolite alteration in epithelial-mesenchymal transition-induced cells using GCMS-based metabolomics
WPS26-09	Hayakawa, Eisuke	Kyushu university	A Strategy to Determine Metabolite Elemental Compositions using Isotopic Fine Structure Information from High-Resolution Mass Spectrometry
WPS26-10	Fischer, Kirsten	F. Hoffmann-La Roche Ltd.	Metabolic soft spot identification workflow: Efficient analyses, review, reporting and storage of accurate mass data using Mass-MetaSite and WebMetaBase
WPS26-11	Astarita, Giuseppe	Istituto Zooprofilattico Sperimentale di Puglia e Basilicata	Ion-Mobility-Derived Collision Cross Section as an Orthogonal Measure for Metabolomic Phenotyping
WPS26-12	Debrauwer, Laurent	INRA Toxalim - AXIOM Platform	Untargeted analysis of reactive aldehydes produced by lipid peroxidation using selective derivatisation and detection by LC/HRMS.
WPS26-13	Krüger, Ralf	Max Rubner-Institut	Serum 25-Hydroxyvitamin D Status of Healthy Adults: Results from the Karlsruhe Metabolomics and Nutrition Study (KarMeN)
WPS26-14	Schmidt, Jürgen		Negative ion electrospray tandem mass spectrometry of prenylated fungal metabolites from Suillus species (Basidiomycetes)
WPS26-15	Devenport, Neil	AB SCIEX	Complimentary LC- and GC-Mass Spectrometry Techniques Provide Broader Coverage of the Metabolome
WPS26-16	Witt, Matthias	Bruker Daltonik GmbH	Green or black what's your favorite? Fast biomarker detection and identification in green and black tea using flow injection and FT-ICR mass spectrometry
WPS26-17	Schönenberger, Bernhard	Sigma-Aldrich	Derivatization and Enantioselective Separation of Sugar Metabolites
WPS26-18	Wohlgemuth, Roland	Research Specialties	LC-MS Analysis of Gluconate dehydratase-catalyzed Formation of KDG
WPS26-19	Zhong-hua, Wang	Institute of Materia Medica, Chinese Academy of Medical Sciences and Peking Union Medical College	UFLC-MS based metabolomic profiling reveals oxidative stress related early biological effects induced by ambient air pollutants exposure in general population
WPS26-20	Nam, Myung Hee	Korea Basic Science Institute/Seoul Center	Nontargeted Metabolite Profiling Approach to Investigate the Role of Reactive Oxygen Species and Ethylene in Compatible Plant-Pathogen Interaction
WPS26-21	Xu, Jing	Institute of Materia Medica, Chinese Academy of Medical Sciences & Peking Union Medical College	INTEGRATED METABOLOMICS FOR URINE BIOMARKER DISCOVERY OF ESOPHAGEAL CARCINOMA
WPS26-22	Opekarova, Ivana	Biology Centre, Czech Academy of Sciences, v.v.i.	Metabolite Labeling with Fluorinated Alkyl Chloroformate and Concurrent Liquid Liquid Microextraction for Targeted GC-MS and LC-MS Metabolomics
WPS26-23	Zhi, Zhou	State Key Laboratory of Bioactive Substance and Function of Natural Medicines, Institute of Materia Medica, Chinese Academy of Medical Sciences & Peking Union Medical College	Label-free and standard-free quantitative metabolomics approach by using liquid chromatography mass spectrometry
WPS26-24	Fernández Fernández, Mario	University of Oviedo	STUDY OF GLUCOSE METABOLISM IN SEVERAL PROSTATE CANCER AND NORMAL CELL LINES USING ¹³ C METABOLIC FLUX ANALYSIS AND GC-MS
WPS26-25	Räsänen, Riikka-Marjaana	University of Helsinki	Detection of betulin and its derivatives from birch
WPS26-26	Chervet, Jean-Pierre	Antec BV	Enhanced Pharmaceutical Stability Testing Using On-line Electrochemical Reactions Up-front MS
WPS26-27	Boertz, Jens	Sigma-Aldrich	Analysis of Isoprenoid Pathway Metabolites by LC-MS
WPS26-28	Tabet, Jean-Claude	Université Pierre et Marie Curie,	Development of a standard protocol for high-throughput metabolomic fingerprinting of urine using FIA- and Nano-ESI coupled with FT-ICR MS

WPS26-29	Papouskova, Barbora	Palacky University	Mass spectrometric investigation of biotransformation pattern of palmatine in human hepatocytes
WPS26-30	Andre Baptista Canuto, Gisele	Institute of Chemistry - University of Sao Paulo	A sample preparation protocol for metabolomics studies in Leishmania using gas chromatography-mass spectrometry as analytical tool
WPS26-31	Bruderer, Tobias	Life Sciences Mass Spectrometry	Identification of human metabolites in urine with a high-quality metabolomics library combined with UHPLC SWATH-MS/MS analysis
WPS26-32	Tabet, Jean-Claude	Université Pierre et Marie Curie,	Towards a standardized metabolomics MS/MS databank : advantages and limitations
WPS26-33	Mairinger, Teresa	Austrian Center of Industrial Biotechnology (acib)	Accurate mass GC-qTOFMS - a novel tool in metabolic flux analysis
WPS26-34	Chen, Chao-Yu	Fu Jen Catholic University	Metabolomic study of trans-trans 2, 4-decadienal induced lung lesions in mice by liquid chromatography-mass spectrometry
WPS26-35	Franceschi, Pietro	Fondazione E. Mach	Analysis of untargeted MS-based metabolomics data: the metaMS package for R
WPS26-36	Ortmayr, Karin	Department of Chemistry, University of Natural Resources and Life Sciences (BOKU) Vienna	The potential of two-dimensional chromatography in non-targeted metabolome analysis
WPS26-37	Allard, Pierre-Marie	University of Geneva	HRMS dereplication and MS/MS networking to decipher cryptic metabolite pathways in fungal microorganisms
WPS26-38	Gimenez-Cassina Lopez, Begoña	UNICAMP	Identification of two plant sources of red propolis by UHPLC-MS
WPS26-39	Sugahara, Kohtaro	Suntory Institute for Life Sciences	Localization of Flavonoids Affects Blue Color Expression of Flower Petals
WPS26-40	Ozeki, Miho	Osaka University	Metabolomic Analysis of Gingival Crevicular Fluid Using GC/MS
WPS26-41	Bucher, Rahel	Department of Chemistry, University of Zurich	Analyzing Durable Anti-fungal Resistance Processes in Cereals by Metabolomics Using UHPLC-HR-MS
WPS26-42	Kasparovska, Jitka	Masaryk University, Faculty of Science, Department of Biochemistry	Determination of soybean-derived isoflavones in the rumen fluid by HPLC-MS-TOF
WPS26-43	Tabet, Jean-Claude	CEA-Genoscope/UMR8030	Identification of an unexpected de novo metabolite from Acinetobacter baylyi ADP1 : a particular challenge for the HRMS and HR/MSn arsenal
WPS26-44	Jung, Youngae	Korea Basic Science Institute	Gender-specific metabolic profiling study in patients with myocardial infarction using UPLC/Q-TOF MS
WPS26-45	Hann, Stephan	University of Natural Resources and Life Sciences, BOKU Vienna	GC-qTOFMS for determination of accurate isotopologue ratios and tandem mass isotopomer ratios for metabolic flux analysis of the central carbon metabolism
WPS26-46	Jahn, Sandra	Life Sciences Mass Spectrometry (LSMS), University of Geneva	Characterization of the Hepatocellular Metabolome and its Changes upon Primaquine Exposure Using LC/MS
WPS26-47	Köhling, Rudi	Research Specialties	LC-MS of Chiral Hydroxycarboxylic Acids
WPS26-48	Sawaya, Alexandra	UNICAMP	Dereplication of aporphine, oxoaporphine and protoberberine alkaloids from Guatteria australis by ESI IT MS
WPS26-49	Sawaya, Alexandra	UNICAMP	UHPLC-MS analysis of damage-induced variation in metabolites in species of medicinal plants: Mikania glomerata Sprengel and Mikania laevigata Schultz
WPS26-50	Trausinger, Gert	Joanneum Research Forschungsgesellschaft mbH	Potential of high resolution mass spectrometry and additional all ion fragmentation mass spectrometry for targeted and untargeted metabolomics
WPS26-51	Afzan, Adlin	Phytochimie et Produits Naturels Bioactifs Ecole de Pharmacie Genève Lausanne Section des Sciences Pharmaceutiques Université de Genève	UHPLC-HRMS metabolomics as a tool to decipher complex chemotaxonomic relationships in plants: the case of the Gentianaceae

WPS26-52	Langridge, Jim	Waters	A NOVEL APPROACH FOR ACQUIRING AND PROCESSING LC-MS METABOLOMICS DATA
WPS26-53	Wagner, Michel	UQAM - Department of chemistry	Quantitative metabolomics using isotope-labeling, differential analysis and RP-LC-HRMS: Investigation of metabolic perturbations in a cellular model of cancer
WPS26-54	Kovac, Andrej	Institute of Neuroimmunology of Slovak Academy of Sciences	UPLC/MS method for determination of panel of neurotransmitters in rat cerebrospinal fluid: application to the rat model for tauopathy
WPS26-55	Friedecký, David	Palacky University Olomouc	Influence of mass spectrometry resolution on metabolite coverage in plasma
WPS26-56	Syslova, Kamila	ICT Prague	Molecular insight into the postoperative state of diabetic patients
WPS26-57	Huang, Yingying	Thermo Fisher Scientific	Metabolomic Profiling of Anionic Metabolites in Oral Cancer Cells by Capillary Ion Chromatography HR/AM Mass Spectrometry
WPS26-58	Kumar, Yashwant	National chemical Laboratory	Metabolomics of plant fungal interaction
WPS26-59	Hankemeier, Thomas	Leiden University	Large-scale metabolomics & lipidomics to discover biomarkers of healthy aging and personalizing medicine
WPS26-60	Menezes, Riya C	Max Planck Institute for Chemical Ecology	Combining Raman microscopy and LESA-HR mass spectrometry to identify and image metabolites produced by Schizophyllum commune in fungal co-cultures
WPS26-61	Demeyer, Marie	University of Mons	Molecular Diversity and Body Distribution of Saponins in the Sea Star Asterias rubens by Mass Spectrometry
WPS26-62	Moreau, Stephane	SHIMADZU Europa GmbH	High Sensitivity Analysis of Metabolites in Serum Using Simultaneous SIM and MRM Modes in a Triple Quadrupole GC/MS/MS
WPS26-63	Kay, Lorraine	LECO Instruments UK Ltd.	Myth Busters: The Truth About Metabolomics & Gas Chromatography-High Resolution Time-of-Flight Mass Spectrometry
WPS26-64	Koch, Wendelin	Helmholtz Zentrum München	Sensitivity improvement in negative mode electrospray ionization mass spectrometry using 2-(2-methoxyethoxy)ethanol (2-MEE) for non-targeted metabolomics
WPS26-65	Varesio, Emmanuel	University of Geneva	Integrated analytical platform including automated Bligh and Dyer extraction and dual-column UHPLC-MS/MS separations for metabolomic analyses of cells extracts
WPS26-66	Fatangare, Amol	Mass spectrometry research group, Max Planck institute for chemical ecology, Jena.	A combined metaXCMS and automated fragmentation trees alignment approach for rapid characterization of differentially induced metabolites.
WPS26-67	Crawford, Elizabeth	Institute of Chemical Technology Prague	Chamomile characterization combining ambient ionization & LC-ESI MS/MS high resolution data for a novel metabolomics approach

WPS27 - Small Molecules – Data Acquisition and Analysis

Abstract No.	Presenting Author	Affiliation	Abstract Title
WPS27-01	Schwab, Nicolas	Department of Chemistry - York University/ Thomson Lab - Unicamp	The porous size effect in functionalized porous silicon surfaces by desorption electrospray ionization mass spectrometry analysis
WPS27-02	Alsohaimi, Ibrahim	King Saud University	Quantitative analysis of bromate in non-alcoholic beer using ultra performance liquid chromatography-electrospray ionization mass spectrometry
WPS27-03	Abrahamsson, Anna	AstraZeneca	Comparison of metabolite formation for CYP specific substrates in human and rat lung S9 using single or pooled incubations.
WPS27-04	Mokochinski, Joao Benhur	UNICAMP	A new UHPLC-MS method to evaluate S/G ratio in lignin
WPS27-05	Schymanski, Emma	Eawag	Towards a high-throughput workflow via the Critical Assessment of Small Molecule Identification (CASMI) 2013 using MetFrag, MetFusion and MOLGEN-MS/MS
WPS27-06	Stokes, Peter	University of Durham	Incorporation of a modified Waters APGC system into an open access environment for the rapid, automated analysis of small organic molecules.

WPS27-07	Liigand, Jaanus	Institute of Chemistry, University of Tartu	Solvent effects on electrospray ionization
WPS27-08	Witt, Matthias	Bruker Daltonik GmbH	Analysis of crude oil mixtures by Atmospheric pressure photoionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry
WPS27-09	Ugarov, Michael	Agilent Technologies	Establishing A New Standard in Triple Quadrupole Detection Limits
WPS27-10	Ohara, Kazuaki	Tokushima Bunri University	Continuous Complexation of CoCl ₂ and Admantane-Based Ligands observed by CSI-MS
WPS27-12	Chen, Yet-Ran	Academia Sinica	iElement: New UHRM Signal Handling Approach for More Accurate Elemental Composition Determination
WPS27-13	Cabello, Noemí	ICIQ (Institute of Chemical Research of Catalonia)	Solvent free analysis of biphenyl-hydroxyacids by APCI- Direct Insertion Probe-High Resolution Mass Spectrometry (APCI-DIP-TOF-HRMS)
WPS27-15	Miraval, Tommaso	Actelion Pharmaceuticals Ltd.	Detection and structural characterization of reactive metabolites using liquid chromatography coupled with high resolution mass spectrometry.
WPS27-16	Grüning, Anja	Shimadzu Europa GmbH	Maximizing Efficiency in UHPLC-MS/MS Method Development for multi component analysis
WPS27-17	Bressac, Didier	Inventiva	A Rapid LC-hrMS Method for Metabolite Identification Simultaneously to Metabolic Stability Assessment on Microsomes at an Early Screening Stage
WPS27-18	Sage, Ashley	AB SCIEX	Routine Targeted Quantitation and Identification of Pesticide Residues using Triple Quadrupole LC-MS/MS and Advanced Scheduling of MRM Transitions
WPS27-19	Ball, Andy	Durham University	Characterisation of small pharmaceutical molecules by electron-transfer dissociation
WPS27-20	Hayakawa, Eisuke	Kyushu university	A combination of quantitative structure-property relationship and machine learning to predict MALDI efficiency of metabolites
WPS27-21	Watanabe, Kyoko	Life Sciences Mass Spectrometry, School of Pharmaceutical Sciences, University of Geneva, University of Lausanne	High-speed MRM quantification for multiple metabolites in biological samples using parallel UHPLC-MS/MS system with fast electrospray polarity switching
WPS27-22	Nørgaard, Asger W.	The National Research Centre for the Working Environment	Direct analysis of complex impregnation products by thermal solid phase extraction GCMS and low temperature plasma ionization MS
WPS27-23	Borges, ANTONIO CESAR DE AMORIM	UFRGS	MECHANISM STUDIES OF ULLMANN-TYPE COUPLING REACTIONS: ESI-MS Detection of Intermediates by Using an Ionically-Tagged Ligand
WPS27-24	Schimek, Denise	JOANNEUM RESEARCH Forschungsgesellschaft mbH, HEALTH-Institute for Biomedicine and Health Sciences	We have the analyte – but where is the dross? A systematic approach to investigate the matrix removal during sample preparation
WPS27-25	Chandra, Preeti	CSIR-Central Drug Research Institute	Quality Control Assessment of Polyherbal Formulation Based on Quantitative Determination Multimarker Approach by UPLC-ESI-MS/MS using Polarity Switch Technique
WPS27-26	Dresen, Sebastian	AB SCIEX	Identification and Quantitation of Designer Drugs in Urine by LC-MS/MS
WPS27-27	Osuga, Junichi	JEOL (Europe) SAS	Outgas analysis for zeolites by DIP-GC-HR-TOFMS and Complementary Interpretation by NMR and FE-SEM
WPS27-28	Novak, Ondrej	Umeå Plant Science Centre	Ultrarapid auxin metabolite profiling for high-throughput Arabidopsis mutant screening
WPS27-29	Takeuchi, Takae	Nara Women's University/Department of Chemistry, Faculty of Science	Development of Software for Identifying Fungal Species with PLS Analysis of SPME GC/MS and IMS Data of Microbial Volatile Organic Compounds
WPS27-30	Hvattum, Erlend	GE Healthcare	Deiodination of iodinated aromatic compounds with electrospray ionization mass spectrometry
WPS27-31	Cherubini, Cristina	CNR	Mass spectrometric studies of free radiolyzed amino acids and in analogous meteoritic matrix
WPS27-32	Mülele, Melanie	Universität Würzburg, Institut für Pharmazie und Lebensmittelchemie	The importance of matrix effect investigations in human biological matrices for accurate and sensitive quantification of polyphenols with LC-ESI/MS/MS

WPS27-33	Gonzalez, Oskar	Division of Analytical Biosciences, Leiden Academic Centre for Drug Research, Leiden University/ Analytical Chemistry Department, Faculty of Science and Technology, University of the Basque Country (UPV/EHU)	Matrix effect correction in drug analysis for a LC- TOF platform using post column infusion
WPS27-34	Lucassen, Arnas	Sandia National Labs	Improving resolving power for complex reactive and instable gas mixtures by combining tunable synchrotron radiation with advanced mass spectrometric techniques
WPS27-35	Guy, Philippe	Philip Morris	A Gas Chromatography High Resolution Time-of-Flight Mass Spectrometry Method to Characterize and Semi-Quantify Constituents in Aerosol Fractions

WPS28 - Biomolecular Conformation in the Gas-Phase and in Solution

Abstract No.	Presenting Author	Affiliation	Abstract Title
WPS28-01	Kim, Hugh	Pohang University of Science and Technology	Porbing Structural Dynamics of Intrinsically Disordered Proteins in Heterogeneous Systems from Solution to the Gas Phase
WPS28-02	Raznikov, Valerii	The Branch of Talrose Institute for Energy Problems of Chemical Physics of Russian Academy of Sciences	Further development of decomposition method of charge-state distributions of biopolymer ions produced by electrospray ionization of solutions
WPS28-03	Lee, Jong Wha	Pohang University of Science and Technology	Acid-induced Expansion of Lysozyme Structure during Electrospray Ionization
WPS28-04	Groves, Kate	LGC	Characterisation of immunoassay antibody-antigen interactions: ion mobility mass spectrometry as a potential tool
WPS28-05	Kosevich, Marina	B.Verkin Institute for Low Temperature Physics and Engineering of the National Academy of Sciences of Ukraine	Complexes of nucleic acid bases with polyethylene glycol oligomers: from solution to the gas phase
WPS28-06	Thorsen, Michael	DuPont	Simultaneous protein N- and C-termini identification using tandem mass spectrometry, isotope labelling and database searches.
WPS28-07	Fang, Jing	Waters	An Improved HDX MS System for online Digestion, Separation and Data Analysis
WPS28-08	Lavanant, Helene	Normandie Univ	Differentiation of topoisomeric peptides by ion mobility - mass spectrometry
WPS28-09	Kukacka, Zdenek	Faculty of Science, Charles University in Prague	Chemical Cross-linking and Mass Spectrometry - Tools for Characterization of Conformational Changes in Proteins
WPS28-10	Halada, Petr	Institute of Microbiology	Immobilization of aspartic protease nepenthesin-1 for protein digestion in hydrogen/deuterium exchange mass spectrometry
WPS28-11	Kurulugama, Ruwan	Agilent Technologies	Structural analyses of gas phase molecules using different drift gases in a high resolution ion mobility time-of-flight mass spectrometer
WPS28-12	Cianferani, Sarah	CNRS - IPHC - LSMBO	Real-time native MS to monitor the effect of point mutations, inhibitor or tRNA binding on Tgt subunit exchange and dimer stability
WPS28-13	Saikusa, Kazumi	Hiroshima University	Behavior of the disordered tail regions of the histone H2A/H2B dimer
WPS28-14	Rauschenbach, Stephan	Max-Planck-Institute for Solid State Research	Active Control of Protein Conformation on Surfaces by Hyperthermal Ion-Surface Interaction

WPS28-15	Chervet, Jean-Pierre	Antec	Controlled Reduction of Disulfide Bonds in Biopharmaceuticals Using an Electrochemical Reactor Cell online with LC/MS
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WPS29 - Ambient Ionization and Miniaturization

Abstract No.	Presenting Author	Affiliation	Abstract Title
WPS29-01	Schwab, Nicolas	Department of Chemistry - York University/ Thomson Lab - Unicamp	Functionalized porous silicon surfaces as DESI-MS substrates for small molecules analysis
WPS29-02	McCullough, Bryan	LGC	Investigation of Programmable Temperature Vaporisation as a Sample Introduction Method for Ambient Ionisation MS
WPS29-03	Bristow, Tony	AstraZeneca	On-line monitoring of continuous flow chemical synthesis using a portable, small footprint mass spectrometer
WPS29-04	Gross, Jürgen	Heidelberg University	Substantial Release of Silicones from Household Items and Baby Articles Analyzed by Direct Analysis in Real Time-Mass Spectrometry
WPS29-05	Barrios-Collado, César	ETH Zurich, Department of Chemistry and Applied Biosciences; SEADM. S. L.; Valladolid University, Energy and Fluid Mechanics Engineering Dep.	Towards an Add-on Secondary Electrospray Ionizer for pre-existing API-MS and for high sensitivity analysis of volatiles
WPS29-06	Hopley, Christopher	LGC	A comparison of ion mobility spectrometry and direct ionisation mass spectrometry for the detection of trace explosives on hand swabs.
WPS29-07	Inoue, Hiroyuki	National Research Institute of Police Science	On-site detection of ecstasy tablets by portable mass spectrometer
WPS29-08	Huang, Minzong	National Sun-Yat Sen University	Thermal Desorption/Electrospray+Atmospheric Pressure Chemical Ionization/Mass Spectrometry for Simultaneously Detecting Polar and Nonpolar Compounds in Complica
WPS29-09	Benham, Kevin	Georgia Institute of Technology	Atmospheric pressure vacuum ultraviolet ionization via microplasma ionization sources
WPS29-11	Kim, Sunghwan	Kyungpook National University	Mechanistic understanding on factors determining ionization efficiencies of (+) APPI-MS
WPS29-12	Jones, Emrys	Imperial College London	Alternative ionization methodologies for the broadening of intra-operative applications of rapid evaporative ionization mass spectrometry
WPS29-13	Farrell, Ross	Australian Centre for Research On Separation Science, UTAS	Direct-infusion and paper spray ionisation mass spectrometry for high-throughput screening of rapid oak extracts
WPS29-14	Pfeuffer, Kevin	Indiana University	Halo-shaped flowing atmospheric pressure afterglow for ambient desorption/ionization mass spectrometry

WPS44 - Very Large Biomolecules and Structural Biology

Abstract No.	Presenting Author	Affiliation	Abstract Title
WPS44-01	Husser, Christophe	F. Hoffmann-La Roche Ltd.	In vivo catabolism of the fusion protein Tetranectin-Apolipoprotein A1 in rabbit
WPS44-02	Tseng, Mei-Chun	Academia Sinica	Ion-mobility mass spectrometry analysis of the conformational conversion of amyloid aggregation
WPS44-04	Hsu, Chun-Hua	National Taiwan University	Ion-mobility mass spectrometry analysis reveals quaternary structural and conformational changes for thermal-induced activation of thermophilic SNR
WPS44-05	Boelt, Sanne Grundvad	BMB, SDU	There goes the neighbourhood – Mapping protein proximity in highly complex samples, using chemical cross-linking, LC-MS and novel bioinformatics.
WPS44-06	Fioramonte, Mariana	UNICAMP	A New Cross-Linker targeting Asp/Glu residues

WPS44-07	Lima, Tatiani	University of Campinas	Insights into the interaction between Human Hsp90 C-terminal and Tom70 by chemical-cross-linking and HDX coupled to mass spectrometry
WPS44-08	Ferrari, Allan	University of Campinas	Cross-linking as a key experimental data in Stanniocalcin-1 structural modeling
WPS44-09	Cianferani, Sarah	CNRS - IPHC - LSMBO	Native MS and Ion Mobility MS (IM-MS) for Antibody Drug Conjugate Characterization
WPS44-11	Akashi, Satoko	Yokohama City University	Native Mass Spectrometry of Reconstituted Human Nucleosome Core Particle
WPS44-12	Nguyen-Huynh, Nha-Thi	Laboratoire de Spectrométrie de Masse des Interactions et des Systèmes (LSMIS) - UMR 7140 CNRS/Université de Strasbourg -	Chemical cross-linking and MALDI-MS for the characterization of intact protein complexes
WPS44-13	Takayama, Mitsuo	Yokohama City University	Mass Spectrometric Estimation of the Flexibility of Intact Proteins
WPS44-14	Spector, Almog	weizmann institute	Investigating the familial Parkinson's disease's mutations in DJ-1 and their affect on the 20S proteasome

Thursday, August 28th

ThPS32 - Ion Mobility MS

Abstract No.	Presenting Author	Affiliation	Abstract Title
ThPS32-01	Ihlenborg, Marvin	CAU Kiel	Comparative study of APCI and MPI/REMPI in atmospheric pressure IMS
ThPS32-02	Li, Haiyang	Key Laboratory of Separation Science for Analytical Chemistry, Dalian Institute of Chemical Physics, Chinese Academy of Sciences	Dopant-Assisted Negative Photoionization Ion Mobility Spectrometry for Explosives Detection and Clinical Monitoring
ThPS32-03	Groessler, Michael	Tofwerk AG	Resolution Enhancement in a Multiplexed, High-Pressure Drift Tube IMS-MS
ThPS32-04	Wang, Yi-Sheng	Academia Sinica	Analysis of Ions Produced By Laser-Desorption Ionization In Air and Liquid – A Theoretical and Experimental Study
ThPS32-05	Queguiner, LAURENCE	JANSSEN R&D	Coupling of ion mobility and mass spectrometry as a new alternative for the analysis of pharmaceutical diastereomers
ThPS32-06	Ujma, Jakub	University of Manchester	A New High Resolution Temperature Regulated Ion Mobility Mass Spectrometer
ThPS32-07	Amantonico, Andrea	Firmenich SA	Monitoring of active ingredients release from different delivery systems by GC-IMS
ThPS32-08	Slováková, Kristína	Regional Centre of Advanced Technologies and Materials, Department of Analytical Chemistry, Faculty of Science, Palacky University	Ion Mobility-Mass Spectrometry of Linear alcohol ethoxylates
ThPS32-09	Rosu, Frédéric	CNRS / Univ. Bordeaux	Ion mobility spectrometry of foldamers
ThPS32-10	Jenkins, Benjamin	MRC-HNR	The Dispersion Characteristics of Lipids in High-Field Asymmetric Waveform Ion Mobility Spectrometry
ThPS32-11	Riebe, Daniel	University of Potsdam	Pressure-tunable, UV- and IR-laser based ion mobility spectrometer for the determination of ion mobilities and the investigation of laser ionization mechanisms
ThPS32-12	Zühlke, Martin	University of Potsdam	HPLC-ESI ion mobility spectrometry: Characterization and applications
ThPS32-13	Kirk, Ansgar	Leibniz University Hannover Institute of Electrical Engineering and Measurement Technology	Direct Sample Ionization and Separation Using a High Kinetic Energy Ion Mobility Spectrometer (HiKE-IMS)

ThPS32-14	Lemr, Karel	Palacký University	"Secondary effects" changing arrival time distribution in ion mobility-mass spectrometry of tyramine-based hyaluronan derivatives
ThPS32-15	Sidibe, Jonathan	University of Geneva	Differential mobility spectrometry of endogenous peptides: Modifiers effect on ion mobility and selectivity
ThPS32-16	Nakamura, Takemichi	RIKEN	Formation of isomeric ions in collision-induced dissociation process probed by energy-resolved ion mobility tandem mass spectrometry (ER-IMS/MS2)
ThPS32-17	Nieland, Bertram	AB SCIEX	Solving Selectivity Challenges in Qualitative and Quantitative Analysis of Drugs and Metabolites
ThPS32-18	Causon, Jason	AB SCIEX	Rapid quantitation of Substance P in plasma using Differential Mobility Spectrometry and Microflow chromatography
ThPS32-19	Azzollini, Antonio	School of Pharmaceutical Sciences , EPGL , University of Geneva, University of Lausanne, Quai Ansermet 30, 1211 Geneva 4, Switzerland	High Resolution IMS-MS and UHPLC-HRMS for the analysis of natural products and complex natural extracts
ThPS32-20	Horner, Julie	Thermo Fisher Scientific	Separation of Lipid Classes, Subclasses and Isobaric/Isomeric Lipids Using a Novel FAIMS Device
ThPS32-21	Burgess, Jennifer	Waters Corporation	Using Ion Mobility Mass Spectrometry to Identify Multiple Protonation Sites and Different Fragmentation Patterns For The Fluoroquinolone Class of Antibiotics
ThPS32-22	McCullagh, M.	Waters Corporation	Using the Routine Separation Dimension and Identification Criteria of UPLC Ion Mobility to Enhance Specificity in Profiling Complex Samples
ThPS32-23	Gosciny, Séverine	Scientific Institute of Public Health	Collision Cross Section a powerful parameter for the identification of pesticides in food
ThPS32-24	Zhang, Wen	Max Planck Institute for Polymer research	Elucidation of unexpected reaction pathways during synthesis of strained PAH macrocycles by ion mobility mass spectrometry
ThPS32-25	Porta, Tiffany	FOM Institute AMOLF	Direct visualization of intact protein ion beam focusing transmitted by an ion funnel using a position-sensitive detector at elevated pressure
ThPS32-26	Stafford, George	Agilent Technologies	Multiplexed IM-QTOF analysis of complex proteomics and metabolomics samples using a real-time dual filtering technique
ThPS32-27	Chipperfield, John	Waters	Characterisation of metabolites by utilising Collision Cross Section measurements in conjunction with an integrated microfluidic device
ThPS32-28	Bellina, Bruno	University of Manchester	Photodissociation of trapped ions selected by drift-time separation. IMS-UVPD-MS

ThPS33 - Data Analysis – General

Abstract No.	Presenting Author	Affiliation	Abstract Title
ThPS33-01	Trubitsyn, Andrey	Ryazan State Radio Engineering University	Adaptive noise smoothing of the mass spectra
ThPS33-02	Li, Detian	Company Science and Technology on Vacuum & Cryogenics Technology and Physics Laboratory,	A new calibration method of vacuum mass spectrometer
ThPS33-03	Okada, Yutaka	Ritsumeikan University	The relationship between electron-ionization mass spectra and conformation of (substituted phenyl)ferrocenes
ThPS33-04	Todua, Nino	National Institute of Standards and Technology	Analytical application of alkylation for the study of amino acids
ThPS33-05	Rajan J Methikkalam, Rabin	Indian Institute of Technology, Madras	Development of ultralow energy (1-10 eV) ion scattering spectrometry coupled with RAIRS and TPD for the investigation of molecular solids

ThPS33-06	Im, Sohee	Korea Research Institute of Chemical Technology (KRICT)	Determination of mesoridazine by liquid chromatography–tandem mass spectrometry and its application to pharmacokinetic study in rats
ThPS33-07	Schollee, Jennifer	Eawag, Swiss Federal Institute of Aquatic Science and Technology	A Workflow for Nontarget Screening of Transformation Products formed in Biological Wastewater Treatment using Multivariate Analysis
ThPS33-08	Cuyckens, Filip	Pharmacokinetics, Dynamics & Metabolism, Janssen R&D, Beerse, Belgium	The choice for centroid or profile data in high-resolution MS quantification: more than a detail?
ThPS33-09	González Méndez, Ramón	University of Birmingham	DEVELOPMENT AND APPLICATIONS OF PROTON TRANSFER REACTION-MASS SPECTROMETRY FOR HOMELAND SECURITY: TRACE DETECTION OF EXPLOSIVES
ThPS33-10	Zhang, Terry	ThermoFisher	Structure characterization of intact monoclonal antibody using Orbitrap Tribrid mass spectrometer
ThPS33-11	Patiny, Luc	EPFL	Recent developments of ChemCalc (www.chemcalc.org) : an online tool for mass spectrometrists
ThPS33-12	Menin, Laure	EPFL	Structure of arene-linked dinuclear ruthenium(II) organometallics–peptide complexes
ThPS33-13	Takeuchi, Takae	Nara Women's University/Department of Chemistry, Faculty of Science	Development of Software for Identifying Fungal Species with PLS Analysis of SPME GC/MS and IMS Data of Microbial Volatile Organic Compounds
ThPS33-14	Caldwell, Anna	King's College London	An AMDIS-based GC/MS Procedure for the Rapid Characterization of Algal Liquefaction Products and Process Optimization
ThPS33-15	Emami Khoonsari, Payam	Uppsala University	Cerebrospinal Fluid Proteome of Patients Diagnosed with Alzheimer Disease: Focus on Data Analysis
ThPS33-16	Urban, Jan	Institute of Complex Systems, Faculty of Fisheries and Protection of Waters, University of South Bohemia	False precision and mass peak deconvolution
ThPS33-17	Kozhinov, Anton N.	Ecole Polytechnique Fédérale de Lausanne	New methods of data analysis for FTMS with improved analytical performance

ThPS35 - Elemental and isotopics, MS, ICP-MS General, Cultural Heritage and Archeology

Abstract No.	Presenting Author	Affiliation	Abstract Title
ThPS35-01	Dubkov, Michael	Ryazan State Radio Engineering University	Methods to improve analytical characteristics of monopole mass spectrometers
ThPS35-02	Kim, Sook Heun	Korea Research Institute of Standards and Science	Development of a Certified Reference Material (KRISS CRM 114-01-001) for the Determination of Hazardous Elements in Cosmetics
ThPS35-03	Bednařík, Antonín	Masaryk University	Simple cobalamin speciation using TLC-DLTV ICP MS
ThPS35-04	Varga, Janos	Helmholtz Zentrum München	Investigation of Sulfur Allotropes with Thermal Analysis – Single Photon Ionization Mass Spectrometry
ThPS35-05	Besic, Denis	PLIVA Hrvatska d.o.o.	Determination of elemental impurities in active pharmaceuticals by single ICP-MS run after prior stabilisation of osmium
ThPS35-06	Jägerová, Kateřina	Masaryk University	Coupling of single HPLC separation run to ESI, MALDI and SALD ICP MS for metallothionein characterization
ThPS35-07	Zhiming, Li	Northwest Institute of Nuclear Technology	Determination Age of Uranium and Plutonium Material by MC-ICPMS
ThPS35-08	Aggarwal, Suresh Kumar	Bhabha Atomic Resaerch Centre	Electrospray Ionisation Mass Spectrometry for the Complexation of Palladium with Thiourea, Benzoylthiourea and N,N-diethyl N'-benzoylthiourea
ThPS35-09	Aggarwal, Suresh Kumar	Bhabha Atomic Resaerch Centre	Investigation of Uranyl-Hydroxycarboxylic Acid Complexes by Electrospray Ionization Mass Spectrometry
ThPS35-10	Adler, Lewis	University of New South Wales	A Comparison of Groundwater $\delta^{18}\text{O}$ and Speleothem-derived water $\delta^{18}\text{O}$ isotopes.

ThPS35-11	Lee, Chi-Gyu	Korea Atomic Energy Research Institute	Ultra-trace analysis of plutonium isotopes by thermal ionization mass spectrometry with a continuous heating technique without chemical separation
ThPS35-12	Desprez, Alain	IPREM/LCABIE	Size distribution of Sulfur, Vanadium and Nickel in four crude oils complete distillation series using GPC ICP HR MS
ThPS35-13	Hattendorf, Bodo	ETH Zurich, Laboratory for Inorganic Chemistry	Occurrence and Impact of Doubly Charged Alkaline Earth Argon Ions [MAr] ²⁺ in ICPMS.
ThPS35-14	Yim, Yong-Hyeon	KRISS	Development of Simplified Nanoparticle Quantification Protocols
ThPS35-15	Molchanov, Vladimir	Far East Geological Institute (FEGI FEB RAS)	Current evaluation of powder geological samples elemental analysis using laser-ablation inductively coupled plasma mass-spectrometry
ThPS35-16	Tanner, Martin	Tofwerk AG, Uttigenstrasse 22, 3600 Thun	ICP-TOFMS based on iCAP Qc ion source and interface

ThPS36 - Advanced MS in Food and Nutrition

Abstract No.	Presenting Author	Affiliation	Abstract Title
ThPS36-01	Lee, ye ji	Gyeongbuk Branch office of National Agricultural Products Quality Management Service	Simultaneous analysis of flonicamid and its metabolites in agricultural products by liquid chromatography tandem mass spectrometry
ThPS36-02	Holzschuh, Maribete	Faculdade de Farmácia - UFRGS	Phenolic Compounds from the Leaves of <i>Vitis labrusca</i> and <i>Vitis vinifera</i> L. as a Source of Waste Byproducts: Validation of LC Method and Antichemotactic Activity
ThPS36-03	Cho, Soon-Kil	National Agricultural Products Quality Management Service	A residual feature of gibberellin in pears using the LC/MS/MS determination
ThPS36-04	Muscarella, Marilena	Istituto Zooprofilattico Sper. Puglia e Basilicata	Confirmatory LC/MS/MS methods for monitoring of feedingstuffs contamination by authorized coccidiostats at carry-over level
ThPS36-05	Martins-Froment, Nathalie	Université Paul Sabatier Service Commun Spectrométrie de Masse	Accurate determination of adulterants in dietary supplements using shotgun high-resolution tandem mass spectrometry
ThPS36-06	Kim, Byungjoo	Korea Research Institute of Standards and Science	Development of ID-LC-MS/MS for the Accurate Determination of Ochratoxin and Application to the Certification of Fermented Soybean Paste Reference Material
ThPS36-07	Frerot, Eric	FIRMENICH S.A.	Analysis of Stevia Extracts by Ultra Performance Liquid Chromatography coupled with High-Resolution Quadrupole-Orbitrap Mass Spectrometry (UPLC [®] -HRMS).
ThPS36-08	Lee, Joongoo	Ministry of Food and Drug Safety	Method Validation for Determination of polycyclic aromatic hydrocarbons in food by GC-MS
ThPS36-09	Sarathchandra, Ghadevaru	Pharmacovigilance Laboratory for Animal Feed and Food, Directorate Centre for Animal Health Studies, Tamilnadu Veterinary and Animal Sciences University	Surveillance of chloramphenicol residues in milk, eggs and Chicken meat by LCMSMS
ThPS36-10	Ueda, Yoshihisa	JEOL Ltd.	Structural analyses of marine polyether toxins by means of high-energy CID MS/MS using MALDI SpiralTOF-TOF tandem MS system
ThPS36-11	Nuñez, Oscar	University of Barcelona	Liquid Chromatography-Mass Spectrometry and Chemometric Techniques for the Authentication of Natural Extracts using the Compositional Profiles of Polyphenols
ThPS36-12	Hebert, Yann	Bruker Daltonics Inc.	Enhanced reduction of matrix effects using LC-MS/MS with online extraction for the rapid quantitation of antibiotics in milk
ThPS36-13	Engst, Wolfram	German Institute of Human Nutrition Potsdam- Rehbrücke	Determination of protein adducts originating from 1-methoxy-3-indolylmethyl glucosinolate using isotope-dilution UPLC-ESI-MS/MS

ThPS36-14	Burger, Udo	Shimadzu Schweiz GmbH	Quantification of Micropollutants in Ground Water with LCMS-8050 - Qualifier and Quantifier ions with different Polarity Modes
ThPS36-15	Maljers, Louis	Bruker Daltonics Inc.	Screening and Quantitation of About 250 Pesticides in Fruit Juices with Positive/Negative Switching LC/MS/MS
ThPS36-16	Felician, Muntean	Bruker Daltonics Inc.	Comparison of Ionization Techniques for the Analysis of Trace-Level Pyrethroid Insecticides by GC/MS/MS
ThPS36-17	Szesny, Matthias	Bruker Daltonik GmbH	Ultra High Performance LC-QTOF workflow for Multi-Residue Pesticide Screening using Diagnostic Ion Enhanced Confirmation Criteria
ThPS36-18	Fabrega Prats, Marta	University of Padua dept. DAFNAE	Identification of low molecular weight thiols in plants by fluorescence derivatization and LC-MS/MS
ThPS36-19	Quek, Yi Ling	Health Sciences Authority	Screening Of Toxic Natural Substances in Herbal Products by Liquid Chromatography-Coupled Quadrupole Tandem Mass Spectrometry
ThPS36-20	Xiao, Peng	National Institute of Metrology, P.R.China.	Determination of Collision Cross-Section and Analysis of Isomeric Vitamin K1 Using Electrospray Ion Mobility Time-of-Flight Mass Spectrometry
ThPS36-21	Lee, Seung hwa	National agricultural products quality management service, Gyeongnam provincaill office	Residue patterns of flonicamid and its metabolites in paprika cultivated using manually pulled trolley sprayer
ThPS36-22	Tsipi, Despina	GENERAL CHEMICAL STATE LABORATORY	GC-MS/MS and LC-MS/MS
ThPS36-23	Hyung, Seok-Won	Korea Research Institute of Standards and Science	Demonstration of Two-Dimensional Liquid Chromatography for the Elimination of Matrix Effects in the Food Analysis
ThPS36-24	Yunin, Maxim	FGBU VGNKI	Development of a rapid method for the analysis of anabolic steroids and stilbenes in bovine muscle using liquid chromatography tandem mass spectrometry
ThPS36-25	Scheibner, Olaf	Thermo Fisher Scientific	Quick and sensitive analysis of multiclass veterinary drug residues in animal products using a benchtop Orbitrap mass spectrometry system
ThPS36-26	Glauner, Thomas	Agilent Technologies Inc.	Eliminating matrix effects during multi-residue pesticide analysis by extensive dilution using the high-sensitive 6495 triple quadrupole MS
ThPS36-27	Dr. Lelik, László	Corvinus University of Budapest	Investigation of nicotine contents of chamomile samples by HPLC/TOF-MS method
ThPS36-28	Wuest, Bernhard	Agilent Technologies Inc.	Determination of 8 Estrogens in Milk by the 1290 UHPLC and Highly Sensitive 6495 Triple Quadrupole Mass Spectrometer
ThPS36-29	Kim, Eunjung	Gyeongin MFDS	Multi-residue method for the determination of 262 pesticides in crops by gas chromatography- mass spectrometry
ThPS36-30	Pandey, Renu	CSIR-Central Drug Research Institute	Quality Control Strategy for Leaf Extracts and Marketed Herbal Formulations of Ocimum sanctum based on MRM Determination of Multiple Markers by UPLC-QTRAP-MS/MS
ThPS36-31	Stahl-Zeng, Jianru	AB SCIEX	Vitamin B complex detection in infant formula by LC/MS/MS
ThPS36-32	Crawford, Elizabeth	IonSense, Inc.	HPTLC combined with ambient mass spectrometry: Current trends in food & natural product analysis
ThPS36-33	Westphal, Yvonne	Unilever R&D Vlaardingen	NPLC-APPI-MS for the separation and identification of sterols, steradienes, and sterol oxides
ThPS36-34	Park, Su-Jeong	Ministry of Food and Drug Safety (MFDS), Seoul Regional FDA	Multi-residue screening method of 47 veterinary drugs in fishery products by ultra performance liquid chromatography-tandem mass spectrometry
ThPS36-35	Benozzi, Elisabetta	Fondazione Edmund Mach	Proton-Transfer-Reaction Mass Spectrometry for the study of the aromatic impact of yogurt starter cultures
ThPS36-36	Gallo Hermosa, Blanca	Euskal Herriko Unibertsitatea (UPV/EHU)	MSE strategy for characterization of phenolic compounds
ThPS36-37	Wang, Jia	Thermo Fisher Scientific	Analysis of 200+ Pesticides in a Short LC Run Using Non-Timed SRMs on Triple Quadrupole Mass Spectrometer

ThPS36-38	Juvonen, Minna	University of Helsinki	The structural identification of cereal-based arabinooligosaccharides by ESI-MSn
ThPS36-39	Silcock, Paul	Thermo Fisher Scientific	Fast SRM Transition Speeds for High Sensitivity, High Capacity and Selective Multi-Residue Pesticide GC-MS/MS Analysis
ThPS36-40	Pollack, Leonhard	Markes International	Enhanced aroma profiling by GC-TOF MS with variable-energy electron ionisation
ThPS36-41	Dr. Lelik, László	Corvinus University of Budapest	GC-MS volatile profiles of ground spice from Hungary extracted by HS-SPME compared with distillation techniques
ThPS36-43	Godin, Simon	LCABIE, Université de Pau et des Pays de l'Adour, IPREM UMR CNRS 5254	Influence of selenium species in aquaculture feeds on the selenium status of farmed rainbow trout
ThPS36-44	Gallo Hermosa, Blanca	Euskal Herriko Unibertsitatea (UPV/EHU)	Application of HPLC-ESI(+)-CID-MS/MS in MRM mode to determine the evolution profile of pyranoanthocyanins in red wine from Rioja.
ThPS36-45	Kiuchi, Masato	AIST	Dispersion of olive oil in aqueous fine bubbles
ThPS36-46	Sagi-Kiss, Virag	University of Reading	Flavonoid profiling of meat products treated with selected plant extracts using HPLC-MS/MS
ThPS36-47	Hird, Simon	Food and Environment Research Agency	The Analysis of Horsemeat for the Banned Drug Phenylbutazone
ThPS36-48	Le Quéré, Jean-Luc	INRA - SFC	A comprehensive approach of Cognac 'crus' typicity by GC-O and GC-MS analysis of extracts and PTR-MS direct analysis of samples headspace
ThPS36-49	Kim, Hyeo Joong	Korea Yakult	New methods for assessing quality of milk powder using particle size analysis and NIR technique

ThPS37 - Hyphenated Techniques – Applications

Abstract No.	Presenting Author	Affiliation	Abstract Title
ThPS37-01	Niemi, Anneli	Finnish Food Safety Authority Evira	Monitoring of coccidiostat residues in eggs according to the EU legislation using liquid chromatography tandem mass spectrometry
ThPS37-02	Lamoree, Marja	Institute for Environmental Studies, VU University	On-line trapping LC-MS for the determination of DEHP metabolites, PFOS and PFOA in breast milk and cord plasma samples from European birth cohorts
ThPS37-03	Preisler, Jan	Masaryk University	Liquid chromatography with substrate-assisted laser desorption/ionization mass spectrometry for determination of sterols
ThPS37-04	Dier, Tobias	Universität des Saarlandes	Detailed analysis of lignin cleavage products from electrochemical degradation by high resolution mass spectrometry
ThPS37-05	Wohlfahrt, Sebastian	Helmholtz Zentrum München	Rapid characterization of crude oils by thermogravimetry coupled to fast modulated gas chromatography-single photon ionization time-of-flight mass spectrometry
ThPS37-06	Tomalová, Iva	Masarykova univerzita	Off-line CE-MALDI/SALD-ICP MS coupling: What can we acquire from a single separation run?
ThPS37-07	Weber, Waldemar	MEET UNI-Münster	GC-MS for Identification of Volatile Organophosphates in Thermal Aged LiPF6-Based Electrolyte
ThPS37-08	Kraft, Vadim	University of Münster, MEET	IC-ESI-MS/MS for Investigation of the Organophosphates in LiPF6-Based Electrolyte
ThPS37-09	Bakkour, Rani	Eawag	Using molecularly-imprinted polymers for compound-specific isotope analysis of polar organic micropollutants
ThPS37-10	Deng, Yan	EPFL	Highly sensitive detection of typical fluoroquinolones in milk by FESI-CE coupled with electrostatic spray ionization MS
ThPS37-11	Grützke, Martin	University of Münster, MEET Battery Research Center, Institute of Physical Chemistry	Structure Determination of Aging Products in Lithium-Ion Battery Electrolytes with Gas Chromatography using Chemical Ionization Mass Spectrometry
ThPS37-12	Zangrando, Roberta	Institute for the Dynamics of Environmental Processes-CNR	Target and untarget analysis of water soluble compounds in urban aerosols using an innovative coupling of IC-HRMS.

ThPS37-13	Bourgogne, Emmanuel	Laboratoire de toxicologie, Hopital Lariboisière, AP-HP	Historical amphetamines are still here. Development of a reliable turbulent flow LC-MS/MS assay for following intoxication admitted in intensive care unit
ThPS37-14	Soichot, Marion	Laboratoire de toxicologie, Hopital Lariboisière, AP-HP	Input of bonded fluoro(pentafluorophenyl) used as normal phase for determination of Cocaine and Opiates drugs of abuse in plasma
ThPS37-15	Alechaga, Élida	University of Barcelona	FIA-HRMS/MS FOR THE ANALYSIS OF RECREATIONAL DRUGS AND LEGAL HIGHS
ThPS37-16	Koulman, Albert	MRC HNR	Ion exchange chromatography with non-volatile buffers hyphenated through on-line liquid-liquid extraction to electrospray MS for the analysis of lipoproteins
ThPS37-17	Roig-Navarro, Antoni F.	Universitat Jaume I. IUPA	Comparison of different quantification approaches to deal with matrix effects in LC-ESI-MS/MS based determinations of mycotoxins in selected spices
ThPS37-18	Vojs Stanova, Andrea	Comenius University, Faculty of Natural Sciences, Department of Analytical Chemistry	Buffer salt effects in off-line coupling of capillary electrophoresis and mass spectrometry
ThPS37-19	Molnárné Guricza, Lilla	Max-Planck Institut für Kohlenforschung	Compositional analysis of heavy crude oil samples using size exclusion chromatography in combination with ultrahigh resolution mass spectrometry
ThPS37-20	Rathore, Atul S	CARPS, Poona College of Pharmacy, Bharati Vidyapeeth University	Determination of Corilagin by Hybrid Solid-Phase-Extraction UPLC-ESI-MS/MS in Rat Plasma and its Application to Pharmacokinetic and Bioavailability Studies
ThPS37-21	Loge, Eike	AB SCIEX	Routine high throughput quantitative analysis with increased sensitivity using micro flow LC-MS/MS.
ThPS37-22	Herniman, Julie	University of Southampton	Utilising open access UPC2-MS within a Chemistry environment
ThPS37-23	Nokihara, Kiyoshi	HiPep Laboratories	The routine sequencing method for one peptide immobilized on a gel-type single bead prepared by the solid-phase synthesis focusing on drug discovery
ThPS37-24	Choi, Soowan	College of pharmacy, Kyung-Hee university	Validated LC-MS/MS method for the determination of enantiomeric purity of S-Amlodipine in human plasma : Application to pharmacokinetic study.
ThPS37-25	Naudé, Yvette	University of Pretoria, Department of Chemistry, South Africa	Lipid residue analysis by derivitisation and comprehensive Gas Chromatography – Time of Flight Mass Spectrometry as applied to South African Iron Age pottery
ThPS37-26	Subramanyam, Saravanan	Indian Institute of Chromatography & Mass Spectrometry	Application of novel “nMS2” technique towards characterisation of “Bio-Active” molecules of Andrographis paniculata extracts.
ThPS37-27	Clench, Malcolm	Sheffield Hallam University	FAFOSS : Fast Automated Food Safety Screening
ThPS37-28	Aurand, Craig	Supelco	Investigation of Solid Phase Micro Extraction in Bioanalysis
ThPS37-29	Senior, Adam	Biotage GB Ltd	Development of Optimized Multiclass Clean-up Methods for LC-MS/MS Analysis of Mycotoxins in Multiple Food/Feed Matrices Incorporating a Novel SPE Column
ThPS37-30	Langridge, James	Waters Corporation	Characterisation of the Performance of an Ultra High Pressure Liquid Chromatography System
ThPS37-31	Righi, Davide	UNIVERSITY OF GENEVA	Methodological development for the establishment of efficient normal phase MS directed purification of natural products at the preparative scale
ThPS37-32	Smit, Elize	University of Pretoria	Characterisation of the polar fraction of diesel using accurate mass spectrometry: the effects of sample preparation, ionisation methods and pre-separation
ThPS37-33	Alonso Salces, Rosa Maria	Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Instituto de Investigaciones en Biodiversidad y Biotecnología (INBIOTEC)	UHPLC-UV-MSE analysis for the characterization of carotenoids and chlorophylls in Synechococcus sp. PCC 7002 cyanobacterium
ThPS37-34	Absalon, Christelle	ISM - University of Bordeaux	Isolation and Characterization by HRMS of a new compound in Red Wine

ThPS37-35	Azzollini, Antonio	School of Pharmaceutical Sciences , EPGL , University of Geneva, University of Lausanne, Quai Ansermet 30, 1211 Geneva 4, Switzerland	Development of an LC-MS-based purification strategy for the Mass Spectrometry targeted isolation of bioactive compounds
ThPS37-36	Berezovski, Maxim	University of Ottawa	Kinetic Capillary Electrophoresis Coupled On-line with Mass Spectrometry to Study Conformational Dynamics of DNA G-Quadruplex in Solution
ThPS37-37	Marakova, Katarina	Faculty of Pharmacy, Comenius University	Capillary Electrophoresis On-line Hyphenated with Mass Spectrometry Used for Analysis of Vitamins B in Pharmaceuticals
ThPS37-38	Wendt, Juergen	LECO Instrumente GmbH	HIGH PERFORMANCE TIME-OF-FLIGHT MASS SPECTROMETRY FOR COMPREHENSIVE PETROLEUM ANALYSIS
ThPS37-39	Wendt, Juergen	LECO Instrumente GmbH	Utilizing Hydrogen Carrier Gas for High Throughput Gas Chromatography - High Resolution Time of Flight Mass Spectrometry (GC-HRT): Application Compendium
ThPS37-40	Ammann, Adrian	EAWAG	Endogenous metabolite separation by multimode gradient HPLC and detection by MS
ThPS37-41	Lee, Joon Seok	ThermoFisher Korea	Identification and Relative Quantification of Anions in Battery Samples with the course of time using Ion chromatography and High Resolution Mass Spectrometer
ThPS37-42	Tranchida, Peter	Dipartimento SCIFAR, University of Messina, Italy	The combination of "fast" triple-quad MS with flow-modulated comprehensive 2D gas chromatography for the untargeted and targeted analysis of complex mixtures
ThPS37-43	Langley, John	University of Southampton	Qualitative and quantitative application of UPC2-MS to biofuel screening.
ThPS37-44	Babaev, Vasily	A.E. Arbuzov Institute of Organic and Physical Chemistry of the Russian Academy of Sciences	ESI mass spectrometry investigation of the chiral recognition of amino acid esters by lariat ethers
ThPS37-45	Isobe, Toshiaki	Tokyo Metropolitan University	Automated LC-LC-MS/MS system for comprehensive analysis of small RNAs in functional RNP complexes
ThPS37-46	Sun, Cuirong	Zhejiang University	Chiral Discrimination of Amino Acids Based on Cyclofructans (CFs) in Mass Spectrometry
ThPS37-47	Ollikainen, Elisa	University of Helsinki	Rapid Phosphopeptide Analysis by Microchip Electrophoresis-Electrospray Ionization Mass Spectrometry
ThPS37-48	Pereira, Fiona	CSEM	Improved Sequence Coverage for PMF using a Droplet Interface for Nano-LC MALDI-MS
ThPS37-49	Oldrati, Vera	Atheris Laboratories; School of Pharmaceutical Sciences, University of Geneva	High-resolution peptidomic and transcriptomic profiling of spider venom: a rapid and comprehensive method for assessment of complex venom composition.
ThPS37-50	Petras, Daniel	TU Berlin	Top-down venomomics - High resolution mass spectrometry as a fast and accurate tool for the profiling of snake venoms
ThPS37-51	Gasilova, Natalia	LEPA, EPFL	On-chip spyhole mass spectrometry for droplets-based microfluidics: Studying β -lactoglobulin interaction with liposoluble vitamins
ThPS37-52	Burkhardt, Therese	TU Muenchen	Hyphenation of effect-directed enzymatic reactions to mass spectrometry
ThPS37-53	Loge, Eike	AB SCIEX	Exploring the effect of DMSO as a mobile phase additive for improving protein identification and SWATH acquisition by NanoLC/MS/MS
ThPS37-54	Sikanen, Tiina	University of Helsinki	GLASS SEPARATION CHIPS WITH SHARP, MONOLITHICALLY INTEGRATED ELECTROSPRAY EMITTER FOR RAPID BIOANALYSIS
ThPS37-55	Alonso Salces, Rosa Maria	Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Instituto de Investigaciones en Biodiversidad y Biotecnología (INBIOTEC)	UHPLC-UV-MSE analysis for the characterization of carotenoids and chlorophylls in <i>Scenedesmus obliquus</i> microalgae

ThPS38 - Non-Covalent Interactions			
Abstract No.	Presenting Author	Affiliation	Abstract Title
ThPS38-01	Cabrera, Gabriela	DQO-UMYMFOR, FCEN, Universidad de Buenos Aires	Study by Electrospray Ionization Mass Spectrometry of the Complexation of Histone Deacetylase Inhibitors With Divalent Metal Ions
ThPS38-02	Gavriilidou, Agni Faviola Mika	ETH Zurich, Department of Chemistry and Applied Biosciences	Effect of Buffer Concentration on Protein-Ligand Binding Affinities Measured by Native ESI-MS
ThPS38-03	Perret, Cécile	Laboratoire de Spectrométrie de Masse des Interactions et des Systèmes (LSMIS), CNRS-UMR 7140, University of Strasbourg	MALDI-MS quantitative analysis of organometallic complexes: application to anti-cancer drug candidates.
ThPS38-04	Ruhe, Lena	Humboldt-Universitaet zu Berlin	Characterization of a Cisplatin-DNA-Antibody and its Corresponding Antibody-Antigen-Complexes by Mass Spectrometry under Native Conditions
ThPS38-05	Gulbakan, Basri	ETH Zurich	Native nano-ESI mass spectrometry studies of aptamer-ligand complexes
ThPS38-06	Chhoden, Tashi	University of Southern Denmark/ NRCWE	Interaction of phospholipid pulmonary surfactants with nanoparticles studied in liquid media by LC MS and MALDI TOF MS
ThPS38-07	Guérineau, Vincent	CNRS/ICSN	CHARACTERIZATION OF CALCIUM PHOSPHATE SALT CATALYSTS BY MALDI-TOF MASS SPECTROMETRY
ThPS38-08	Rosati, Sara	Utrecht University	High Resolution Native Mass Spectrometry allows rapid characterization of therapeutic monoclonal antibodies: from PTM to antibody-drug conjugates analysis.
ThPS38-09	Rafalik, Monika	University of Gdansk	The application of mass spectrometry to identification of the epitope in human cystatin C – monoclonal antibody HCC3 complex.
ThPS38-10	Bildl, Wolfgang	Institute of Physiology, University of Freiburg, Hermann-Herder-Str. 7, 79104 Freiburg, Germany	A high-resolution quantitative BN-MS approach for comprehensive analysis of protein complexes
ThPS38-11	Czaplewska, Paulina	University of Gdansk	Mass spectrometry as a powerful tool in antigen-antibody studies.
ThPS38-12	Schlosser, Gitta	Research Group of Peptide Chemistry, Hungarian Academy of Sciences, Eotvos L. University	Association behavior of Ser-Ser dipeptide: magic clusters and metal ion binding
ThPS38-13	Prądzińska, Martyna	University of Gdansk	Identification of epitopes and characteristic of anti cystatin C antibodies.
ThPS38-14	Behrendt, Izabela	University of Gdansk	Mass spectrometry technique in studies of interactions of human cystatin C with antibodies
ThPS38-15	Williams, Jonathan	WATERS CORPORATION	Size-exclusion chromatography combined with Native MS and Ion Mobility MS of Protein complexes
ThPS38-16	Sulc, Miroslav	Institute of Microbiology ASCR	Mapping the protein-protein interactions employing the combination of photo cross-linking protein nanoprobe with high resolution mass spectrometry
ThPS38-17	Abb, Sabine	Max-Planck-Institute for solid state research	Peptide folding on metal surfaces in UHV
ThPS38-18	Tabet, Jean-Claude	Université Pierre et Marie Curie,	Three-body fragment ion in Positive and Negative ESI for Location of Non-covalent Binding Sites in DNA/Peptide complexes
ThPS38-19	Ptackova, Renata	Department of Biochemistry, Charles University in Prague, Czech Republic	Mapping of protein-protein interactions in 14-3-3zeta homodimer: Combination of photo cross-linking protein nanoprobe with mass spectrometry.
ThPS38-20	Thurn, Heinke V.	Christian-Albrechts-Universität zu Kiel	1c2p-REMPI of non-covalent anisole complexes
ThPS39-01	Haas, Bernd	Biocrates Life Sciences AG	Mass spectrometry based metabolomics work area and data management software "From sample to metabolic pathways"

ThPS39 - Informatic tools for MS			
Abstract No.	Presenting Author	Affiliation	Abstract Title
ThPS39-02	Mercier, Jean	Genedata AG	Mass Spectrometry software tool enabling full characterization of biopharmaceutical molecules
ThPS39-03	Winkler, Robert	CINVESTAV Unidad Irapuato	MASSyPup: A Linux Live DVD for the analysis of mass spectrometry data
ThPS39-04	Trede, Dennis	SCiLS GmbH	A spatially-aware peak picking method for MALDI-imaging data from TOF and FTICR mass analyzers
ThPS39-05	Broeckx, Valérie	KU Leuven	Comparison of protein extraction buffers in formalin-fixed paraffin-embedded tissue
ThPS39-06	Bilbao, Aivett	LSMS/SIB	Towards demultiplexing of SWATH spectra for peptide identification: similarity analysis of fragment elution profiles
ThPS39-07	Clench, Malcolm	Sheffield Hallam University	Do You See What I See ?
ThPS39-08	Gorshkov, Vladimir	University of Southern Denmark	Expanding the current performance of precursor ion-based protein quantification using complementary fragment ions
ThPS39-09	Loos, Martin	Eawag	Clustering-based ion chromatogram extraction and peak-picking for high-resolution LC-MS data
ThPS39-10	Rasmussen, Morten Ib	BMB, SDU	Probing the structure of human protein disulfide isomerase by chemical cross-linking combined with LC-MS
ThPS39-11	Eliuk, Shannon	Thermo Fisher Scientific	A "Universal" data-dependent mass spectrometry method that eliminates time-consuming method optimization for achieving maximal identifications from each sample
ThPS39-12	De Grave, Kurt	KU Leuven	Prediction of peptide fragment ion intensity: a priori partitioning reconsidered
ThPS39-13	Becker, Christopher	Protein Metrics Inc.	Toward a comprehensive bottom-up and top-down analysis of a reference monoclonal antibody
ThPS39-14	Leeming, Michael	The University of Melbourne	Twin-Ion Metabolite Extraction: Combining stable isotopic labels and LCMS data mining software for non-targeted identification of drug metabolites

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