

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Polymers and synthetic macromolecules		
Theme: Biomaterials		
#	Abstract Title	Presenter
77	MASS SPECTROMETRY STUDY OF THE PHOTOISOMERIZATION AND THERMAL BACK-ISOMERIZATION OF AZOBENZENE-FUNCTIONALIZED PEPTOIDS FOR THE CHEMICAL STORAGE OF SOLAR ENERGY	Benjamin Tassignon
78	IMITATION IS THE HIGHEST FORM OF FLATTERING SWAMP-MS: A NEW SYSTEMATIC WORKFLOW OF ANALYZING MULTIPLE- FRAGMENTED POLYMERS WITH MASS SPECTROMETRIC	Ynze Mengerink
157	MASS SPECTROMETRY AND PHOTOCHEMICAL STUDY OF PHOTOISOMERIZATION AND THERMAL BACK-ISOMERIZATION OF SUBSTITUTED AZOBENZENE ANCHORED ON PEPTOIDS FOR THE CHEMICAL STORAGE OF SOLAR ENERGY	Gwendal Henrard
265	APPLICATION OF MALDI-TOF MS FOR THE STRUCTURAL IDENTIFICATION OF NEW POLYOL BUILDING BLOCKS FOR POLYURETHANES	Katalin Czifrák
277	PATTERN TARGETING SOFTWARE FOR THE DETECTION AND ASSIGNMENT OF POLYMERIC COMPOUNDS IN DATA ACQUIRED USING LIQUID CHROMATOGRAPHY-ION MOBILITY-MASS SPECTROMETRY	Jeff Goshawk
282	THE POLYDISPERSITY RATIO AND ITS IMPLEMENTATION FOR THE INTERPRETATION OF PLURONICS	Gergő Róth
292	MONITORING AND CHARACTERIZATION OF SUCROSE-HDI COOLIGOMER FORMATION BY MALDI-TOF MASS SPECTROMETRY	Csilla Lakatos
300	INFORMATION CODING BY PEG – ALIPHATIC ISOCYANATE REACTION AND DECODING BY MALDI-TOF MS	Bence Vadkerti
304	DETAILED KINETIC STUDY ON THE REACTIVITIES OF THE EIGHT HYDROXYL GROUPS OF SUCROSE IN URETHANE FORMING REACTION	Lajos Nagy
324	ANALYSIS OF MULTIBLOCK COPOLYMERS BY MASS SPECTROMETRY	Tibor Nagy
335	DEVELOPMENT OF CHEMICAL BARCODES AND THEIR READING BY DART-MS	Veronika Csilla Pardi-Tóth
340	MONITORING THE REACTIONS OF 1,5-ISOCYANAMINAMINAPHTHALENE IN THE PRESENCE OF WATER/PROTIC SOLVENT MIXTURES AND HG (II) IONS BY FLUORIMETRIC AND MASS SPECTROMETRIC METHODS	Anita Dékány-Adamoczky
353	MASS SPECTRAL FILTERING BY MASS-REMAINDER ANALYSIS (MARA) AND ITS APPLICATION TO FLAVONOID SCREENING	Ákos Kuki
435	ANALYSIS OF POLYBUTADIENE POLYDISPERSITY BY ION MOBILITY COUPLED WITH A TIME OF FLIGHT MASS SPECTROMETRY	Caroline Damseaux
973	MALDI ANALYSIS OF NON-IONIC SURFACTANTS : STRUCTURAL CHARACTERIZATION AND MIXTURE ANALYSIS	Christelle Absalon
996	STRUCTURAL FEATURES AND COMPLEXATION PROPERTIES OF A SOLOMON LINK STUDIED BY ION MOBILITY MASS SPECTROMETRY	Anniina Kiesilä
857	HIGH RESOLUTION MS FOR SINGLE-USE SYSTEMS EXTRACTABLE AND LEACHABLE ANALYSIS	Kate Comstock
924	CONFIRMATION OF SYNTHESIS OF SPARINGLY SOLUBLE COMPOUNDS BY ACCURATE MALDI-TOF MASS SPECTROMETRY	Ei-ichi Matsuo
948	ION MOBILITY MASS SPECTROMETRY AS A TOOL TO STUDY STRUCTURAL CHEMISTRY OF METAL COORDINATION CAGES AND GOLD CLUSTERS	Eliina Kalenius
961	STRUCTURAL CHARACTERIZATION OF HARDWOOD XYLAN WITH DIRECT-INFUSION ESI FT-ICR MASS SPECTROMETRY	Janne Jänis
917	ELECTROCHEMISTRY MEETS IMAGING – ELECTRODE SURFACE ANALYSIS BY MEANS OF MALDI-TOF-MS	Arne Behrens

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Biosimilars, Biobetters and Glycoengineering		
Theme: Food and (Bio)Pharma		
#	Abstract Title	Presenter
126	USE OF PASEF FOR ACCELERATED PROTEIN SEQUENCE CONFIRMATION AND DE NOVO SEQUENCING WITH HIGH DATA QUALITY	Detlev Suckau
137	AUTOMATED ANNOTATION OF CLIPPING RELATED HETEROGENEITIES IN VEDOLIZUMAB	Christian Albers
149	FORCED DEGRADATION STUDY OF A MONOCLONAL ANTIBODY BY HRMS AT INTACT, SUBUNIT AND PEPTIDE LEVELS	Geert Van Raemdonck
574	ACCELERATED SOLVENT EXTRACTION AND ULTRA-HIGH PERFORMANCE LIQUID CHROMATOGRAPHY COUPLED WITH HIGH-RESOLUTION MASS SPECTROMETRY FOR THE ANALYSIS OF ADDITIVES IN POLYMERS FOR BIOMANUFACTURING PROCESSES	Sandra Rontree
743	ANTIBODY;GLYCAN	Andrea Krumm
890	A ROBUST WORKFLOW FOR BIOSIMILAR COMPARABILITY ASSESSMENT VIA INTACT AND SUBUNIT RPLC-MS AND NATIVE IEX-MS WITH A BENCHTOP QTOF	Jayne Kirk
889	BIOSIMILAR PEPTIDE MAPPING CHARACTERIZATION AND MAM WORKFLOW USING A BENCHTOP QTOF WITH AN APP-BASED ACQUISITION AND DATA PROCESSING PLATFORM	Jayne Kirk

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Imaging in Food & Pharma		
Theme: Food and (Bio)Pharma		
#	Abstract Title	Presenter
342	MICROPLASTIC CHARACTERIZATION IN SEAFOOD BY MASS SPECTROMETRY IMAGING	Lidia Molina Millán
350	SAMPLE PREPARATION STRATEGIES OF MUSHROOM AS A MODEL FOR FOOD QUALITY ASSESSMENT USING MASS SPECTROMETRY IMAGING	Mudita Vats
437	SPATIAL LOCATION OF MONOTERPENOID INDOLE ALKALOIDS IN RAUWOLFIA TETRAPHYLLA BY MALDI-MSI	Marcus Lorensen
557	PHARMACOKINETICS OF CATIONIC AMPHIPHILIC ANTIHISTAMINES IN CANCER MODELS STUDIED BY WHOLE-BODY DESI-MSI	Christian Janfelt
729	MULTIMODAL SPECTROSCOPIC IMAGING OF PLANT METABOLITES IN ROOT NODULES	Anna Sroka-Bartnicka
911	DETERMINATION OF N-NITROSO SALBUTAMOL IN SALBUTAMOL PRODUCTS BY LC-MS/MS	Jing Quan Lim
927	INVESTIGATION OF DRUG DISTRIBUTION IN RENAL TISSUE USING HIGH RESOLUTION MALDI MS IMAGING	Eva-Maria Stemp

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Toxicology and metabolism		
Theme: Food and (Bio)Pharma		
#	Abstract Title	Presenter
3	IDENTIFICATION AND CHARACTERIZATION OF IN VIVO, IN VITRO AND REACTIVE METABOLITES OF ZORIFERTINIB USING LIQUID CHROMATOGRAPHY ION TRAP MASS SPECTROMETRY	Nasser Alshakliah
33	A SENSITIVE LC-ESI-MS/MS METHOD FOR THE QUANTITATIVE DETERMINATION OF 54 PYRROLIZIDINE ALKALOIDS AND TWO TROPANE ALKALOIDS IN COWS' MILK	Lisa Klein
67	FATE OF TOXIC TROPANE AND PYRROLIZIDINE ALKALOIDS DURING FOOD PROCESSING OR STORING: CURRENT STATUS AND PERSPECTIVES	Florian Kaltner
75	HIGH-THROUGHPUT RESIDUAL SOLVENT ANALYSIS ACCORDING TO USP 467 USING SIFT-MS	Arnd Ingendoh
110	MICROWAVE-ASSISTED DESULFATION OF THE HEMOLYTIC SAPONINS EXTRACTED FROM HOLOTHURIA SCABRA VISCERA	Philippe Savarino
119	ELIMINATION PROFILE OF MICRODOSED ZILPATEROL MIMICKING CONSUMPTION OF CONTAMINATED CATTLE MEAT	Luisa Euler
428	EFFICIENT CHARACTERISATION AND RATIONALISATION OF METABOLITE STRUCTURES FOR BIOTRANSFORMATION STUDIES USING THE SELECT SERIES™ CYCLIC™ IMS INSTRUMENT	David Higton
496	APPLICATION OF MICRO PILLAR ARRAY COLUMNS FOR METABOLITE IDENTIFICATION	Arnaud Lubin
685	IN VITRO IDENTIFICATION OF PHASE I BIOTRANSFORMATION PRODUCTS OF NEW PLASTICIZERS WITH SUSPECT AND NON-TARGET SCREENING WORKFLOWS ON HIGH RESOLUTION MASS SPECTROMETRY	Adrian Covaci
945	PROFILING OF LIPID METABOLITE IN LIPID DROPLET REVEALS THAT LIPID DROPLETS ARE ESSENTIAL ORGANELLE IN HCV REPLICATION	Kwang-Hyeon Liu
971	ENHANCING THE ASSESSMENT OF FORMATION OF REACTIVE METABOLITES BY USING MSXELERATOR WITH DIFFERENT UNLABELED: STABLE ISOTOPE LABELED GLUTATHIONE ON SEVERAL HIGH RESOLUTION MASS SPECTROMETERS PLATFORMS	Marco Ruijken
841	INVESTIGATIONS INTO THE CONCENTRATION AND METABOLITE PROFILES OF ANABOLIC STEROIDS IN BLOOD PLASMA AND SEMINAL FLUID USING LIQUID CHROMATOGRAPHY- HIGH-RESOLUTION MASS SPECTROMETRY.	Johanna Breuer
859	AMINO FUNCTIONALIZED METAL-ORGANIC FRAMEWORK FOR MAGNETIC SOLID PHASE EXTRACTION COMBINED WITH HPLC-MS/MS FOR THE DETECTION OF PARABENS	Hui-Ling Lee

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Data sciences in MS / AI/ Chemometrics/identification/modelling		
Theme: Instrumentation and methods		
#	Abstract Title	Presenter
63	A NOVEL HIGH-RESOLUTION MASS SPECTROMETRY TOOLBOX FOR UNRAVELLING THE CHEMICAL EXPOSOME	Saer Samanipour
153	PATROON 2.0: NON-TARGET SCREENING WORKFLOWS FOR AUTOMATED TRANSFORMATION PRODUCT SCREENING AND OTHER MAJOR IMPROVEMENTS	Rick Helmus
237	SPATIAL PROBABILISTIC MAPPING OF METABOLITE ENSEMBLES IN MASS SPECTROMETRY IMAGING	Denis Abu Sammour
244	Δ MR: INTER-PEAK DISTANCE FOR SPECTRAL ALIGNMENT AND RESOLUTION ESTIMATION	Eduardo Jacobo Miranda Ackerman
281	VENDOR-NEUTRAL, BROWSER-BASED MS DATA PROCESSING	Anne Marie Smith
295	ANNOTINE: AUTOMATED WORKFLOW FOR MS1 ANNOTATION AND COMPARISON ACROSS IMAGING MASS SPECTROMETRY EXPERIMENTS.	Lukasz Migas
373	ACCURATE PREDICTION OF FRAGMENT INTENSITIES WITH N-DIMENSIONAL POLYNOMIAL REGRESSION FOR LIPID QUANTIFICATION	Kai Schuhmann
408	PEAKONLY: A PRECISE ALGORITHM FOR DETECTING PEAKS IN LC-MS DATA USING NEURAL NETWORKS	Vadim Yanshole
500	INCREMENTAL PRINCIPAL COMPONENT ANALYSIS WITH LOW MEMORY USAGE FOR LARGE MASS SPECTROMETRY IMAGING DATASET ANALYSIS	Kasper Krijnen
534	A UNIFYING, SPECTRUM-CENTRIC APPROACH FOR THE ANALYSIS OF PEPTIDE TANDEM MASS SPECTRA	Martin Frejno
536	AN END-TO-END MACHINE LEARNING WORKFLOW FOR MS-BASED PROTEOMICS	Martin Frejno
548	PREDICTION OF SCHEDULE AND GAS CHROMATOGRAPHIC RETENTION INDICES FOR GC/MS IDENTIFICATION OF CHEMICALS RELATED TO CHEMICAL WEAPONS CONVENTION BY MATCHED MOLECULAR PAIRS AND MACHINE LEARNING METHODS	Albert Kireev
564	ADDING A NEW DIMENSION TO SPATIAL OMICS: PYXIS, COMPREHENSIVE SOFTWARE FOR ION MOBILITY MS IMAGING DATA ANALYSIS	Sara Tortorella
577	FIDELITYCHECK™ SOFTWARE FOR IDENTIFICATION OF AMINO ACID VARIANTS IN RECOMBINANT AND PURIFIED PROTEINS	Tyler Fletcher
652	SHAPLEY VALUE AS A QUALITY CONTROL FOR MASS-SPECTROMETRY DATA	Denis Zavorotnyuk
725	PIPELINES AND SYSTEMS FOR THRESHOLD AVOIDING QUANTIFICATION OF LC-MS/MS DATA (PASTAQ)	Peter Horvatovich
741	GOING BEYOND SIMPLE LIBRARY SEARCHING: INCORPORATING ACCURATE M/Z, MOLECULAR WEIGHT AND CHROMATOGRAPHIC INFORMATION FOR QUALITATIVE ANALYSIS.	Robert Cody
745	COMPARISON OF GC-MS AND GCXGC-MS ANALYSIS OF VOLATILES AND PYROLYSIS PRODUCTS	Robert Cody
806	MACHINE LEARNING APPROACH FOR THE PREDICTION OF THE NUMBER OF SULFUR ATOMS IN PEPTIDES USING THE THEORETICAL AGGREGATED ISOTOPE DISTRIBUTION.	Annelies Agten
839	HANS 1.0: A VENDOR-INDEPENDENT ALGORITHM FOR DETECTION OF IMPURITIES	Kevin Kretschmer
860	A STATISTICAL FRAMEWORK FOR DECONVOLUTED ION CHROMATOGRAM FOR THERAPEUTIC OLIGONUCLEOTIDES	Piotr Prostko
895	IMPROVED HPLC-MS IDENTIFICATION OF SHORT PEPTIDES IN COMPLEX FOOD SAMPLES USING SEQUENCE-BASED RETENTION TIME PREDICTIONS	Boudewijn Hollebrands
983	MERGEION: A SOLUTION FOR BUILDING MULTIFUNCTIONAL R PIPELINES FOR PROCESSING, SEARCHING, AND ORGANIZING SMALL MOLECULE LC-MS/MS DATA	Youzhong Liu
879	POINTLESS4DNA: PREDICTION OF THE ISOTOPE DISTRIBUTION FOR AVERAGE DNA AND RNA MOLECULES	Melvin Geubbelmans
906	A MODERN APPROACH TO MASS SPECTROMETRY IMAGING DATA SEGMENTATION WITH SPATIAL-DGMM AND MASSERSTEIN	Michal Ciach
1011	ENVEMIND: ACCURATE MONOISOTOPIC MASS DETERMINATION BASED ON ISOTOPIC ENVELOPE	Piotr Radziński
974	NEW CCS PREDICTION WORKFLOW TO EXTEND MS/MS SPECTRAL LIBRARIES ON THE FLY WITH CCS INFORMATION	Matthew Lewis
891	IN-DEPTH ANALYSIS OF ELECTRON IONIZATION MASS SPECTRA OF MONOTERPENES WITH HELP OF MOLECULAR NETWORKS	Natan Horacek

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: High resolution mass spectrometry		
Theme: Instrumentation and methods		
#	Abstract Title	Presenter
1018	POLYMERS OF MICRO(NANO)PLASTIC IN HOUSEHOLD TAP WATER OF THE BARCELONA CITY (SPAIN)	Marinella Farre
849	DEVELOPMENT OF A CERTIFIED REFERENCE MATERIAL FOR THE DETERMINATION OF ARSENIC, LEAD AND MERCURY IN LIPSTICK	Deborah Sim
896	SEPARATION OF MONOMERIC FLAVONOIDS BY CYCLIC ION MOBILITY MASS SPECTROMETRY	Carlo De bruin
910	FLOW INJECTION ANALYSIS MASS SPECTROMETRY FOR HIGH THROUGHPUT QUANTIFICATION IN COMPLEX MATRICES	Wouter Coppes
952	DEVELOPMENT OF A LIQUID CHROMATOGRAPHY-HIGH RESOLUTION MASS SPECTROMETRY METHOD FOR THE FREE FATTY ACID PROFILING OF GREEK YOGURT	George Kokotos
809	DEVELOPMENT AND VALIDATION OF AN ANTIBIOTIC ANALYSIS METHOD IN THE BACTERIAL EXTRACTS BY ORBITRAP LC-HRMS	Christine Enjalbal
821	IMPURITY PROFILING OF ORGANIC BY-PRODUCTS OF A NEWLY DEVELOPED GD BASED CONTRAST AGENT	Sonja Weishaupt
834	MULTI-DISSOCIATIONS;MULTI-STAGE FRAGMENTATIONS;IQ-X TRIBRID MS	Kate Comstock
878	ENSURING CONFIDENT ANALYSIS OF EXTRACTABLES AND LEACHABLES SCREENING USING HIGH-RESOLUTION QUADRUPOLE TIME OF FLIGHT TECHNOLOGY	Rachel Sanig
904	SICYLIA-TMT: A MULTI-STEP LABELLING STRATEGY FOR GLOBAL REDOX PROTEOMICS	Sergio Lilla
928	TARGETED FORENSIC SCREENING AND SEMI-QUANTITATION OF DRUGS IN URINE USING A NOVEL HIGH-RESOLUTION ACCURATE-MASS MASS SPECTROMETER	Claudio De Nardi
980	DEVELOPMENT OF A LIQUID CHROMATOGRAPHY-HIGH RESOLUTION MASS SPECTROMETRY METHOD FOR THE LIPIDOMICS ANALYSIS OF FREE FATTY ACIDS IN HUMAN PLASMA OF HEALTHY AND DIABETIC SUBJECTS	George Kokotos
1006	A NOVEL STABLE ISOTOPE LABELING DATA PROCESSING WORKFLOW FOR LC-MS AND LC-TIMS-MS DATA	Sven Meyer
1019	LEVERAGING A HIGHER DUTY CYCLE DIA ACQUISITION FOR ENHANCED PROTEOMICS ANALYSIS ON A ZENOTOF 7600 FOR ENHANCED PROTEOMICS ANALYSIS	Katherine Tran
1021	A COMPLETE AND AUTOMATED SAMPLE PREPARATION STRATEGY FOR HIGH-THROUGHPUT AND STANDARDIZED PROTEOMICS APPLIED TO A CLINICAL COHORT OF PATIENT PLASMA SAMPLES	Nicolai Bache
1027	IMPLEMENTATION OF PASEF AND IMPROVED IONIZATION CHARACTERISTICS IN IMMUNOPEPTIDOMICS	Daniel Flender
972	IMPLEMENTATION OF CCS-M/Z TRENDLINES IN THE IDENTIFICATION PROCESS OF QUATERNARY AMMONIUM COMPOUNDS (QACS) IN INDOOR DUST SAMPLES THROUGH DRIFT TUBE ION-MOBILITY QUADRUPOLE TIME-OF-FLIGHT MASS SPECTROMETRY	Lidia Belova
992	QUANTIFICATION OF ENDOCANNABINOIDS USING A SOLID PHASE EXTRACTION IN COMBINATION WITH MICRO FLUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY (SPE- μ L-MS/MS)	Robert Gurke
262	DEVELOPMENT AND VALIDATION OF AN ANTIBIOTIC ANALYSIS METHOD IN THE BACTERIAL EXTRACTS BY ORBITRAP LC-HRMS	Christine Enjalbal
26	ACHIEVING PPM-MASS ACCURACY FOR IONS UP TO M/Z 17,000 WITH MATRIX-ASSISTED LASER DESORPTION/IONIZATION ON A TRAPPED ION MOBILITY-QUADRUPOLE-TIME-OF-FLIGHT MASS SPECTROMETER	Jürgen Gross
38	COMBINING THE DATA-DRIVEN AND HYPOTHESIS-DRIVEN APPROACHES IN ONE GO VIA A NOVEL INTELLIGENT DATA ACQUISITION HYBRID-DIA MASS SPECTROMETRY STRATEGY	Yue Xuan
52	ACCURATE MASS LIBRARY FOR NATURAL PRODUCTS BASED ON COMPOUNDS IDENTIFIED IN HEMP OIL	Sofia Nieto
147	HIGH THROUGHPUT SEQUENCE CONFIRMATION AND IMPURITY LOCALISATION OF SYNTHETIC OLIGONUCLEOTIDES USING MASS SPECTROMETRY (MS/MS AND MSE)	Chris Knowles
216	RHAMNOLIPID IDENTIFICATION AND STRUCTURAL CHARACTERIZATION IN COMPLEX BIOTECHNOLOGICAL SAMPLES BY SFC-HRMS/MS AND KENDRICK MASS DEFECT PLOTS	Anna Lipphardt
217	MS/MS BASED DISTINCTION OF GLYCOPEPTIDE ISOMERS	Joshua Maliepaard
274	HALOGENATED POPS NON-TARGETED SCREENING BY GC-APCI-HRMS AND ION MOBILITY SPECTROMETRY	Fan Yang
275	DEEPER AND HIGHER CONFIDENT ANNOTATION OF COMPLEX METABOLOMICS DATA BY COMPLEMENTARY LARGE-SCALE SPECTRAL LIBRARIES	Mohamed Elsadig
299	TEMPERATURE-CONTROLLED CYCLIC ION MOBILITY MASS SPECTROMETRY – A NOVEL ANALYTICAL STRATEGY FOR THE CHARACTERIZATION OF BIOPHARMACEUTICALS	Philipp Bittner
303	HIGHLY EXOTHERMIC PROTON TRANSFER REACTIONS FROM PROTONATED ARGON TO METHANOL AND ACETONE	Maximilian Münt
318	DEEP METAPROTEOME ANALYSIS USING A NEW AUTOMATED SAMPLE PREPARATION PLATFORM AND A VANQUISH NEO UHPLC SYSTEM COUPLED TO AN ORBITRAP ECLIPSE TRIBRID MASS SPECTROMETER WITH FAIMS PRO INTERFACE	Amirmansoor Hakimi
320	FROM UNKNOWN TO KNOWN: UTILITY OF HIGH QUALITY CURATED HRAM MSN SPECTRAL LIBRARIES AND REAL TIME LIBRARY SEARCH FOR HIGH CONFIDENCE ANNOTATION OF METABOLITES	Rahul Deshpande
323	INTELLIGENT DATA ACQUISITION WORKFLOW TO OPTIMIZE QUANTITATION OF LOW ABUNDANT METABOLITES IN HIGH QUANTITATIVE DYNAMIC RANGE SAMPLES	Bashar Amer
325	AN AUTOMATED SAMPLE PREPARATION PLATFORM FOR ROBUST MICRO-FLOW LC-MS PROTEOMICS ANALYSIS IN MAMMALIAN PERIPHERAL BLOOD MONONUCLEAR CELLS	Yang Liu
378	DECONVOLUTION OF HIGH RESOLUTION SPECTRA FOR TOP-DOWN PROTEOME	Anatoly Verenchikov
389	AN AUTOMATED END TO END SAMPLE PREPARATION PLATFORM FOR HUMAN PLASMA PROTEOMICS ANALYSIS	Woong Kim

396	PHOSPHOPEPTIDES: FLOW PEPTIDE SYNTHESIS AND STRUCTURAL CHARACTERIZATION BY CYCLIC IMS-MS	Adina Noemi Borbely
466	TWO APPROACHES TO IDENTIFY DIFFERENTIAL COMPONENTS BETWEEN TWO POLYMER SAMPLES BY USING INTEGRATED QUALITATIVE ANALYSIS WITH PYROLYSIS-GAS CHROMATOGRAPH MASS SPECTROMETRY AND DIRECT MASS ANALYSIS WITH FIELD DESORPTION MASS SPECTROMETRY	Yoshihisa Ueda
537	INVESTIGATING STRUCTURAL INTERCONVERSION OF GAS PHASE ISOMERS OF OLIGONUCLEOTIDES WITH TANDEM ION MOBILITY MASS SPECTROMETRY	Alexey Barkhanskiy
555	TOTAL CORRELATION MASS SPECTROMETRY (TOC-MS) ON A LINEAR ION TRAP	Nathan Cassidy
568	STREAMLINING WORKFLOW FROM CHARACTERIZATION TO QUALITY CONTROL OF THERAPEUTIC OLIGONUCLEOTIDES IMPURITIES ACROSS IPRP-LC-HRAM-MS PLATFORMS	Hao Yang
588	PHOTODISSOCIATION OF ATOMIC CLUSTERS IN A MULTI-REFLECTION TIME-OF-FLIGHT MASS SPECTROMETER	Paul Fischer
616	NITROGEN MUSTARDS-GLUTATHIONE CONJUGATIONS: IN VITRO STUDY	Nurhazlina Hamzah
620	NON-TARGETED ANALYSIS OF CHEMICALS MIGRATING FROM BEER CANS	Ana Kovačič
663	IMPROVEMENT OF DATA QUALITY IN FT-ICR MS ANALYSIS OF COMPLEX MIXTURES BY INDEPENDENT ACQUISITION AND PROCESSING OF TIME-DOMAIN TRANSIENT DATA	Alessandro Vetere
700	ESTABLISHING A HIGH THROUGHPUT WORKFLOW FOR COMPREHENSIVE YEAST PROTEOMICS	Marian Scherer

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Imaging MS - instrumentation and methods		
Theme: Instrumentation and methods		
#	Abstract Title	Presenter
134	HIGH RESOLUTION IMAGING PLATFORM INCORPORATING MALDI AND DESI	Mark Towers
79	ENHANCED LAAPPI-MS FOR IMAGING APPLICATIONS	Juha-Pekka Hieta
104	MS SPIDOC: MASS SPECTROMETRY MEETS SINGLE PARTICLE IMAGING	Thomas Kierspel
112	DESI AND/OR LA-REIMS? ADJACENT AUTOMATED AMBIENT TECHNIQUES FOR THE PRECISE IDENTIFICATION OF CANCER TISSUE	Gabriel Stefan Horkovics-Kovats
140	MS IMAGING OF INTACT 100 KDA MEMBRANE AND SOLUBLE PROTEIN ASSEMBLIES	Oliver Hale
178	MASS SPECTROMETRY IMAGING PROVIDES INSIGHTS INTO THE FATE OF CARNITINE AND ACYLCARNITINES IN ISCHEMIC MOUSE BRAIN	Leonidas Mavrouidakis
211	TOWARDS CELLULAR RESOLUTION OF TRYPTIC PEPTIDES IN MASS SPECTROMETRY IMAGING: A FOCUS ON ENZYME APPLICATION AND REPRODUCIBILITY	Bastian Jahreis
239	MALDI MASS SPECTROMETRY IMAGING WORKFLOWS FOR THE ECOTOXICOLOGICAL MODEL ORGANISMS DAPHNIA MAGNA, DANIO RERIO AND EISENIA FETIDA	Matthias Ochs
276	A FAST METHOD FOR LIPIDS SCREENING USING TLC AND MASS SPECTROMETRY IMAGING	Sophie Rappe
306	REVEALING ESGASTRIC CANCER SPECIFICITY BY MALDI-MS IMAGING AND SPIDERMASS	Lea Ledoux
332	FAST MOLECULAR PROFILING VIA TARGETED SINGLE-CELL MALDI MSI	Christian Croissant
333	SOFT-MATERIAL SURFACE SAMPLING WITH ULTRASONIC METHOD FOR MASS SPECTROMETRY	Ari Salmi
351	REVISITING THIN LAYER CHROMATOGRAPHY BY MASS SPECTROMETRY IMAGING AND IN SOURCE DECAY (ISD)	Edwin De pauw
352	INNOVATIVE MASS SPECTROMETRY APPROACH BASED ON MSI-GUIDED TARGETED METABOLOMIC TO IDENTIFY AND CHARACTERIZE NEW NATURAL PRODUCTS SPECIFIC TO BACTERIAL CO-CULTURE.	Pierre Burguet
363	DOPANT-ASSISTED MALDI-2-MSI: A DOUBLE BOOSTER FOR HIGHLY RESOLVED IMAGING OF LIPIDS AND METABOLITES	Christoph Bookmeyer
382	CORRELATIVE CHEMICAL IMAGING TO UNDERSTAND NEURITIC PLAQUE PATHOLOGY IN ALZHEIMERS DISEASE	Jörg Hanrieder
442	MASS SPECTROMETRY OF CHIRAL MIXTURES BY MICRO-GC CHIRAL-MS	Maurice Janssen
597	LASER DESORPTION – RAPID EVAPORATIVE IONISATION MASS SPECTROMETRY, A NOVEL METHOD FOR SAMPLE PREP-FREE TISSUE IMAGING AND CANCER SURGERY	Daniel Simon
600	THE CUMULATIVE INFLUENCE OF SALT ADDITIVES COUPLED WITH MATRIX SUBLIMATION/RECRYSTALLIZATION ON MALDI LIPIDS IMAGING	Mariya Shamraeva
628	TAKING A CLOSER LOOK AT SAMPLE PREPARATION FOR LIPID DETECTION IN MALDI MSI USING DIFFERENT SPRAYING DEVICES	Peter Sandbichler
632	THE OPTIMAL PARAMETERS OF FLOW FOCUSING MECHANISM FOR MASS SPECTROMETRY IMAGING OF CLINICAL SAMPLES	Vincen Wu
661	THE SEPARATION OF HOMOGENEOUS REGIONS OF INTEREST IN MASS SPECTROMETRY IMAGING DATA WITHOUT DIMENSION REDUCTION	Stanislav Pekov
708	MULTIDRUG QUANTIFICATION BY MALDI-MSI	Michael Tuck
720	COMPARISON OF MAPPING STRATEGIES IN LA-ICPMS: SINGLE PULSE, MULTIPLE DOSAGE, AND 2D OVERSAMPLING / DECONVOLUTION	Martin Šala
727	ACCURATE PRE-PROCESSING OF MASS SPECTROMETRY IMAGING DATA WITH HIGH SPECTRAL RESOLUTION	Peter Horvatovich
734	AP-SMALDI ORBITRAP IMAGING OF SMALL AND COMPLEX BIOLOGICAL OBJECTS	Bernhard Spengler
970	STUDYING THE METALLOME AT SINGLE CELL LEVEL BY LA-ICP-TOFMS IMAGING - A PROOF OF PRINCIPLE STUDY IN MACROPHAGE SUBTYPES	Anna Schoeberl
803	HIGH RESOLUTION IMAGING PLATFORM INCORPORATING MALDI AND DESI	Mark Towers
916	COMBINING FORCES OF TISSUE IMAGING, SHOTGUN AND NANOLC-MALDI ULTRA-HIGH-RESOLUTION-MASS SPECTROMETRY (UHR-MS): A UNIQUE WORKFLOW FOR UNTARGETED BIOMARKER DISCOVERY AT SANOFI, A STRATEGIC VIEW	Bogdan Munteanu
956	RECENT METHODOLOGICAL DEVELOPMENTS AND APPLICATIONS OF MALDI-2 MASS SPECTROMETRY IMAGING	Klaus Dreisewerd
1020	DEVELOPMENT OF A FULL MSI-LC-MS/MS WORKFLOW FOR LIPID LOCALIZATION, QUANTIFICATION AND IDENTIFICATION IN A PARKINSON'S DISEASE MODEL	Tim Hendriks
898	MICROGRID TECHNOLOGY FOR ROBUST HIGH LATERAL RESOLUTION IMAGING DOWN TO THE (SUB)CELLULAR LEVEL	Arne Behrens
932	SPATIAL METABOLOMICS ON A NOVEL DUAL-FUNNEL LDI – ORBITRAP EXPLORIS FOR MATRIX- AND SURFACE-ASSISTED LASER DESORPTION IONIZATION MS IMAGING	Christoph Bookmeyer
940	FROM LIPIDS AND DRUGS TO PROTEINS: IDENTIFYING CO-LOCALIZED MOLECULES ACROSS MULTIPLE CLASSES USING MALDI-HIPLEX-IHC	Joshua Fischer
997	SPATIALOMX AT ITS BEST: COMPARISON OF DIFFERENT STAINING PROCEDURES AND SLIDE TYPES	Corinna Henkel
1033	DNA-BARCODED SIGNAL AMPLIFICATION FOR IMAGING MASS CYTOMETRY ENABLES SENSITIVE AND HIGHLY MULTIPLEX TISSUE IMAGING	Bernd Bodenmiller

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Ion Spectroscopy, physical and chemical principles underlying MS (fundamentals)		
Theme: Instrumentation and methods		
#	Abstract Title	Presenter
29	DERIVING ENERGETICS OF POLYMETALLIC COMPLEXES WITH ION MOBILITY MASS SPECTROMETRY	Niklas Geue
74	GAS PHASE INVESTIGATION OF CONCAVE-CONVEX INTERACTIONS BETWEEN C60 AND SADDLE-SHAPED Π -EXTENDED PORPHYRINS	Johanes Oschwald
105	DISSOCIATION BEHAVIOUR OF DOUBLY FUSED N-HTA SCAFFOLDS IN THE GAS-PHASE STUDIED BY ESI-MS/MS	Marina Kinzelmann
199	INVESTIGATION OF STRUCTURE-STABILIZING ELEMENTS IN PROTEINS BY ION MOBILITY MASS SPECTROMETRY AND COLLISION-INDUCED UNFOLDING	Edwin De Pauw
233	TOWARDS ROUTINE INFRARED ION SPECTROSCOPY IN THE ANALYTICAL LABORATORY	Giel Berden
330	COVALENT MODIFICATION OF LYSINES: IMPACT OF MODIFICATIONS AND THEIR MASS ON ION MOBILITY AND COLLISIONAL INDUCED UNFOLDING OF PROTEINS	Thomas Tilmant
480	DEVELOPMENT OF A NEW ELECTROSPRAY IONIZATION TIME-OF-FLIGHT MASS SPECTROMETER FOR CHIROPTICAL STUDIES	Peter Krüger
501	METASTABLES AS A CAUSE FOR BASELINESHIFT IN QUADRUPOLE MASS ANALYZERS	Markus Langner
514	STUDYING THE KEY INTERMEDIATE OF RNA AUTOHYDROLYSIS BY CRYOGENIC GAS-PHASE INFRARED SPECTROSCOPY	Kim Greis
516	MASS SPECTROMIC PRODUCT STUDY IN THE INTERACTION OF SELECTED METAL SURFACES WITH H ₂ PLASMA GENERATED SPECIES	Joshua Rieger
527	MOLECULAR DYNAMIC SIMULATION OF ESI DROPLET FRAGMENTATION IN MS VACUUM STAGES	Leonie Grashoff
528	AN INVESTIGATION OF FRAGMENTATION MECHANISM ON NIFEDIPINE-TYPE NITRO-CONTAINING MOLECULES BY TANDEM MASS SPECTROMETRY AND ION MOBILITY SPECTROMETRY	Peiliang Han
598	EFFECTS OF ESI SOURCE PARAMETERS ON CHARGED DROPLETS OBSERVED IN API-MS SYSTEMS	Laura Lehmann
655	IDENTIFICATION OF DRUG METABOLITES WITH INFRARED ION SPECTROSCOPY – APPLICATION TO IN VITRO INCUBATIONS OF MIDAZOLAM	Rianne van Outersterp
657	STRUCTURAL ELUCIDATION IN MALDI MASS SPECTROMETRY IMAGING WITH INFRARED ION SPECTROSCOPY	Jelle Schuurman
671	KINETICS AND THERMODYNAMICS INSIGHTS IN CONFORMATIONAL RELAXATION FROM TRAP AND RELEASE TANDEM-IMS MEASUREMENTS	Fabien Chivot
736	STRUCTURAL CHARACTERIZATION BASED ON ISOTOPIC SHIFTS IN HIGHRESOLUTION ION MOBILITY/MASS SPECTROMETRY SPACE	Alexandre Shvartsburg
852	INTEGRATION OF A VARIABLE SOFT SPHERE COLLISION MODEL INTO THE IDSIMF ION TRAJECTORY SIMULATION FRAMEWORK	Sanna Benter
855	IMPLEMENTATION OF A MOLECULAR DYNAMICS COLLISION MODEL FOR DETERMINATION OF ION MOBILITIES IN THE ION DYNAMICS SIMULATION FRAMEWORK (IDSIMF)	Michelle Rajkovic
894	BAND CROSSING EVIDENCE IN PB1-XSNXTE OBSERVED BY SIMS MEASUREMENTS	Zeinab Khosravizadeh
938	COLLISION CROSS SECTIONS OF POLYOXOMETALATE ANIONS AND DETERMINATION OF LENNARD-JONES INTERACTION PARAMETERS OF MO AND W IN HE AND N ₂	Hélène Lavanant
966	GAS-PHASE FRAGMENTATION OF METALLO-SUPRAMOLECULAR AGGREGATES	Marianne Engeser
995	MASS SPECTROMETRY AS AN ALTERNATIVE TO NMR SPECTROSCOPY FOR SOLUTION STUDIES	Quentin Duez
756	TOF-SIMS;OLED;MATRIX	Pierre Hirchenhahn
776	EFFECT OF DIFFERENT DOPANTS ON THE SENSITIVITY OF ION MOBILITY-MASS SPECTROMETRY TOWARD AUXIN PLANT HORMONES	Vahideh Ilbeigi
831	DETECTION OF THE RARE GALACTOFURANOSE SUGAR IN LICHEN POLYSACCHARIDES USING MS-IR SPECTROSCOPY	Oznur Yeni
905	FORMATION AND STABILITY OF HOST-GUEST COMPLEXES BETWEEN CYCLOPARAPHENYLENES AND CROWN ETHERS	Lei Ye

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Ionization technologies		
Theme: Instrumentation and methods		
#	Abstract Title	Presenter
877	REACTANT ION POPULATION IN HIGH KINETIC ENERGY ION MOBILITY SPECTROMETRY (HIKE-IMS) AT VARYING CORONA IONIZATION SOURCE VOLTAGE AND OPERATING PRESSURE	Florian Schlottmann
903	ENHANCING PROTEOME COVERAGE USING NEGATIVE ION MODE PROTEOMICS	Pelayo Alvarez penanes
955	COLDSPRAY IONIZATION-MS: THE SEARCH FOR A MISSING LINK IN AN ARTIFICIAL PHOTOSYNTHESIS MODEL	Noemí Cabello
990	IMPROVED SENSITIVITY FOR LOW ABUNDANT LIPIDS USING A VACUUM INSULATED HEATED ESI SOURCE	Matthias Szesny
39	APCI, APPI, APLI, AND LTP: UNCOMMON IONISATION METHODS FOR GC-MS	Oliver Schmitz
118	STRUCTURAL CHARACTERIZATION OF SUBSTANCE P USING GOLD NANOPARTICLES IN SALDI "IN-SOURCE DECAY" MASS SPECTROMETRY	Gauthier Eppe
201	FRAGMENTATION OF PRODUCT IONS IN HIGH KINETIC ENERGY ION MOBILITY SPECTROMETRY	Christoph Schäfer
222	COUPLING DROPLET-BASED MICROFLUIDICS WITH ION MOBILITY-MASS SPECTROMETRY TO STUDY THE EARLY STEPS OF PROTEIN AGGREGATION	Iuliia Stroganova
248	INTELLIGENT INTERNAL RECALIBRATION	Harry Taylor
293	OPTIMIZATION OF HUMAN PLASMA PROTEOME HIGH-THROUGHPUT ANALYSIS USING FAIMS PRO INTERFACE	Dana Hein
297	A NOVEL EI SOURCE OPTIMIZED FOR USE WITH HYDROGEN CARRIER GAS IN GC/MS AND GC/MS/MS	Bruce Quimby
487	SIGNATURES OF LIQUID DROPLETS FROM ELECTROSPRAY IN THE MASS ANALYZER REGION OF AN COMMERCIAL ESI-TOF-MS	Chris Heintz
493	3D PRINTED OFFLINE NANO-ELECTROSPRAY IONIZATION SOURCE FOR BRUKER MASS SPECTROMETERS	Michael Götz
497	SOLVENT EFFECT AND COMPETITIVE REACTIONS IN AN ATMOSPHERIC PRESSURE CHEMICAL IONIZATION ION SOURCE	Younes Valadbeigi
524	CONTROL OF METAL ADDUCT FORMATION IN ELECTROSPRAY AND ITS BENEFITS FOR ELECTRON INDUCED DISSOCIATION AND DIFFERENTIAL MOBILITY SPECTROMETRY	David Ruskic
543	DETECTION OF EXPLOSIVES FROM VAPOUR PHASE UTILIZING MION INLET EQUIPPED API-TOF-MS	Paxton Juuti
580	PERMEATION TUBE ASSISTED REAGENT ION MANIPULATION ON A GC-EC-TOF FOR IMPROVED NON-TARGET ANALYSIS APPROACHES	Sonja Klee
670	INTACT LIPID MOLECULAR-CATIONS AND -ANIONS OF REACTIVE COMPOUNDS	Mathias Linden
682	MULTI-SCHEME CHEMICAL IONIZATION INLET (MION) FOR ATMOSPHERIC PRESSURE CHEMICAL IONIZATION MASS SPECTROMETRY (CIMS) APPLICATIONS	Jyri Mikkilä
684	PESTICIDES RESIDUE PRE-SCREENING USING KARSA MION INLET COUPLED TO MS WITH SELECTIVE CHEMICAL IONIZATION	Fariba Partovi
702	QUALITATIVE AND QUANTITATIVE DISTINCTION OF ISOMERS BY MEANS OF CHIRPED FEMTOSECOND LASER IONIZATION	Karl-Michael Weitzel

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Miniaturization, lab-on-a-chip, in situ applications		
Theme: Instrumentation and methods		
#	Abstract Title	Presenter
683	FURTHER STEPS IN MINIATURIZED TISSUE SAMPLING WITH A NANOSECOND INFRARED LASER (NIRL) FOR QUANTITATIVE PROTEOMICS	Jan Hahn
871	MODIFIED TARGET SURFACE TO ENHANCE PERFORMANCE DURING MALDI ANALYSIS	Andreas Baumeister
1001	MINIATURIZATION OF 3D TISSUE SAMPLING WITH A NANOSECOND INFRARED LASER (NIRL) FOR DIFFERENTIAL QUANTITATIVE PROTEOMICS	Antonia Gocke
969	INCREASING SENSITIVITY IN PROTEOMICS REQUIRED ALSO DECREASING SAMPLE ADSORPTION ON CONTAINER SURFACES	Wafa Hechiche
810	QUANTIFICATION OF ENDOCANNABINOIDS IN HUMAN CEREBROSPINAL FLUID USING A NOVEL MICRO-FLOW LIQUID CHROMATOGRAPHY-MASS SPECTROMETRY METHOD	Thomas Hankemeier

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Metabolomics		
Theme: Life Sciences & Health		
#	Abstract Title	Presenter
19	NMR BASED CSF METABOLOMICS IN TUBERCULOUS MENINGITIS: CORRELATION WITH CLINICAL AND MRI FINDINGS	Rashmi Parihar
23	ANTI-INFLAMMATORY EFFECTS OF HOP BITTER ACIDS IN DENTRITIC CELLS REVEALED BY MRMS METABOLOMIC STUDIES	Matthias Witt
37	ACCURATE MASS SPECTRAL AND RETENTION INDEX LIBRARY FOR METABOLOMICS BASED ON QUADRUPOLE TIME-OF-FLIGHT GAS CHROMATOGRAPHY/MASS SPECTROMETRY	Sofia Nieto
50	SUPERCHARGING IN LC-MS/MS HORMONE ANALYSES: ENHANCING IONIZATION, NOT SENSITIVITY	Vera de Kleijne
69	METABOLIC SIGNATURE PANEL SURROGATES THE HUMAN DRUG EXPOSURES - A METFORMIN MODEL	Anas Abdel Rahman
171	THE USE OF DRIED BLOOD SPOT SAMPLE FOR LC-MS/MS MONITORING OF PATIENTS WITH TYROSINEMIA TYPE I.	Josef Bartl
182	INVESTIGATIONS INTO THE IN VITRO METABOLISM OF HGH AND IGF-I EMPLOYING STABLE-ISOTOPE LABELLED DRUGS AND MONITORING DIAGNOSTIC IMMONIUM IONS BY HIGH RESOLUTION/HIGH ACCURACY MASS SPECTROMETRY	Sophia Krombholz
337	DEVELOPMENT, VALIDATION AND APPLICATION OF AN LC-MS/MS METHOD TO INVESTIGATE THE ROLE OF GLUTAMINE: GLUTAMATE RATIO AS A POTENTIAL DIAGNOSTIC BIOMARKER IN A HEART FAILURE COHORT	Helen Jordan
440	APPLICATION OF THE HRMS TO METHOD DEVELOPMENT AND VALIDATION OF THE QUANTITATION OF TECOVIRIMAT IN HUMAN PLASMA.	Alexander Chernonosov
444	DEVELOPMENT AND VALIDATION OF A MULTIPLE REACTION MONITORING METHOD TO DETERMINE TECOVIRIMAT AS THE PRIMARY NIOCH-14 METABOLITE IN HUMAN PLASMA.	Galina Zakabluk
477	INTEGRATION OF METABOLOMICS RESEARCH INTO TRANSLATIONAL CLINICAL CARE: CEREBROSPINAL FLUID BIOMARKERS FOR NEUROINFLAMMATION	Jinni Jingya Yan
478	GC-MS ANALYSIS OF A NEW 20-KETO-STEROID S42	Hui-Chung Wen
491	ENHANCED 4D WORKFLOWS USING TIMS FOR ADVANCING SMALL MOLECULE RESEARCH	Aiko Barsch
517	TANDEM MASS SPECTRAL LIBRARY IN METABOLOMICS: FRAGMENTATION SPECTRA OF SODIATED SPECIES AS ADDITIONAL AND VALUABLE METABOLITE IDENTIFIER	Annelaure Damont
521	MULTIDIMENSIONAL SEPARATION IN METABOLOMICS BASED ON DIFFERENTIAL MOBILITY SPECTROMETRY WITH BINARY MODIFIERS AND HIGH RESOLUTION MASS SPECTROMETRY	Lysi Ekmekciu
590	CCS-ENABLED TIMSTOF PRO WORKFLOW FOR IN VITRO HUMAN LIVER MICROSOME DRUG METABOLITES PROFILING AND CHARACTERIZATION	Xuejun Peng
593	DISTINCTIVE METABOLOMICS PATTERN ASSOCIATED WITH HYPERTHYROIDISM TREATMENT	Hicham Benabdelkamel
594	HIGH RESOLUTION ION MOBILITY TIMSTOF PRO FOR THE FAST SEPARATION AND CHARACTERIZATION OF ISOMERIC BILE ACIDS	Xuejun Peng
619	CCS-ENABLED TIMSTOF PRO WORKFLOW FOR IN VITRO HUMAN LIVER MICROSOME DRUG METABOLITES PROFILING AND CHARACTERIZATION	Xuejun Peng
662	PHYSIOLOGICAL AND POSTTRAINING EFFECTS OF TAKING ECDYSTEROIDS SUPPLEMENT. A MULTIVARIATE ANALYSIS OF THE HUMAN SERUM METABOLOME	Patrizia Leogrande
672	UTILIZATION OF DUAL COLUMN LC-HRMS FOR NON-TARGETED METABOLOMICS TO INVESTIGATE ALTERED ROOT EXUDATE EXPRESSION IN THE PRESENCE OF PLANT NEIGHBORS	Alexandra Bennett
946	EVALUATION THE DRUG-INDUCED LIVER INJURY POTENTIAL OF SAXAGLIPTIN THROUGH THE IDENTIFICATION OF REACTIVE METABOLITES	Kwang Hyeon Liu
947	IN VIVO METABOLISM OF DONEPEZIL IN RATS USING NON-TARGETED METABOLOMICS	Kwang-Hyeon Liu
949	ASSOCIATION OF TRYPTOPHAN PATHWAY-RELATED METABOLITES: DEPLETION OF DIETARY ARYL HYDROCARBON RECEPTOR LIGANDS INDUCED ATOPIC DERMATITIS IN MICE	Jeeyoun Jung
943	METABOLIC SIGNATURE OF ETHANOL-INDUCED HEPATOTOXICITY IN HEPARG CELLS BY LC-MS- BASED UNTARGETED METABOLOMICS	Elias Iturrospe
976	METABOSCAPE AS A QUALITY-FOCUSED SOFTWARE SOLUTION FOR EXPLORING METABOLIC PROFILING DATASETS	Nikolas Kessler
991	STUDY AND STATISTICAL ANALYSIS OF SMALL MOLECULES IN SNAKE VENOM	Luis Alonso
1012	A MULTI-ACQUISITION-MODE STRATEGY FOR IN-DEPTH METABOLOMICS ANALYSIS	Katherine Tran
1017	COMPREHENSIVE METABOLITE CHARACTERIZATION USING ORTHOGONAL MS/MS DATA	Katherine Tran
984	ENHANCED UNTARGETED METABOLOMICS WORKFLOW USING LC-QTOF AND METABOSCAPE FOR ANALYSIS OF GUT MICROBIAL METABOLISM	Erica Forsberg
842	DIFFERENTIATION OF AYAHUASCA SAMPLES ACCORDING TO ORIGIN AND RELIGIOUS GROUPS USING MULTIVARIATE STATISTICAL ANALYSIS OF LC-MS DATA	Taynara Matos
738	FINGERPRINTING OF TEA VARIETIES USING A NOVEL UNTARGETED METABOLOMICS WORKFLOW	Daniel Hermanson
747	NEW PEAK DETECTION (PYCO) AND ISOTOPE GROUPING (PRISM) ALGORITHMS FOR AN IMPROVED COMPOUND DETECTION WORKFLOW	Pedro Navarro
817	MICROBIAL DEGRADATION OF HYALURONAN: STABLE ISOTOPE LABELLING STRATEGY	Matěj Šimek
827	A NOVEL LC-MS/MS METHOD FOR THE DETERMINATION OF SELECTED VITAMIN D METABOLITES AND ITS CLINICAL APPLICATION	Ludmila Máčová
838	RAPID EVAPORATIVE IONISATION MASS SPECTROMETRY (REIMS) FOR OXIDATIVE STRESS BIOMARKER DISCOVERY IN PSEUDOMONAS AERUGINOSA	Rob Bradley
771	TECHNOLOGIES FOR CHARACTERIZATION, DETECTION AND ISOLATION OF EXTRACELLULAR VESICLES AS BIOMARKERS	Masood Kamali-Moghaddam

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: MS in Structural biology - Crosslinking MS		
Theme: Life Sciences & Health		
#	Abstract Title	Presenter
885	STRUCTURAL REFINEMENT OF THE TUMOR SUPPRESSOR P53 BY MASS SPECTROMETRY- GUIDED COMPUTATIONAL MODELING	Christian Ihling
32	STUDYING NUCLEOTIDE AND NUCLEOTIDE - PROTEIN PHOTO-CROSSLINKING USING CRYOGENIC IR SPECTROSCOPY	Kevin Pagel
177	A PROTEIN-NUCLEIC ACID CROSSLINKING NODE FOR PROTEOME DISCOVERER 2.5 SOFTWARE	Bernard Delanghe
384	CROSS-LINKING MASS SPECTROMETRY ON P-GLYCOPROTEIN	Gabriella Gellen
407	BLUE LIGHT PHOTOACTIVATABLE DIAZO COMPOUNDS AS A NOVEL CROSS-LINKING REACTIVE GROUP	Fabio Gozzo

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Proteomics: Post-translational modifications and their cross-talk		
Theme: Life Sciences & Health		
#	Abstract Title	Presenter
27	PERSONALIZED (GLYCO)PROTEOGENOMIC FEATURES OF THE SERUM HISTIDINE-RICH GLYCOPROTEIN REVEALED BY MASS SPECTROMETRY	Yang Zou
95	IN-DEPTH CHARACTERIZATION OF THE CLOSTRIDIODES DIFFICILE PHOSPHOPROTEOME TO IDENTIFY SER/THR KINASE SUBSTRATES	Mariette Matondo
99	CHARTING THE PROTEOFORM LANDSCAPE OF THE SERUM PROTEINS BY HIGH-RESOLUTION NATIVE MASS SPECTROMETRY	Dario Cramer
416	INTEGRATED MASS SPECTROMETRY-BASED PIPELINE FOR CHARACTERIZATION OF TAU IN HUMAN ALZHEIMER'S BRAIN: DEVELOPMENT AND COMPARISON OF SAMPLE PREPARATION METHODS	Rita Azevedo
475	THE TRYPTOPHAN IMMONIUM ION IS A MARKER FOR INSECT ADIPOKINETIC HORMONES	Simone König
1014	ANALYSIS OF POST-TRANSLATIONAL MODIFICATIONS USING FAST ELECTRON ACTIVATED DISSOCIATION (EAD)	Katherine Tran
929	EFFECTS OF AGEING AND CALORIE RESTRICTION ON ROS-INDUCED PROTEIN DAMAGE IN MITOCHONDRIA OF DIFFERENT TISSUES FROM RATTUS NORVEGICUS	Ansgar Poetsch
968	PHOSPHOPROTEOME DYNAMICS IN RESPONSE TO SYNAPTIC UP- & DOWN-SCALING	Kristina Desch

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Proteomics: Quantification		
Theme: Life Sciences & Health		
#	Abstract Title	Presenter
858	SIMULTANEOUS DETECTION AND QUANTIFICATION OF ANGIOTENSIN I, II, 1-7 AND 1-9 BY LC-MS/MS IN HUMAN PLASMA	Loreen Huyghebaert
1004	QUANTIFICATION OF THERAPEUTIC MONOCLONAL ANTIBODIES IN HUMAN PLASMA BY MEASURING THE INTACT LIGHT CHAIN USING 2D-LC ORBITRAP HRMS	Magnus Olin
853	MASS SPECTROMETRY-BASED DIFFERENTIAL QUANTITATIVE PROTEOMICS OF INFLAMED MURINE AND HUMAN BLADDERS FOR THE IDENTIFICATION OF BIOMARKERS AND NOVEL TARGETS TO TREAT URINARY TRACT INFECTIONS	Bente Siebels
875	IMPROVING THE QUANTIFICATION OF HEAVY ISOTOPE-LABELLED HISTONE SPECIES	Thomas Mair
886	LONGITUDINAL PROTEOTYPING OF PLASMA FROM ACUTE COVID-19 PATIENTS USING PARALLEL MRM AND DIA METHODS	Yassene Mohammed
893	QUANTIFICATION OF ASIALOGLYCOPROTEIN RECEPTOR SUBUNITS IN HBV INFECTED AND NON-INFECTED MICE LIVER USING LIQUID CHROMATOGRAPHY TANDEM MASS SPECTROMETRY (LC-MS/MS)	Emmanuel Njunge Ediage
897	PHARMACOLOGICAL INFLUENCE ON THE NEURONAL PROTEOME AS A PATHOPHYSIOLOGICAL TRIGGER FOR THE DEVELOPMENT OF MENTAL ILLNESS, ESPECIALLY DEPRESSION	Sam Thilmany
923	GLOBAL ANALYSIS OF INTEGRATED ACYLOME PROFILING IN SEPSIS	Sangkyu Lee
988	PHOSPHOPROTEOMICS PROFILING OF BLADDER CANCER FOR THE DISCOVERY OF ANTI-METASTASIS PATHWAY	Sangkyu Lee
787	COMPARING THE PROTEOMES OF SPATIALLY RESOLVED EPITHELIAL CELL REGIONS AND WHOLE LUNG TISSUE TO STUDY ACUTE EPITHELIAL LUNG INJURY IN MICE	Eva Griesser
833	SINGLE CEREBRAL ORGANOID MASS SPECTROMETRY ANALYSIS: TOWARDS NEURODEGENERATIVE DISEASES	Marketa Nezvedova
55	FASTCAT WORKFLOW FOR CONSISTENT AND MULTIPLEXED ABSOLUTE QUANTIFICATION OF PROTEINS IN CLINICAL SAMPLES	Ignacy Rzagalinski
123	BENCHMARKING THE QUANTITATIVE ACCURACY OF LABEL-FREE PROTEOMICS BY DIA	Tobias Jumel
158	ABSOLUTE QUANTIFICATION OF 500 HUMAN PLASMA PROTEINS IN COLON CANCER PLASMA SAMPLES BY PRM-PASEF.	Pierre-Olivier Schmit
179	MASS SPECTROMETRY-BASED PROTEOMICS BIOMARKER DISCOVERY IN A CORONARY ARTERY DISEASE COHORT	Colleen Maxwell
234	SWEAT PROTEOMICS IN CYSTIC FIBROSIS AND COVID-19 – TOWARDS PROTEIN BIOMARKERS FOR NON-INVASIVE, PRECISION MEDICINE	Bastien Burat
261	THE TEMPORAL PROTEOME DYNAMICS OF THE MODEL EUKARYOTE YEAST DURING GLUCOSE EXHAUSTION	Maxime den Ridder
269	MULTIPLEX QUANTIFICATION OF TAU PROTEOFORMS BY MASS SPECTROMETRY FOR THE DIFFERENTIAL DIAGNOSIS OF NEURODEGENERATIVE DISEASES	Jacquemin Chloé
273	MULTIPLEXED LC-HRMS/MS QUANTIFICATION OF NINE SEPSIS PROTEIN BIOMARKERS IN HUMAN SERUM	Maxence Derbez-Morin
296	DETERMINATION OF FOOD AUTHENTICITY OF INSECT-BASED NOVEL FOODS BY MASS SPECTROMETRY-BASED IMMUNOASSAYS	Oliver Poetz
314	QUANTITATIVE ANALYSIS OF PHOSPHORYLATED PROTEINS FROM MULTIPLE SIGNALING PATHWAYS USING THE TMT AND SUREQUANT TARGETED MASS SPECTROMETRY ASSAY PANEL REAGENTS	Bhavin Patel
315	AN AUTOMATED SAMPLE PREPARATION SOLUTION FOR MASS SPECTROMETRY-BASED PROTEOMICS	Maowei Dou
319	HIGH-THROUGHPUT PROTEOMIC ANALYSIS OF STORED RED BLOOD CELLS FROM NON-DOMESTIC CAT SPECIES	Amirmansoor Hakimi
359	MS-BASED ASSAY FOR THE DETERMINATION OF NATRIURETIC PEPTIDES IN SALIVA AND PLASMA SAMPLES	Alessio Lenzi
413	A HIGH-THROUGHPUT LABEL-FREE QUANTITATIVE PROTEOMICS PLATFORM TO SPEED-UP MICROBIAL STRAIN CHARACTERIZATION	Nicolas Abello
414	QUALITATIVE AND QUANTITATIVE CHARACTERIZATION OF ELASTIN-LIKE POLYPEPTIDES COMBINING A NOVEL PROALANASE BOTTOM-UP APPROACH AND INTACT PROTEIN ANALYSIS	André Vente
664	COMPARATIVE ASSESSMENT OF QUANTIFICATION METHODS FOR TUMOR TISSUE PHOSPHOPROTEOMICS	Kathrin Thedieck
689	ADDRESSING THE CHALLENGES OF PROTEOMICS DATA PROCESSING TO SUPPORT DRUG DISCOVERY AND DEVELOPMENT	Giuseppe Infusini

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Proteomics: Top down		
Theme: Life Sciences & Health		
#	Abstract Title	Presenter
49	MULTIDIMENSIONAL MULTIPLE-STAGE TOP-DOWN ANALYSIS OF INTACT NON-REDUCED ANTIBODIES IN THE OMNITRAP PLATFORM COUPLED TO ORBITRAP MASS SPECTROMETRY	Athanasios Smyrnakis
64	TISSUE-BASED PROTEOMIC PROFILING IN HYPERPLASIA AND ENDOMETRIAL CANCER PATIENTS	Hicham Benabdelkamel
68	RANA ARVALIS: PEPTIDOMES COMPARISON OF CENTRAL SLOVENIAN AND MOSCOW REGION POPULATIONS	Irina Vasileva
87	PERSONALIZED LONGITUDINAL MONITORING OF SERUM IGG1 AND IGA1 REPERTOIRES IN SEVERE COVID-19 PATIENTS PROVIDES A VIEW AT PATIENT SPECIFIC IMMUNE RESPONSES	Max Hoek
98	MANIPULATING CHARGE STATE AND CHARGE SITES TO IMPROVE TOP-DOWN FRAGMENTATION	Tanja Habeck
152	NATIVE LESA MASS SPECTROMETRY OF INTACT PROTEINS AND PROTEIN COMPLEXES DIRECTLY FROM LIVING BACTERIAL COLONIES	Yuying Du
197	UTILIZATION OF FAST PHOTO-OXIDATION OF PROTEINS AND TOP DOWN MASS SPECTROMETRY FOR STRUCTURAL CHARACTERIZATION OF PROTEINS	Petr Novak
207	THERE BE DRAGONS: THE DANGERS ASSOCIATED WITH ASSIGNING INTERNAL FRAGMENT IONS OF PROTEINS	David Kilgour
289	SQUEEZE EVERY DROP	Bruno Bellina
326	ENABLING THE HIGH-THROUGHPUT ANALYSIS OF LARGER PROTEOFORMS FROM MAMMALIAN CELLS USING A REFINED TARGETED PROTON TRANSFER CHARGE REDUCTION (TPTCR) DATA ACQUISITION STRATEGY	Luca Fornelli
539	TWO DIMENSIONAL MASS SPECTROMETRY AS A TOOL FOR BIOTHERAPUTICS ANALYSIS USING ULTRAVIOLET PHOTODISSOCIATION AND ELECTRON-BASED DISSOCIATION TECHNIQUES	Peter O'Connor
613	ION MOBILITY ASSISTED GLYCOPROTEOMICS ON TIMS-TOF	Andris Jankevics
666	QUANTIFYING PERFORMANCE DIFFERENCES IN DECONVOLUTION FOR TOP-DOWN PROTEOFORM IDENTIFICATION	Kyowon Jeong
1003	DETECTION OF INTERMEDIATES IN THE HYDROXYL RADICAL DERIVED OXIDATION OF PEPTIDES BY MS AND LC-MS	Nik Vagkidis
967	SMALL PROTEIN DISCOVERY IN PROKARYOTES BY COMBINED TOP-DOWN & BOTTOM-UP SEQUENCING AND PROTEOGENOMICS	Jakob Meier-Credo
979	USING TOP-DOWN MASS SPECTROMETRY TO STUDY THE PROTEOFORM CHANGES CAUSED BY VPS35-D620N PROTEIN MUTATION OF PARKINSON'S DISEASE	Pui Yiu Lam
999	HIGHLY EFFICIENT AND REPRODUCIBLE SAMPLE HOMOGENISATION FOR PROTEOMIC ANALYSES OF VARIOUS ORGANS UP TO 50 MG	Ina Aretz

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Single cell MS / in cell MS		
Theme: Life Sciences & Health		
#	Abstract Title	Presenter
1015	IMPROVED DATA-INDEPENDENT ACQUISITION (DIA) AND DATA-DEPENDENT ACQUISITION (DDA) PERFORMANCE ON LOW- LEVEL PROTEOMIC SAMPLES USING A NOVEL ZENO TRAP	Katherine Tran
1022	ROBUST AND HIGH-THROUGHPUT SINGLE CELL ANALYSIS WITH THE EVOSEP ONE	Nicolai Bache
150	TAKING PROTEOMICS DOWN TO THE SINGLE CELL LEVEL	Pierre-Olivier Schmit
703	LABEL-FREE SINGLE CELL ANALYSIS WORKFLOW ON THE TIMSTOF SCP MASS SPECTROMETER USING THE CELLENONE PLATFORM	Christoph Krisp

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Translational MS – Cancer and immunology, and MS		
Theme: Life Sciences & Health		
#	Abstract Title	Presenter
97	HUMAN IMMUNOGLOBULIN REPERTOIRES ARE SIMPLE, UNIQUE, AND DYNAMIC	Albert Bondt
155	SURVEYING THE CELL-CELL INTERACTION BETWEEN TUMOR AND NATURAL KILLER (NK) CELLS USING PROXIMITY LABELING (PL) AND SHOTGUN PROTEOMICS.	Maria Cristina Trueba Sanchez
159	COMPARATIVE ANALYSIS OF PRIMARY CELL LINES WITH RESPECTIVE PARENTAL TUMOUR TISSUES BY RAPID EVAPORATIVE IONIZATION MASS SPECTROMETRY: CAN WE REPRODUCE THE COMPLEXITY OF THE ORIGINAL TUMOUR FROM THE CELL LINE CULTURED FROM IT?	Adrienn Molnár
214	ADVANTAGES OF A DYNAMIC POLYGON FOR MHC CLASS I AND II IMMUNOPEPTIDES	Pierre-Olivier Schmit
312	TARGETED MASS SPECTROMETRY METHOD TO STUDY THE INHIBITORY EFFECT OF THE SELECTED APTAMERS ON CD28-B7 CO-STIMULATORY BATHWAY	Abeer Malkawi
401	MOVING TRANSLATIONAL MASS SPECTROMETRY IMAGING TOWARDS TRANSPARENT AND REPRODUCIBLE DATA ANALYSES: A CASE STUDY OF AN UROTHELIAL CANCER COHORT ANALYZED IN THE GALAXY FRAMEWORK	Melanie Föll
426	CANCER CELL SURFACE PROTEINS STUDY FOR HIGHLIGHTED NEW POTENTIAL TARGETS FOR IMMUNOTHERAPY	Melanie Rose
430	THE NECROSOME COMPLEX AS A POTENTIAL THERAPEUTIC TARGET; FINDING NEW REGULATORS OF NECROPTOSIS THROUGH IP-MS BASED ANALYSIS	Anastasia Piskopou
509	A MASS SPECTROMETRY-BASED METHOD FOR THE DETERMINATION OF IN VIVO BIODISTRIBUTION OF SMALL MOLECULE-METAL CONJUGATE	Ettore Gilardoni
650	LIPID PROFILE OF PATIENTS WITH ORAL SQUAMOUS CELL CARCINOMA	Tialfi Bergamin de Castro
692	GENETIC ANCESTRY VARIATION IN BREAST CANCER COLLAGEN STROMA FROM BLACK WOMEN	Peggi Angel
731	A NOVEL CHARACTERISATION OF PROTEOLYSIS TARGETING CHIMERAS USING TANDEM MASS SPECTROMETRY AND TWO-DIMENSIONAL MASS SPECTROMETRY	Peter O'Connor
870	CHEMORESISTANT CANCER CELL LINES ARE CHARACTERIZED BY MIGRATORY, AMINO ACID METABOLISM, PROTEIN CATABOLISM AND IFN1 SIGNALLING PERTURBATIONS	Manuela Klingler-Hoffmann
913	PROTEOMICS CHARACTERIZATION OF FFPE LUNG CANCER SAMPLES	Lilla Turiak
930	CHOLESTEROL PROFILE OF BREAST CANCER, USING TOF-SIMS	Auraya Manaprasertsak
962	AUTOMATED AND GENERIC WORKFLOW FOR PERSONALIZED MINIMAL RESIDUAL DISEASE MONITORING USING REAL-TIME DATA INDEPENDENT ACQUISITION – NEURAL NETWORK PROCESSING (DIA-NN) ON PASER	Charissa Wijnands
805	IDENTIFICATION OF THE CANCER EXTRACELLULAR VESICLE SURFACE PROTEOME AND ITS APPLICATION TO DETECT CANCER IN URINE	Irene Bijnsdorp
823	FROM TUMOUR HETEROGENEITY IN GLIOBLASTOMA TO PRECISION THERAPY	Salzet Michel
926	UNTARGETED METABOLITE PROFILING OF GINKGO EXTRACT EGB 761 WITH LC-HRMS	Markus Schmitt

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Cultural heritage and conservation science		
Theme: Mass spectrometry across disciplines		
#	Abstract Title	Presenter
757	DYE ANALYSIS OF HISTORICAL TEXTILES USING DESI-MS	Edith Sandström
994	CHARACTERIZATION OF ARCHEOLOGICAL RESIDUES BY PYROLYSIS-GCMS	Christelle Absalon
1031	IDENTIFICATION OF ORGANIC PIGMENTS AND DYES IN HISTORIC COLOUR CHARTS OF ARTISTS' PAINTS - THE "DEUTSCHES FARBENBUCH" (1925)	Alina Astefanei
368	MINIMALLY-INVASIVE LIQUID MICROJUNCTION SAMPLING TO IDENTIFY DYE ON A 17TH CENTURY SPANISH ILLUMINATED MANUSCRIPT	Hannah Lawther
452	GETTING UNDER THE SKIN: TOWARDS ON-TISSUE DIGESTION OF COLLAGEN IN PARCHMENT	Antonia Malissa
587	MINIMALLY INVASIVE PROTEOMICS WORKFLOW TO DETERMINE THE SPECIES OF ORIGIN OF IVORY OBJECTS	Catherine Gilbert
595	IDENTIFYING PAINT BINDERS IN PAINTINGS BY MARK TOBEY USING MASS SPECTRAL TECHNIQUES	Vanessa Johnson
623	IDENTIFICATION AND DISCRIMINATION OF METAL-CONTAINING PIGMENTS AND ADDITIVES IN OIL PAINTS EXPLORED BY ULTRA-HIGH RESOLUTION (FT-ICR) MASS SPECTROMETRY.	Elena Giaretta

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Forensic Sciences		
Theme: Mass spectrometry across disciplines		
#	Abstract Title	Presenter
17	FIRST STEPS TOWARD UNCOVERING GENE DOPING WITH CRISPR/CAS BY IDENTIFYING SPCAS9 IN PLASMA VIA HPLC-HRMS/MS	Alina Paßreiter
25	FORENSIC INVESTIGATION OF BLOODSTAINS AND BLOOD FINGERMARKS BY MALDI MSI	Simona Francese
56	INVESTIGATIONS INTO THE ELIMINATION PROFILES AND METABOLITE RATIOS OF MICRO-DOSED SELECTIVE ANDROGEN RECEPTOR MODULATOR LGD-4033 FOR DOPING-CONTROL PURPOSES	Felicitas Wagener
180	PROBING FOR FACTORS INFLUENCING EXHALED BREATH DRUG TESTING IN SPORTS – PILOT STUDIES FOCUSING ON THE TESTED INDIVIDUAL'S TOBACCO SMOKING HABIT AND SEX	Ann-Marie Garzinsky
376	SPATIAL CHEMOMETRICS AND CORRELATIVE CHEMICAL IMAGING BASED MOLECULAR HISTOPATHOLOGY DELINEATES ANATOMICAL HETEROGENEITY AT CELLULAR LENGTH SCALES	Jörg Hanrieder
388	CREATININE TAUTOMERISM AS PREDICTOR OF SOLUTION PHASE PRESERVATION IN THE GAS PHASE	Maria Florencio
482	UNIDIRECTIONAL DOUBLE AND TRIPLE HYDROGEN REARRANGEMENT REACTIONS PROBED BY IR ION SPECTROSCOPY	Mathias Schäfer
542	OXYGEN 16O/18O ISOTOPE EXCHANGE FOR SMALL MOLECULE LC-MS BASED IDENTIFICATION	Sergey Osipenko
767	VALIDATION OF THE METABOLITE ERGOTHIONEINE AS A FORENSIC MARKER IN BLOODSTAINS	Hee-Gyoo Kang
768	DISCOVERY OF THE FORENSIC MARKER FOR ESTIMATION OF THE AGE OF BLOODSTAIN USING METABOLOMIC APPROACH	Jiyeong Lee
909	ISOTOPE ANALYSIS OF U AND PU FOR 6TH COLLABORATIVE MATERIALS EXERCISE (CMX-6) SAMPLES BY MC-ICP-MS IN KAERI	Ranhee Park
936	SYNTHESIS AND MASS SPECTROMETRIC CHARACTERIZATION OF THE SELECTIVE ANDROGEN RECEPTOR MODULATOR SARM 2F FOR DOPING CONTROL PURPOSES	Tristan Möller

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Homeland security, explosives and environmental monitoring		
Theme: Mass spectrometry across disciplines		
#	Abstract Title	Presenter
964	STICKING IT TO COLLECTION AND ANALYSIS: UTILIZING PRESSURE-SENSITIVE ADHESIVE PAPER COMBINED WITH PORTABLE MASS SPECTROMETRY FOR DETECTION OF THREATS	Dan Carmany

POSTERSESSION A (MONDAY 29 & TUESDAY 30 AUGUST 2022)		
Session: Young MS Scientists		
Theme: Other		
#	Abstract Title	Presenter
343	KIT QUANTA – STANDARDIZATION KIT FOR ABSOLUTE PROTEIN QUANTITATION: CONTROL OF THE LIQUID CHROMATOGRAPHY SETUP-DEPENDENT ARTEFACTUAL METHIONINE OXIDATION OF PEPTIDES	France Baumans
21	COMPETITIVE BINDING SCREENING ASSAY BASED ON LC-TANDEM MS FOR NATURAL PRODUCT INHIBITOR OF TNF-ALPHA	Yongsoo Choi