Wednesday 4th September

Theatre - *denotes an early-career scientist

TIME	
15:00	**WELCOME FROM BMSS CHAIR AND BSPR PRESIDENT** **OPENING PLENARY LECTURE Chair:** Andrea Lopez-Clavijo *Babraham Institute* **Corinne Spickett, Aston University** Lipidomics, ox-lipidomics and the biological effects of oxidatively-modified phospholipids
	MULTIOMICS **Chair: Gina Eagle** *Sciex*
16:00	**Keynote: Julio Saez-Rodriguez** *European Bioinformatics Institute (EMBL-EBI)* Combining proteomics (and other omics) and biological knowledge into machine-learning models to extract disease mechanisms
16:30	**Charles Eldrid** *University of Manchester* Multi-Omics investigation of mAb expressing CHO cell lines in fed batch bioreactors*
16:50	**Elisabete Pires** *University of Oxford* Unwrapping malformation biomarkers in an Egyptian foetus Mummy using multi-omics*
17:10	**Sadr ul Shaheed** *University of Oxford* Multi-omics approach to identify the molecular signature of primary non function prior to transplantation in deceased donor kidneys*
17:30	**C-MASS UPDATE** THEATRE **CAREERS WORKSHOP** WOODS-SCAWEN ROOM
17:30	**EXHIBITION**
19:00	*END OF ACADEMIC DAY*
19:30	**DAI GAMES SYMPOSIUM & MEXICAN SUPPER NETWORKING EVENT**

Thursday 5th September AM

Theatre

TIME	ORAL TRACK A
09:00	**POSTER BROWSING & EXHIBITION**
10:00	**FLASH PRESENTATIONS 1** **Chair: Rebecca Nash** *LGC Group* Flash Oral Talks (3min, no questions)
11:00	**TEA/COFFEE & EXHIBITION & POSTER SESSION** Flash Presenters: Sessions 1 & 3 ODD numbered posters
	APPLICATIONS I (NATURAL SCIENCES)
	Chair: Erik van Balderen *Bruker*
12:00	**Keynote: Nanna Bjarnholt** *University of Copenhagen* Mass spectrometry imaging for plant science, and why plants are so challenging
12:30	**Benedict Gannon** *University of Warwick* Effects of sustainable rejuvenator on aged British roads compared with commercial bitumen binder rejuvenator by FT-ICR MS*
12:50	**Christopher McElroy** *LGC Group* Simultaneous Screening of 9 Allergens in plant milks by mass spectrometry
13:10	**Luciana da Costa Carvalho** *University of Oxford* Do I smell a (dead) rat? Exploring carrion mimicry in aroid and Rafflesia flowers using thermal desorption GC-MS/MS*
13:30	**BUFFET LUNCH & EXHIBITION**

Thursday 5th September PM

Theatre

TIME	ORAL TRACK A
	APPLICATIONS II (LIFE SCIENCES)
	Chair: Emma Sisley *OMass Therapeutics*
14:30	**Keynote: Ana Rodriguez-Mateos** *King's College London* The role of Mass Spectrometry in Precision Nutrition
15:00	**Lily Adair** *University of Reading* Advances in Peptide and Protein Identification by LAP-MALDI MS and MS/MS Analysis*
15:20	**Rachelle Black** *AstraZeneca* Characterisation of phosphothioate oligonucleotides and the effect of lipid conjugation via HPLC-high resolution MS
15:40	**Sandra Martin-Guerrero** *Queen Mary University of London* Quantitative proteomics and phosphoproteomics approaches for exploiting MASTL as a new therapeutic target for Acute Myeloid Leukaemia
16:00	**TEA/COFFEE & EXHIBITION & POSTER SESSION** Flash Presenters: Session 2 EVEN numbered posters
	PARTNER PRESENTATIONS 1
	Chair: Liam Heaney *Loughborough University*
17:00	**WATERS CORPORATION: Matthew Daly** *Pushing the Boundaries of Science with Multi Reflecting Time-of-Flight Technology*
17:15	**SHIMADZU: Alan Barnes** Characterising unknowns; new developments in lipid characterisation and non-targeted screening by HRMS
17:30	*END OF ACADEMIC DAY* **BSPR AGM** (Woods-Scawen Room)
18:00	**LGBTQ+ PRE-DINNER SOCIAL GET TOGETHER (PANORAMA SUITE)**
19:00	**DRINKS RECEPTION AND CONFERENCE DINNER (CHANCELLORS SUITE)**

Thursday 5th September AM
Studio

TIME	ORAL TRACK B
09:00	**POSTER BROWSING & EXHIBITION**
10:00	**FLASH PRESENTATIONS 2** **Chair: Cara Jackson** *University of Strathclyde* Flash Oral Talks (3min, no questions)
11:00	**TEA/COFFEE & EXHIBITION & POSTER SESSION** Flash Presenters: Sessions 1 & 3 ODD numbered posters
	CHEMICAL BIOLOGY
	Chair: Jack Houghton *Imperial College London*
12:00	**Keynote: Megan Wright** *University of Leeds* Chemical proteomic approaches to unveil the mode of action of anti-infective compounds
12:30	**Amy George** *Newcastle University* Comprehensive Characterisation of CDK4/6 Inhibitor Trilaciclib in Acute Myeloid Leukaemia Using Proteomics Approaches*
12:50	**Tia Hawkins** *Rosalind Franklin Institute* Functional Evolution of Nipah Virus G protein glycosylation*
13:10	**Kleitos Sokratous** *OMass Therapeutics* Mass spectrometry-based screening and characterization of electrophile molecules for hit identification of Gasdermin D
13:30	**BUFFET LUNCH & EXHIBITION**

Thursday 5th September PM

Studio

TIME	ORAL TRACK B
	INSTRUMENTAL & FUNDAMENTAL MS
	Chair: Emma Marsden-Edwards *Waters Corporation*
14:30	**Keynote: Amy Burton** *GSK* Using an acoustic ejection mass spectrometry platform to develop label-free workflows for biochemical and cell-based assays in early-stage drug discovery
15:00	**Christopher Wootton** *Bruker Daltronics* A prototype TIMS-FT-ICR MS instrument capable of deep characterisation of complex samples and biomolecules
15:20	**Niklas Geue** *University of Manchester* Visualizing Conformational Dynamics of Biomacromolecules by Coupling Ion Mobility Mass Spectrometry to Electron Microscopy*
15:40	**Felicia Green** *Rosalind Franklin Institute* New generation of microscope mode secondary ion mass spectrometry imaging
16:00	**TEA/COFFEE & EXHIBITION & POSTER SESSION** Flash Presenters: Session 2 EVEN numbered posters
	UK TECHNOLOGY SPECIALISTS NETWORK (TSN) PRESENTATION
	Chair: Lindsay Harding *University of Huddersfield*
17:00	**Julie Herniman** *University of Southampton* Research Technical Professional Opportunities, Knowledge and Skills (ROKS)
17:30	*END OF ACADEMIC DAY* **BSPR AGM** (Woods-Scawen Room)
18:00	**LGBTQ+ PRE-DINNER SOCIAL GET TOGETHER (PANORAMA SUITE)**
19:00	**DRINKS RECEPTION AND CONFERENCE DINNER (CHANCELLORS SUITE)**

Thursday 5th September AM

Woods-Scawen Room

TIME	ORAL TRACK C
09:00	**POSTER BROWSING & EXHIBITION**
10:00	**FLASH PRESENTATIONS 3** **Chair: Colleen Maxwell** *University of Leicester* Flash Oral Talks (3min, no questions)
11:00	**TEA/COFFEE & EXHIBITION & POSTER SESSION** Flash Presenters: Sessions 1 & 3 ODD numbered posters
	PROTEOMICS (ONE HEALTH & NON-HUMAN)
	Chair: Jo Kirkpatrick *Thermo Fisher Scientific*
12:00	**Keynote: Paola Roncada** *University Magna Graecia of Catanzaro* One Health Proteomics: exploring the potential of integrated approach in public health domain
12:30	**Scott Peterman** *Thermo Fisher Scientific* Semi-quantification of triglycerides with resolved fatty acid composition using a targeted MS3 approach on a novel hybrid nominal mass instrument
12:50	**Alistair Hines** *AstraZeneca* Comparative spatial proteomics as a tool to understand difficult-to-express molecules in CHO cell lines
13:10	**Patchara Sittishevapark** *University of Liverpool* LC-MS/MS analysis of four medically important venomous snake venoms from to identify functional proteinaceious venom components*
13:30	**BUFFET LUNCH & EXHIBITION**

Thursday 5th September PM

Woods-Scawen Room

TIME	ORAL TRACK C
	CLINICAL PROTEOMICS
	Chair: Karin Barnouin *Merck Sharpe & Dohme*
14:30	**Keynote: Pietro Fratta** *University College London* Detecting the consequences of RNA processing dysfunction in ALS
15:00	**Richard Kay** *University of Cambridge* LC-MS/MS shows raised maternal plasma levels of GDF15 in pregnancy is produced almost entirely from the fetus
15:20	**Nikita Bhakta** *University of Leicester* Developing Quantitative SRM Assays for Biomarkers of Heart Failure with Preserved Ejection Fraction (HFpEF) Using a Novel Heavy Labelling Technique*
15:40	**Giles Drinkwater** *LGC Group* Development of mass spectrometric reference methods: α-synuclein in CSF
16:00	**TEA/COFFEE & EXHIBITION & POSTER SESSION** Flash Presenters: Session 2 EVEN numbered posters
	PARTNER PRESENTATIONS 2
	Chair: Edward Emmott *University of Liverpool*
17:00	**EVOSEP: Joanna Freeke** Standardized Proteomics – an easy solution and today's reality
17:15	**LECO: Richard Spence** A Novel Long-Lifetime Ion Detector for GCxGC-TOFMS with Sub-Femtogram Detection Limits
17:30	*END OF ACADEMIC DAY* **BSPR AGM**
18:00	**LGBTQ+ PRE-DINNER SOCIAL GET TOGETHER (PANORAMA SUITE)**
19:00	**DRINKS RECEPTION AND CONFERENCE DINNER (CHANCELLORS SUITE)**

Friday 6th September AM
Theatre

TIME	ORAL TRACK A
	AMBIENT IONISATION AND IMAGING
	Chair: Stefania Maneta Stavrakaki *Imperial College London*
9:00	**Keynote: Ingela Lanekoff** *Uppsala University* Nano-DESI MS: One tool – diverse applications
9:30	**Rachel McGuire & Catherine Welsh** *AstraZeneca* Optimisation and validation of ambient ionisation assay method of a compound in pharmaceutical drug development using ASAP-MS*
9:50	**Sophie Pearce** *Sheffield Hallam University* An Investigation into the Chemotherapy Drug-Induced Response of Osteosarcoma Multicellular Tumour Spheroids by Multimodal Mass Spectrometry Imaging*
10:10	**Emmanuelle Claude** *Waters Corporation* Mapping of pharmacological dosed drug/ metabolites using the sensitive and fast targeted DESI MRM MS imaging
10.30	**TEA/COFFEE & EXHIBITION**
	SMALL MOLECULES
	Chair: Stephen Holman AstraZeneca
11:30	**Keynote: Chris Hopley** LGC Group Harmonisation and Standardisation in small molecule clinical measurement
12:00	**Christopher Green** Loughborough University Investigating the efficacy of exhaled breath condensate as an alternative biosample to assess circulating short-chain fatty acid levels*
12:20	**Julie Herniman** University of Southampton Use of 2D GC-MS to Interrogate Complex Fuels
12:40	**Amar Rai** Imperial College London Use of the Universal Fragmentation Model and ion mobility spectrometry/mass spectrometry to enhance pharmaceutical structural elucidation*

Friday 6th September PM
Theatre

TIME	ORAL TRACK A
13:00	**BUFFET LUNCH & EXHIBITION**
	LIPIDOMICS & METABOLOMICS **Chair: Adam King** *Waters Corporation*
14:00	**Keynote: Howbeer Muhamadali** *University of Liverpool* Spectroscopic probing of bacterial metabolism at single-cell level
14:30	**Emily Armitage** *Shimadzu Corporation* Novel ionisation and fragmentation techniques enhance biomarker discovery in pancreatic cancer
14:50	**Minhui Zhu** *University of Manchester* Development of a Quantitative MRM assay using Sebum to Diagnose Parkinson's Disease*
15:10	**Yiquan Chen** *University of Oxford* Investigating the role for elevated 2-hydroxyglutarate (2-HG) in IDH1 mutant glioblastoma cells using 13C5 2-HG as a metabolic tracer*
15:30	**TEA/COFFEE BREAK**
16:00	**PRIZE PRESENTATIONS**
16:15	**CLOSING PLENARY & CLOSING REMARKS** **Chair:** Rainer Cramer *University of Reading* **Bernhard Küster, Technical University of Munich** How Mass Spectrometry-based Phosphoproteomics Aids Precision Oncology by Understanding Tumors and Drugs
17:15	*CLOSE*

Friday 6th September AM

Studio

TIME	ORAL TRACK B
	DATA PROCESSING & INFORMATICS
	Chair: Charlotte Hutchings *University of Cambridge*
9:00	**Keynote: Brendan MacLean** *University of Washington* Skyline: Targeted proteomics software free and open source for 15 years
9:30	**Ananth Prakash** *EMBL-European Bioinformatics Institute* Integrated view of baseline protein expression in human, mouse, rat and pig organs by reanalysing public proteomics datasets
9:50	**Bela Paizs** *Rosalind Franklin Institute* Chemical Annotation Propagation for Molecular Networks
10:10	**Kerry Ramsbottom** *University of Liverpool* PTMeXchange species specific PTM builds: Meta-analysis of datasets and dissemination of high-quality PTM data for community use*
10.30	**TEA/COFFEE & EXHIBITION**
	ION MOBILITY
	Chair: Niklas Geue *University of Manchester*
11:30	**Keynote: Valérie Gabelica** *University of Geneva* Interpreting charge state distributions and collision cross section distributions
12:00	**Vanessa Duerr** *University of Manchester* A high-throughput method for HDX-cIM-MS*
12:20	**Lucy Woods** *MOBILion Systems* h-Throughput, Label-Free Cyclic Peptide Soft Spot Identification (SSID) by High-resolution Ion Mobility Mass Spectrometry
12:40	**Michael McCullagh** *Waters Corporation* Elevating Specificity and Identification Confidence for PFAS Liquid Chromatography and Cyclic Ion Mobility Mass Spectrometry

Friday 6th September PM

Studio

TIME	ORAL TRACK B
13:00	**BUFFET LUNCH & EXHIBITION**
	BIOMACROMOLECULAR STRUCTURE
	Chair: Sarah Vickers *University of Birmingham*
14:00	**Keynote: Tarick El-Baba** *University of Oxford* Chronic stress invokes alterations to a metabotropic glutamate receptor
14:30	**Anna Simmonds** *University of Leeds* Towards structural mass spectrometry for fragment-based drug discovery*
14:50	**Cameron Baines** *University of Nottingham* Carbene Footprinting of EF-Tu in Complex with Contrasting Elfamycin Antimicrobials*
15:10	**Kish Adoni** *University College London* A Novel Crosslinker Improves Monolink and Crosslink Identification for Alphafold2 based Integrative Protein Structure Determination Pipeline*
15:30	**TEA/COFFEE BREAK**
16:00	**PRIZE PRESENTATIONS** **THEATRE**
16:15	**CLOSING PLENARY & CLOSING REMARKS** **Chair:** Rainer Cramer *University of Reading* **Bernhard Küster, Technical University of Munich** How Mass Spectrometry-based Phosphoproteomics Aids Precision Oncology by Understanding Tumors and Drugs **THEATRE**
17:15	*CLOSE*

Friday 6th September AM

Woods-Scawen Room

TIME	ORAL TRACK C
	NATIVE MS & PROTEOMICS
	Chair: Kish Adoni *University College London*
9:00	**Keynote: Helen Cooper** *University of Birmingham* Native ambient mass spectrometry imaging of proteins and their complexes
9:30	**Cara Jackson** *University of Strathclyde* Investigating PROTAC Ternary Complexes in Cell-Like Environments Using Native Mass Spectrometry*
9:50	**Nikita Levin** *Rosalind Franklin Institute* Top-down and bottom-up analysis of proteins and PTMs on an Orbitrap-Omnitrap instrument equipped with ExD, UVPD and IRMPD
10:10	**Steven Daly** *MS Vision* Exploring the nature of the volatile salts used in Native MS
10.30	**TEA/COFFEE & EXHIBITION**
	SYSTEMS BIOLOGY & RARE DISEASES
	Chair: James Waddington *Agilent Technologies*
11:30	**Keynote: Albert Sickmann** *Leibniz Institute for Analytical Sciences* Population based proteomics: Platelet data for elucidating mechanisms of cardiovascular diseases
12:00	**Angel Garcia** *University of Hull* Using proteomics to investigate rare diseases*
12:20	**Rob Ewing** *University of Southampton* Multi-omics analysis of the Zika virus – brain tumour interaction to define the mechanisms of a novel oncolytic virotherapy
12:40	**Yuqin Wang** *Swansea University* Application of omics assays in rare metabolic disease diagnosis and monitoring therapeutic response

Friday 6th September PM

Woods-Scawen Room

TIME	ORAL TRACK C
13:00	**BUFFET LUNCH & EXHIBITION**
	EMERGING METHODS & TECHNOLOGIES IN PROTEOMICS
	Chair: Charles Eldrid *University of Manchester*
14:00	**Keynote: Roman Fischer** *University of Oxford* Precision proteomics in human disease
14:30	**Dan McGill** *Rosalind Franklin Institute* Reactions of cold argon plasma with condensed-phase macromolecules*
14:50	**Francesca Robertson** *LGC Group* Novel workflows using combined automated protein digestion and statistical tools for traceable quantification of clinical targets using Isotope Dilution LC-MS
15:10	**Yacine Belgaid** *ACX Instruments Ltd* AM-DMF-SCP: Integrated Single-Cell Proteomics Analysis on an Active-matrix Digital Microfluidic Chip
15:30	**TEA/COFFEE BREAK**
16:00	**PRIZE PRESENTATIONS** **THEATRE**
16:15	**CLOSING PLENARY & CLOSING REMARKS** **Chair:** Rainer Cramer *University of Reading* **Bernhard Küster, Technical University of Munich** How Mass Spectrometry-based Phosphoproteomics Aids Precision Oncology by Understanding Tumors and Drugs **THEATRE**
17:15	*CLOSE*

FLASH PRESENTATIONS 1: THEATRE

1 **Annabel Eardley-Brunt** *University of Oxford* ASAP mass spectrometry and machine learning as a prognostic indicator for vascular disease and cardiology patient outcomes*

3 **Daniyah Alamrani** *University of Birmingham* Quantification of cardiotonic steroids using liquid chromatography-mass spectrometry assay: Application to disease models and patients*

5 **Alisha Henderson** *Loughborough University* Towards Rapid Analysis for the Identification of Prohibited Substances in Sports Supplements using ASAP-MS*

7 **Oscar Ayrton** *King's College London* Development of a GC-MS headspace method for the determination of Residual Solvents

9 **Matthew Harris** *LGC Group* Iso Factor: enabling the quantification of an isotopic distribution from a single isotopologue

11 **Yoshihisa Ueda** *JEOL* Integrated unknown compounds identification method with electron ionization (EI), soft ionization, and EI mass spectra database predicted by artificial intelligence

13 **Harold Cannon** *University of Oxford* A method for the analysis of short chain fatty acids from microbiome-derived samples using anion-exchange chromatography-mass spectrometry (IC-MS)

15 **Anna Cordiner** *University of York* Tandem mass spectrometry based workflows using 2DMS for multiple ions within a single nominal mass window*

17 **Marlene Thaitumu** *Aristotle University of Thessaloniki* Blood Microsampling Devices against plasma in Global Metabolic Profiling Using UHPLC-TOF MS

19 **Fozia Shaheen** *University of Birmingham* Development of a novel thyroid hormone profiling method using liquid chromatography tandem mass spectrometry*

21 **Elmeri Latvanen** *Imperial College London* Using modified surfaces to overcome challenges of analysing complex samples using high throughput Ambient Ionisation Mass Spectrometry (AIMS)*

23 **Isabelle Legge** *University of Oxford* Diethylene Glycol and Ethylene Glycol Contamination in Liquid Medicine

25 **Tianhui Yu** *Loughborough University* Development of Rapid Screening Methods for Herbs used in Traditional Chinese Medicine*

27 **Ruth Walker** *Newcastle University* Developing high-throughput screening MALDI-TOF MS cellular assays for drug discovery in metabolic dysfunction-associated steatotic liver disease*

29 **Chloe Tayler** *GSK* Utilising data-independent acquisition mass spectrometry (DIA-MS) to enable rapid profiling of the human secretome*

FLASH PRESENTATIONS 2: STUDIO

2 **John Headley** *University of Warwick* Investigating the Potential of Slender Wheatgrass Roots for Biotransformation of OSPW-derived Compounds using FT-ICR Mass Spectrometry

4 **Emma Carrick** *CPI* Alchemite TM: A novel machine learning-driven algorithm for oligonucleotide characterisation and manufacturing

6 **Aimee Humphreys** *University of Nottingham* Comparison of Indium Tin Oxide (ITO)-coated and standard glass slides for AP-MALDI-MS-based imaging*

8 **Samuel Weekes** *University of Warwick* Variation of Polyester Fragmentation using Tandem Mass Spectrometry*

10 **Saira Hameed** *Rosalind Franklin Institute* Deciphering dynamics of cellular metabolism in mouse brain by mass spectrometry imaging*

12 **Harry Tata** *University of Bristol* Raw Data Deconvolution for Fragment Ion Abundance Estimation and Impurity Detection in Oligonucleotide Mass Spectra*

14 *Presentation Withdrawn*

16 **Haokai Wang** *University of Warwick* Comparative Analysis of Ionization Techniques in Fast Pyrolysis Bio-oil Derived from Different Feedstocks*

18 *Presentation Withdrawn*

20 **Sidrah Rahman** *University of Nottingham* Exogenous Microbial Metabolite Analysis using MS approaches*

22 **Samuel Mutto** *University of Warwick* Method Optimisation for the Isolation of the Asphaltene Fraction in Bitumen using Automated Soxhlet Extraction*

24 **John Sidda** *University of Oxford* Ion-exchange chromatography-mass spectrometry (IC-MS) for untargeted plant metabolomics

26 **Rachel Harris** *MOBILion Systems* Insights at the Push of a Button: Using the MOBIE System and Lipostar to Unravel the Lipidome

28 **Rebecca Greatorex** *University of Nottingham* Solvent optimisation and matrix enhanced-liquid extraction surface analysis (ME-LESA) for the detection of lipids in brain tissue*

30 **Callan Littlejohn** *University of Warwick* Tools for Polymer Identification using High Resolution Mass Spectrometry*

FLASH PRESENTATIONS 3: WOODS-SCAWEN ROOM

31 **Mariya Misheva** *University of Oxford* Using proteomics to identify novel autoantibodies In Guillain-Barré Syndrome (GBS)

33 **Liuwei Meng** *University of Manchester* Photoactive ion mobility-mass spectrometry reveals the Conformational Changes of fatty acid photodecarboxylase*

35 **Victoria Liu** *Durham University* Proteome-wide identification of clinically relevant carbon dioxide targets

37 **Aisha Ben-Younis** *OMass Therapeutics* A native mass spectrometry approach to investigate novel hit compounds for pyroptosis inhibition*

39 **Cameron Fairweather** *Monash University* RAMP it up! Exploring conformational dynamics of the amylin 3 receptor (AMY3R) using HDX-MS*

41 **Arppana Varughese** *University of Nottingham* Probing protein-protein and ligand-binding interactions of STING using native mass spectrometry and carbene footprinting*

43 **Jaspreet Sound** *University of Birmingham* Native mass spectrometry to detect cyanobacterial fingerprints within natural lake samples*

45 **Charlotte Hutchings** *University of Cambridge* Understanding common and serotype-dependent effects of rAAV-production on host HEK293 cells*

47 **Sarah Vickers** *University College London* A disease-associated conformational ensemble reveals how the folding pathway is subverted in alpha-1-antitrypsin polymerisation*

49 **Feng Qu** *OMass Therapeutics* Enhanced declustering enables native top-down analysis of membrane protein complexes using ion-mobility time-aligned fragmentation*

51 **Leonie Mueller** *Newcastle University* Phenotypic drug discovery screen in human iPSC-derived macrophages using novel MALDI-TOF MS workflows and in-depth diaPASEF proteomics*

53 **Elliot John Gyedu** *University of Leicester* Microwave-assisted extraction of hypertension peptides from dried blood spots for analysis using liquid chromatography tandem mass spectrometry*

55 **Georgina Charlton** *University College London* Using Single Cell Proteomics to Analyse Protein Changes in Huntington's Disease*

57 **Anthony Devlin** *Rosalind Franklin Institute* Understanding glycosaminoglycans: Trapped Ion Mobility Spectrometry (TIMS) as a tool for identification and analysis*

59 **Javeria Mehboob** *University of York* Utilising mass spectrometry as a tool to understand novel transport proteins in Escherichia coli*

POSTERS

POSTERS 1 to 60 in Warwick Arts Centre (Mead) Gallery
POSTERS 61 to 157 in Butterworth Hall

MULTIOMICS

32 **Exploring transcriptional and metabolic regulation in IDH1 mutant glioblastoma cells using IC-MS-based untargeted metabolomics and global RNA-seq**
James McCullagh, Kyla Thomas, Ingvild Hvinden, John Walsby-Tickle, Tom Cadoux-Hudson, Chiara Bardella

34 **Multi-omics investigation of glioblastoma using DESI imaging and LC-MS***
Brittannie Willis, Harry Whitwell, Nelofer Syed, Elizabeth Want

APPLICATIONS I (NATURAL SCIENCES)

36 **Unlocking the full potential of natural vanillin through FT ICR MS-based analysis of carbon and oxygen isotopic ratios**
Jose Ordaz-Ortiz, Yair Cruz-Narváez, Moisés Guerrero-Esperanza, Nayeli L. Romero-García, Anita Arroyo-Silva, Carlos Y. Gómez-Cruz

38 **GCMS ToF : a nice way for global investigation during taste & odor episodes in drinking water**
David Benanou

40 **Gas chromatography-mass spectrometry for phthalate analysis and screening of phthalate leaching from plastic aggregates exposed to a cementitious solution***
Hasanthi Hemantha Kosgahakumbura Kosgahakumbure Nawasiya Mudiyanselage, Damien L. Callahan, Ivan Kourtchev, Sue Charlesworth, Will P. Gates

42 **Solving the PFAS Challenge: Comprehensive Screening of Environmental Samples against 1000s of Compounds in a Single Run**
Erik van Balderen, Eva-Maria Niehaus, Arnd Ingendoh, Andrea Kiehne

44 **Overcoming analytical challenges associated with Per- and polyfluoroalkyl substances (PFAS) analysis in environmental matrices**
Ivan Kourtchev, Omotola Folorunsho, Jishnu Pandamkulangara Kizhakkethil

46 **Fish Speciation Analysis by LAP-MALDI Mass Spectrometry***
Diana Dalia Rangel Casillas, Lily R. Adair, Rainer Cramer

CHEMICAL BIOLOGY

PROTEOMICS (ONE HEALTH & NON-HUMAN)

APPLICATIONS II (LIFE SCIENCES)

63 **Quantitative proteomics and phosphoproteomics approaches for exploiting MASTL as a new therapeutic target for Acute Myeloid Leukaemia**
Sandra M Martin-Guerrero, Tommy Shields, Robert Zach, Pedro Casado, Henry Gerdes, Nadia Afroz Nishat, Vinothini Rajeeve, Helfrid Hochegger, Pedro R. Cutillas

64 **The proteomic background determines the extent by which LSD1 inhibitors sensitize leukaemia cells to gilteritinib and other kinase inhibitors**
Pedro Casado, Nadia Afroz Nishat, Federico Pedicona, Suhana Yasmin, Sandra M. Martin-Guerrero, Vinothini Rajeeve, Pedro R. Cutillas

65 **Accelerating impurity analysis of synthetic oligonucleotides through use of the BioAccord LC-MS System with Waters_connect Informatics**
Kamila Pacholarz

66 **Identification of substandard and falsified vaccines using MALDI mass spectrometry**
John Walsby-Tickle, Rebecca Clarke, Benediktus Yohan Arman, Bevin Gangadharan, James S O McCullagh, The Vaccine Identity Evaluation (VIE) Collaboration

67 **Enhancing Non-Targeted Analysis with GCxGC-HR-TOFMS and a novel Multi-Mode ion source**
Sebastiano Panto, Barry Herschy, Richard Spence, Nick Jones

68 **Developing a method to characterise glycosaminoglycans (GAGs) in human breastmilk***
Melissa Greenwood, Christopher Stewart, Sean Austin, Patricia Murciano Martinez, Sabine Flitsch, Perdita Barran, Janet Berrington

69 **Use of the Thermo Vanquish UHPLC and Exploris 120 Orbitrap in Discovery DMPK**
Iain Beattie, Lucy Burton, Victoria Ford, Rina Mistry, Laie Abello

70 **Longitudinal Monitoring of Steroid Excretion: Hair Analysis**
Fozia Shaheen, Livia Simmonds, Grace Fensome, Rowan Hardy, Farhat Khanim, Renate Reniers, Angela E Taylor

71 **SILAC-MS: Measuring protein turnover and validating mechanism of action in degradation-based drug development**
Gemma Hardman Fowler, Hilary Lewis, Hannah Chesher, Mandy Lawson

72 **Analysis of oligonucleotide therapeutics by LC-MS and MALDI-MS using a single integrated software platform**
Alan Barnes, Michael Nairn, Emily Armitage, Neil Loftus

73 **Quantitative acetylome analysis of aspirin treated AML cell lines using label-free LC-MS/MS reveals potentially cytostatic modifications in cytosolic and mitochondrial proteins***
Luke Higgins, Tommy Shields, Vinothini Rajeeve, Pedro Rodriguez Cutillas

74 **High-throughput workflow for in-depth proteome coverage and quantitative analysis of low sample amounts and single-cells**
Tabiwang Arrey, Robert van Ling, Jenny Ho, Jo Kirkpatrick, Min Huang, Haoran Huang, Eugen Damoc

75 **Developing an automated method for analysis of oligonucleotides by MALDI/MS**
Andrew Ray, Ethan Harrup, Rachelle Black, Stephen Holman

76 **Enhancing the detection of analyte ions in LAP-MALDI MS using ion exchange beads***
Sanduru Thamarai Krishnan, Sela Sezgin, Rainer Cramer

77 **Comprehensive HPAEC-PAD/MS Analysis of N-glycans using SweetSep™ Column***
Andrew Reeder

78 **The Application of Stable Isotopically labelled Proteins to Investigate Protein Digestion in Health and Disease**
Hala Fatani, Abhishek Sheth, Daniel Wilkinson, Ken Smith, Mads S. Larsen, Philip Atherton, Gordon Moran, Matthew Brook

79 **Structural and Functional Significance of Abdala COVID-19 Vaccine Glycosylation***
Sean A. Burnap, Valeria Calvaresi, Gleysin Cabrera, Satomy Pousa, Miladys Limonta, Yassel Ramos, Luis Javier González, David J. Harvey, Weston B. Struwe

80 **Characterisation of the plasma levels of small apolipoproteins in healthy and lean volunteers (BMSS Summer Student 2024)***
J Ted Dennis, AV Punnoose, CA Bannon, PC Fletcher, F Reimann, FM Gribble, RG Kay

INSTRUMENTAL & FUNDAMENTAL MS

81 **Lab2Lab – Automating access to analytical data for the Lab of the Future**
Paul Davey

82 **A prototype TIMS-FT-ICR MS instrument capable of deep characterisation of complex samples and biomolecules**
Christopher Wootton, Alina Theisen, Gregory Brabeck, Julien Maillard, Christopher Ruger, Carlos Afonso, Pierre Giusti

83 **A novel long-life detector for a novel high-speed hybrid nominal mass platform**
Jenny Ho, Ken Cook, Oleg Silivra, Philip Remes, Linfan Li, Charles E Maxey, Cristaia Jacob

84 **A 3D-printed cost-effective plume collection device for improved ion signal detection**
Selahaddin Sezgin, Rainer Cramer

85 **Evaluation of the NIST library similarity matching quality of mass spectra generated by the GC-HR-TOFMS with Multi-Mode Ionization Source**
Barry Herschy, Craig Fowler, Viatcheslav Artaev, Scott Pugh, Richarde Spence, Sebastiano Panto

86 **A Novel Long-Lifetime Ion Detector for GCxGC-TOFMS with Sub-Femtogram Detection Limits**
Richard Spence, Matthew Soyk, Viatcheslav Artaev, Barry Herschy, Sebastiano Panto

87 **High-speed compound quality assessment using Acoustic Ejection Mass Spectrometry**
Nick Bowden

88 **Enabling faster MRM while maintaining instrument robustness**
Melissa McGuinness

CLINICAL PROTEOMICS

89 **Multiplexed absolute quantification of prognostic biomarkers in heart failure with preserved ejection fraction using QconCAT***
Gurnoor Brar

90 **Robust Sample Preparation Workflows for FFPE Samples for Confident Proteomics Data**
Debadeep Bhattacharyya

91 **Haemoglobin interference in dried blood spot bottom-up proteomics***
Hannah Ging, Claire Eyers, Louise Oni, Andrew Chetwynd

92 **Comparing the proteomic analysis of depleted and undepleted plasma for clinical applications**
Rosemary Maher, Claire Eyers

93 **Ultra-deep MS based plasma proteomics in a hand foot and mouth disease cohort**
Iolanda Vendrell, Georgina Berridge, Thanh Tran Tan Thanh, Le Nguyen Thanh Nhan, Garwin Pichler, Zuzana Demianova, Benedikt M Kessler, Le Van Tan, Roman Fischer

94 **Evaluation of Parallel Reaction Monitoring Assays at Discovery Scale on a New Hybrid Nominal Mass instrument for Phosphoproteomics Studies**
Jo Kirkpatrick, Cristina C. Jacob, Hasmik Keshishian, Alan Atkins, Philip Remes, Nikita Kormshchikov, Michael W. Burgess, Claudia P. B. Martins, Steven A. Carr

95 **A Targeted LC-MS/MS plasma protein biomarker panel and Machine Learning can predict Parkinson's disease up to 7-years before symptom onset**
Wendy E Heywood, Sebastian Schade, Mohammed Dakna, Paolo Garagnani, Mariagiulia Bacalini, Chiara Pirazzini, Kailash Bhatia, Maria Xylaki, Sandrina Katharina Weber, Marielle Sophie Ernst, Lucia Muntean, Friederike Sixel-Döring, Claudio Franceschi, Ivan Doykov, Claudia Trenkwalder, Brit Mollenhauer, Sebastian Schreglmann, Justyna Spiewak, Heloise Vinette, Kevin Mills, Jenny Hallqvist

96 **Unique high-throughput workflow for deeper plasma proteome coverage enables discovery of novel biomarkers***
Karin Yeoh, Katharina Limm, Hu Zehan, Andreas Schmidt, Sebastian Mueller, Nils A Kulak

97 **Scalability for high-throughput proteomics – Evotip Pure integration with the Biomek i5 liquid handler for standardized, fully automated sample preparation**
Joanna Freeke

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98 **Dielectric barrier discharge desorption/ionization-mass spectrometry for direct analysis of pharmaceutical tablets***
Habib Ahsan

99 **High resolution low flow DESI imaging using a commercial DESI source**
Mark Towers, Emmanulle Claude, Sheba Jarvis

100 **Interlaboratory Activity and Standardisation in Mass Spectrometry Imaging – Developing Community Awareness and Interaction**
Rory Steven, Martin Metodiev, Angeliki Christakopoulou, Jean-Luc Vorng, Gustavo Trindade, Ian Gilmore, Josephine Bunch

101 **Metabolomic and Glycomic Distribution in Uveal Melanoma Multi-Cellular Tumour Spheroids using Mass Spectrometry Imaging***
Georgia Millard, Neil Cross, Helen Kalirai, Karen Aughton, Laura Cole

102 **Solvent-free Matrix Application by the HTX SubliMATETM for High Quality MALDI Imaging of Lipids and N-glycans**
Sean O'Connor

103 **Mapping Sterol Dynamics in Mouse Brain Using Multi-Platform Mass Spectrometry Imaging***
Eylan Yutuc, Shazia Khan, Joyce Yau, Ruth Andrew, William J Griffiths, Yuqin Wang

104 **Atmospheric pressure solids analysis probe (ASAP) mass spectrometry for in-situ analysis of fentanyl in latent fingerprints***
Katrina Cranfield, Paul Kelly, Jim Reynolds

105 **Ultra-high resolution mass spectrometry MALDI imaging of human kidney on a new TIMS-FTICR-MS prototype**
Alina Theisen, Madeline E. Colley, Jeffrey M. Spraggins, Christopher A. Wootton

106 **Targeted Quantitative Mass Spectrometry Imaging by Triple Quadrupole DESI-MS/MS and Standard Additions (BMSS Summer Student 2023)***
Georgia Millard, Robert Bradshaw, Malcom R Clench, Laura M Cole

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107 **Accelerated Analysis of Structurally Related Components in Complex Samples**
Anne Marie Smith, Alexander Lishchuk, Alexander Sakharov, Baljit Bains

108 **Conversion and integration of OMICS data from a prototype, benchtop multi-reflecting time-of-flight (MRT) platform with third-party informatic workflows**
Lee Gethings

109 **Identification of RDV metabolites from UPLC-MS/MS data by employing a KNIME-based and open-source tools**
Nouf Alourfi

NATIVE MS & PROTEOMICS

110 **Native Mass Spectrometry to Explore Mechanisms Governing Synaptic Communication**
Sophie A. S. Lawrence, Carla Kirschbaum, Jack L. Bennett, Corinne A. Lutomski, Tarick J. El-Baba, Carol V. Robinson

111 **Hybrid Mass Spectrometry methods to evaluate the design of novel photoenzymes***
Jason Michael Drosos Kalapothakis

112 **Can protein structural information be inferred from Native top down electron capture dissociation mass spectrometry?**
Peter Fox

113 **Automated molecular glues screening using native mass spectrometry**
Sue Mayfield

114 **Development of top-down capillary electrophoresis-mass spectrometry to explore labile modifications as part of the histone ‘code’***
Olga Tereszkowska-Kaminska, Andrew J. Chetwynd, Allen Po, Claire E. Eyers

115 **Structural elucidation of FAN1 and MutLalpha complexes involved in DNA repair and Huntington’s disease***
Fanindra Kumar Deshmukh, Konstantinos Thalassinos

116 **Native Mass Spectrometry Reveals Shuttle Protein Conformational Dynamics Under Conditions Promoting and Reversing Liquid-Liquid Phase Separation**
Mxolisi Madoda

117 **Native mass spectrometry for elucidating changes in the oligomeric state of proteins from human pathogens**
Victor Mikhailov, Faisal Alshref, Anka Lucic, Tika Malla, Peijun Zhang, James McCullagh, Christopher Schofield

118 **Expanding native mass spectrometry capabilities for soluble and membrane proteins using a quadrupole-ion mobility-time-of-flight mass spectrometry system**
Dale Cooper-Shepherd, Anthony G Sullivan, Kleitos Sokratos, Mario Hensen, Jonathan T.S. Hopper, James I. Langridge

119 **Improved proteome coverage combined with reproducible quantitation on the timsTOF platform**

Nachal Subramanian, Stephanie Kaspar-Schoenefeld, Andreas Schmidt, Markus Lubeck, Pierre-Olivier Schmit, Torsten Mueller

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120 **HRMS Characterisation of novel psychoactive substances from seized street drug samples**
Alan Barnes, David I. Dixon, Molly F. Millea, Ryan E. Mewis, Chris Titman, Emily Armitage, Oliver B. Sutcliffe, Neil Loftus

121 **Optimisation of Mass Spectrometry Parameters Using Response Surface Modelling**
Rachel Williams, David Bernstein, James McCullagh

122 **Validated quantitative liquid chromatography-tandem mass spectrometry method for a large panel of 29 human urinary steroids***
Joshua T Bain, Fozia Shaheen, Lorna C Gilligan, Angela E Taylor

123 **Investigation of the nitroso radical loss from N-nitrosamines using density functional theory calculations**
Stephen Holman

124 **Contaminants In Recycled PET water bottles**
Steve Corless, Chris Hopley, Rosemary Rupesinghe

125 **A validated LC-MS/MS quantification method for β-lactams intended for use in clinical assays**
Alfred Charlesworth, Dan Lane, Pankaj Gupta, Donald Jones

126 **Investigation of ion suppression from HPLC columns**
Matt James, Tony Edge

127 **Comparison of ionisation techniques for the detection of catecholamines and metabolites**
Rhodri Owen

128 *Poster Withdrawn*

ION MOBILITY

129 **Investigating the metabolic fate of modified oligonucleotide therapeutics using cyclic IMS enabled high resolution mass spectrometry**
Adam King, Rebecca Hansen, Ruisong Pei, Martin Palmer, Emma Marsden-Edwards, Joseph Marini

130 **Exploring the effects of sequence variants on human islet amyloid polypeptide oligomerisation using cyclic ion-mobility mass spectrometry and ECD***
Zijie Dai, Daniel Raleigh, Konstantinos Thalassinos

SYSTEMS BIOLOGY & RARE DISEASES

131 **Investigating metabolic response to Hypoxia in IDH1 mutant glioma cells using IC-MS-based untargeted metabolomics**
Thomas Cadoux-Hudson

132 *Poster Withdrawn*

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133 **Improved non-target and suspect analysis of complex samples by a novel GC-EI/CI-TOF**
Nora Williams, Arnd Ingendoh, Erik van Balderen, Marlene Vetter, Sonja Klee, Steffen Braekling

134 **Characterization of Glucosinolates in Arabis sagittata Extracts using a Multi-Reflecting Q-Tof Mass Spectrometer**
Martin Palmer, Emma Marsden-Edwards, George Just, Isabel Riba, Sabine Metzger, Vera Wewer

135 **Development of a Lipidomics Assay to Further Mechanistic Understanding of Parkinson's Disease***
Caitlin Walton-Doyle, Thomas Hoare, Eleanor Sinclair, Minhui Zhu, Lea Van Dissel, Matthew Russell, Katherine A. Hollywood, Drupad K. Trivedi, Perdita Barran

136 **Comprehensive discovery lipidomic workflow which utilises a novel, multi-reflecting ToF with integrated informatics, providing highly confident lipid characterisation and quantification**
Nyasha Clarence Munjoma, Jayne Kirk, Lee Gethings, Paolo Tiberi, Laura Gorraci, Richard Lock

137 **Mitochondrial oxysterols in Alzheimer's disease brain**
Irundika Dias

BIOMACROMOLECULAR STRUCTURE

138 **Optimizing Data Acquisition and Analysis in Cross-Linking Mass Spectrometry on the Orbitrap Astral Instrument**
Cong Wang

139 **Analysis of Large Biomolecules using Charge Detection Mass Spectrometry***
Anisha Haris, Rebecca J. D'Esposito, Kevin Giles, David, Keith Richardson, Jakub Ujma, Steve Preece

140 *Poster Withdrawn*

EMERGING METHODS & TECHNOLOGIES IN PROTEOMICS

141 **Use of Non-human Sera as a Highly Cost-Effective Internal Standard for Quantitation of Multiple Human Proteins***
Geraldine Williams

142 **Mass spectrometry-based single cell proteomic analysis of primary human neutrophils***
Alejandro J. Brenes, Rupert L. Mayer, Pranvera Sadiku, Leila Reyes, Paul M. Brennan, Ailiang Zhang, Patricia Coelho, Karl Mechtler, Sarah R. Walmsley

143 **Efficient and repeatable peptide desalting with AttractSPE®Disks Tips C18 in manual and fully automated proteomics workflows**
Florine Hallez, Michel Arotçarena, Sami Bayoudh, Kaynoush Naraghi, Florent Dingli, Damarys Loew, Célia Jardin, Soumia Hamada, Cédric Pionneau, Martin Technau, Solenne Chardonnet

144 **Capturing the polyUbiquitylome with pUb-STRACTER (Stringent Trypsin-Resistant Affinity Capture with Targeted Enzymatic Recovery)**
Harvey Johnston, Rahul Samant

145 **Robust and Versatile Two-Dimensional Chromatography system for Proteomics of Nanogram Scale Samples***
Eduardo S Kitano, Gareth Nisbet, Yana Demyanenko, Katarzyna M Kowalczyk, Louisa Iselin, Stephen Cross, Alfredo Castello, Shabaz Mohammed

146 **Mass spectrometry acquisition methods for subcellular spatial proteomics: a direct comparison of resolution and reproducibility***
Kieran McCaskie, Charlotte Hutchings, Yong-In Kim, Eneko Villanueva, Renata Feret, Lisa M. Breckels, Michael J. Deery, Kathryn S. Lilley

147 **Optimizing Sample Preparation Workflows for Single Cell Proteomics***
Atakan Arda Nalbant, Andrew M Frey, Matthias Trost

148 **Improving protein identification and quantitation with ZT Scan DIA**
Tom Ruane

149 **Comparison and characterisation of extracellular vesicles isolation techniques in the context of biomarker discovery***
Oliver Slingsby, Caitlin Maguire, Colleen Maxwell, Natalie Allcock, Tayyiba Shah, Donald Jones, Leong Ng

150 **Unlocking the proteomic potential of FFPE tissues with BeatBox® and iST: A xylene-free, high-throughput workflow for in-depth proteome analysis**
Adam Hughes

151 **High-Quality Human Plasma N-Glycoproteomics on a ZenoTOF using optimized combinations of CID and electron activated dissociation (EAD)**
Shelley Jager, Tatiana M. Shamorkina, Sibylle M. Heidelberger, Heather Chassaing, Victoria South, Karli R. Reiding, Albert J.R. Heck

152 **Quantifying 500 Proteomics Samples Per Day with ZT Scan**
Gina Eagle, Anjali Chelur, Stephen Tate, Claudia Alvarez, Gordana Ivosev, Nic Bloomfield

153 **iprm-PASEF: an integrated workflow for the analysis and interpretation of spatial on-tissue tandem mass spectrometry of lipids**
Mark Churchill, Nannan Tao, Bram Heijs, Tobias Boskamp, Soeren-Oliver Deininger, Nikolas Kessler, Corinna Henkel, Nadine T. Smit, Kate Stumpo, Angela Paul

154 **Dia-PASEF for in-depth immunopeptidomics analysis: Challenges and new opportunities**
Adam Watson, Kundan Sharma, K Marx, Gravel N Hoenisch, J Walz, T Mueller, PO Schmit

155 **Non-small cell Lung cancer single spheroid analysis using the cellenONE with proteoCHIP EVO 96 workflow on the timsTOF Ultra**
Angela Paul, Christoph Krisp, Verena Tellstroem, David Hartlmayr, Anjali Seth, Guilhem Tourniaire, Dorte Bekker-Jensen, Nicolai Bache, Roopesh Krishnankutty, Markus Lubeck

156 **The timsTOF Ultra enables deep global ubiquitinomics of ultra-low protein input samples for validating degrader drug targets**
Roopesh Krishnankutty, Kundan Sharma, Philipp Strohmide, Martin Steger, Uli Ohmayer, Bjoern Schwalb, Torsten Müller, Christian Albers

157 **Enabling scalable high-sensitivity proteomics by utilizing the unique analytical properties of the Evotip Pure with new Whisper Zoom methods**
Djordje Vasiljevic

160 **Identification of new and emerging pollutants and persistent organic pollutants in indoor and outdoor particulate matter using LC- and GC-Orbitrap-HRMS**
CRA Argamino, BG Sebben, G da Costa, S Towers, RHM Godoi, A Bogush, M McKenzie, S Stevanovic, I Kourtchev

161 **The capture of proteins in complex samples using molecular imprinting biopolymer chemistry in the field of proteomics**
Jatinderpal Sandhu, Donald JL Jones, Colleen B Maxwell, Thong H Cao, Paulene Quinn, Leong L Ng

DIGITAL ONLY POSTERS

(AVAILABILE AS PART OF THE POST-MEETING DIGITAL CONTENT)

158 **Multivariate optimization of a dispersive micro solid phase extraction method and HPLC-ESI-Triple Quadrupole Mass Spectrometry for simultaneous quantification of 20 plant growth regulators in algae and algae-based fertilizers**
Carlos Terriente Palacios

159 **Detection of antimicrobial proteins/peptides and bacterial proteins involved in antimicrobial resistance in cow's milk from different breeds**
Cristian Piras, Rosario De Fazio, Carlotta Ceniti, Antonella Di Francesco, Vincenzo Cunsolo, Domenico Britti, Rainer Cramer, Paola Roncada