MSB2017

33rd International Symposium on Microscale Separations and Bioanalysis

Noordwijkerhout
The Netherlands
March 26-29

Programme Book

SYMPOSIUM CO-CHAIRS
Govert W. Somsen *(Vrije Universiteit Amsterdam)*
Rawi Ramautar *(Leiden University)*

MSB2017
THE NETHERLANDS
NOORDWIJKERHOUT
MARCH 26-29

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Welcome from the co-chairs of MSB 2017

It is our great pleasure to welcome you to the 33rd International Symposium on Microscale Separations and Bioanalysis (MSB 2017) being held March 26-29, 2017 at the Conference Center Leeuwenhorst in Noordwijkerhout, The Netherlands.

Originally started in 1989 as HPCE symposium, over the years MSB has evolved into an annual interactive forum for the discussion of research on the frontiers of microscale separation science and bioanalysis. Continuing this development, MSB 2017 will span the full range of microscale separation research, from fundamental technology development to high-impact applications relevant to health, medicine, food, forensics and the environment. The meeting is structured with short courses, plenary and parallel oral sessions, poster sessions and pitches, Science Cafe seminars, and a panel discussion. In order to assist you navigating through the versatile program, the contributed oral presentations have been divided into three main themes that run throughout the conference: Performance, Hyphenation and Impact.

Next to 20 invited plenary and keynote lectures by world-renowned experts, the MSB 2017 scientific program comprises 59 oral presentations that have been selected by blind review, giving ample room to quality and talent. With more than 50% of the oral presenters being 35 years of age or younger, MSB 2017 truly gives the floor to a young generation that will shape the future of separation science.

The success of MSB 2017 will depend not only on the outstanding cast of knowledgeable speakers, but also on the interactions that take place among the attendees. Therefore, in each keynote and oral presentation, 1/3 of the time is rigorously reserved for discussion to stimulate exchange of ideas and information. We call upon you as symposium delegate to participate whole-heartedly in the discussions.

Just mentioning Van Deemter curves and Poppe plots, and you will recognize that MSB 2017 builds upon a rich history and longstanding reputation of separation science in The Netherlands. With respect to microscale dimensions, The Netherlands is also well known for its efficiency, small distances and compactness. The symposium venue will additionally safeguard microscale performance by providing on-site lodging, full catering, and closely-grouped lecture and poster rooms. An extensive social program, which is open to all registered delegates, will further contribute to an intimate atmosphere for optimum scientific interaction.

At the start of the symposium we would like to thank you for your contribution and participation, and acknowledge our sponsors for their generous support. Without delegates and sponsors there would be no symposium. We warmly invite all of you to join us in creating a stimulating microclimate for a vigorous MSB 2017 event.


Govert W. Somsen
Rawi Ramautar
(Co-chairs MSB 2017)

Committees

MSB 2017 Symposium Co-chairs
Govert W. Somsen, Vrije Universiteit Amsterdam
Rawi Ramautar, Leiden University

MSB 2017 Organizing Committee
Govert W. Somsen, Vrije Universiteit Amsterdam
Rawi Ramautar, Leiden University
Gerard Rozing, ROZING.COM Consulting, Karslruhe
Cari Sänger-van de Griend, Kantisto, Baarn
Henk Lingeman, Vrije Universiteit Amsterdam
Rob Haselberg, Vrije Universiteit Amsterdam
Jeroen Kool, Vrije Universiteit Amsterdam

MSB Strategic Program Committee
James Landers, Charlottesville, USA, Committee Chairman
Michael Lämmerhofer, Tübingen, Germany, Committee Secretary
Gerard Rozing, Karlsruhe, Germany, Webmaster
Michael Breadmore, Hobart, Australia
Jeff Chapman, Brea, USA
Herbert Lindner, Innsbruck, Austria
Sergey Krylov, Toronto, Canada
Jörg Kutter, Kopenhagen, Denmark
Julie Schappler, Geneva, Switzerland
Marina Tavares, Sao Paulo, Brazil

Symposium history

Originally established as the International Symposium on High Performance Capillary Electrophoresis (HPCE), the first event was held April 10-12, 1989, at the Park Plaza Hotel in Boston, MA. The meeting was founded by Professor Barry Karger from Northeastern University. This first meeting featured presentations discussing the principles of separation in capillaries under high electrical fields, including instrumentation development and applications, particularly in biotechnology.

The HPCE symposium was introduced at the moment when capillary electrophoresis (CE) branched off from the HPLC community, giving the technology the necessary focus at a time when CE instrumentation was first being commercialized. The symposium series was driven by the Scientific Advisory Board (SAB) under its diligent chairman Barry Karger until 2000, followed by Frantisek Svec. The series was organized world-wide by Prof. Karger until 2000, and after that by CASSS in the USA, and by separate bodies in Europe and Asia.

At HPCE 2004 in Salzburg, the SAB changed the symposium name to MicroScale Bioseparations (MSB), since the attendees' interests expanded into the related techniques of micro- and nano-HPLC, microfluidic separations, and Lab-on-a-Chip applications, while the fascination with CE slowly decreased. The stylized logo was created at the same time, and captured the acronym MSB in a DNA helix motif given the prominent role that electrical driven microseparations have played in DNA sequencing and the early completion of the Human Genome Project.

At MSB 2012 in Geneva, Switzerland, Beckman-Coulter established the prestigious Arnold O. Beckman Medal and Award for Outstanding Scientific Achievements in The Field of Electrodriven Separations Techniques which has become an essential element of the MSB series.

After the MSB 2012 symposium, the SAB changed. Not just by including new members, but especially by introducing new key concepts by which future meetings of the series will be organized. The symposium aims to create a confidential ambience with significant room for discussion and with over seventy percent of the program built from contributed abstracts using a blind review process. The board also changed its name to Strategic Program Committee (SPC).

In order to further broaden the scope of the series to a wider range of scientists, the SPC approved the acronym of MSB to refer to Microscale Separations and Bioanalysis. The new official conference name was used for the first time at MSB 2016 in Niagara-on-the-Lake, Canada.

Previous HPCE and MSB meetings

Year	*Location*	*Chair(s)*
1989	Boston	Barry L. Karger
1990	San Francisco	Barry L. Karger
1991	San Diego	James W. Jorgenson
1992	Amsterdam	Frans Everaerts
1993	Orlando	Barry Karger
1994	San Diego	Shigeru Terabe
1995	Würzburg	Heinz Engelhardt
1996	Orlando	Barry Karger
1997	Anaheim	William Hancock
1997	Kyoto	Shigeru Terabe
1998	Orlando	Barry Karger, S. Fanali
1999	Palm Springs	Edward Yeung
2000	Saarbrücken	Heinz Engelhardt
2001	Boston	Barry Karger, William Hancock
2002	Stockholm	Douglas Westerlund
2003	San Diego	Aran Paulus, Andras Guttman
2004	Salzburg	Wolfgang Lindner
2005	New Orleans	Michael Ramsey
2005	Kobe	Yoshinobu Baba, Koji Otsuka
2006	Amsterdam	Gerard Rozing
2007	Vancouver	Robert Kennedy
2008	Berlin	Andreas Manz
2009	Boston	Jonathan Sweedler
2009	Dalian	Hanfa Zou
2010	Prague	Frantisek Foret
2011	San Diego	Annelise Barron
2012	Geneva	Franka Kalman, Gerard Rozing, Jean-Luc Veuthey
2012	Shanghai	Rong Zeng
2013	Charlottesville	Jeff Chapman, James Landers
2014	Pécs	Ferenc Kilár, Attila Felinger, András Guttman
2015	Shanghai	Fukui Zhang, Pengyuan Yang, Norman Dovichi, Amy Guo
2016	Niagara-on-the-Lake	Philip Britz-McKibbin, Karen Waldron, Sergey Krylov
2017	Noordwijkerhout	Govert Somsen, Rawi Ramautar

Arnold O. Beckman Medal and Award

The Arnold O. Beckman Medal and Award for Outstanding Scientific Achievements in The Field Of Electrodriven Separations Techniques.

This annual award recognizes outstanding contributions to the field of electrodriven separation techniques and comprises a medal, diploma and a $5,000 prize, as well as the reimbursement of reasonable travel expenses to the MicroScale Separations and Bioanalysis (MSB) symposium. The award recipient will have made an outstanding career achievement supported by a significant body of work in the field of electrodriven separations with particular consideration given to the developments of new methods, techniques, and high impact applications.

This award is presented annually during the MSB conferences in a special Award Plenary Session followed by a lecture from the recipient. The award is sponsored by SCIEX in the name of Dr. Arnold O Beckman whose inspiration was a key driver behind the first commercialization of capillary electrophoresis technology. The Arnold O. Beckman Medal and Award for Outstanding Achievements in the Field of Electrodriven Separations is one way that SCIEX continues to celebrate the spirit of scientific innovation that is critical to the advancement of MicroScale Separations.

SCIEX helps to improve the world we live in by enabling scientists and laboratory analysts to find answers to the complex analytical challenges they face. The company's global leadership and world-class service and support in capillary electrophoresis and liquid chromatography-mass spectrometry, have made it a trusted partner to thousands of the scientists and lab analysts worldwide who are focused on basic research, drug discovery and development, food and environmental testing, forensics and clinical research.

More information on Dr. Arnold O Beckman, whom this award is named in honor of, may be found at his foundation's website (http://www.beckman-foundation.org).

Previous winners of the Arnold O. Beckman Medal and Award:

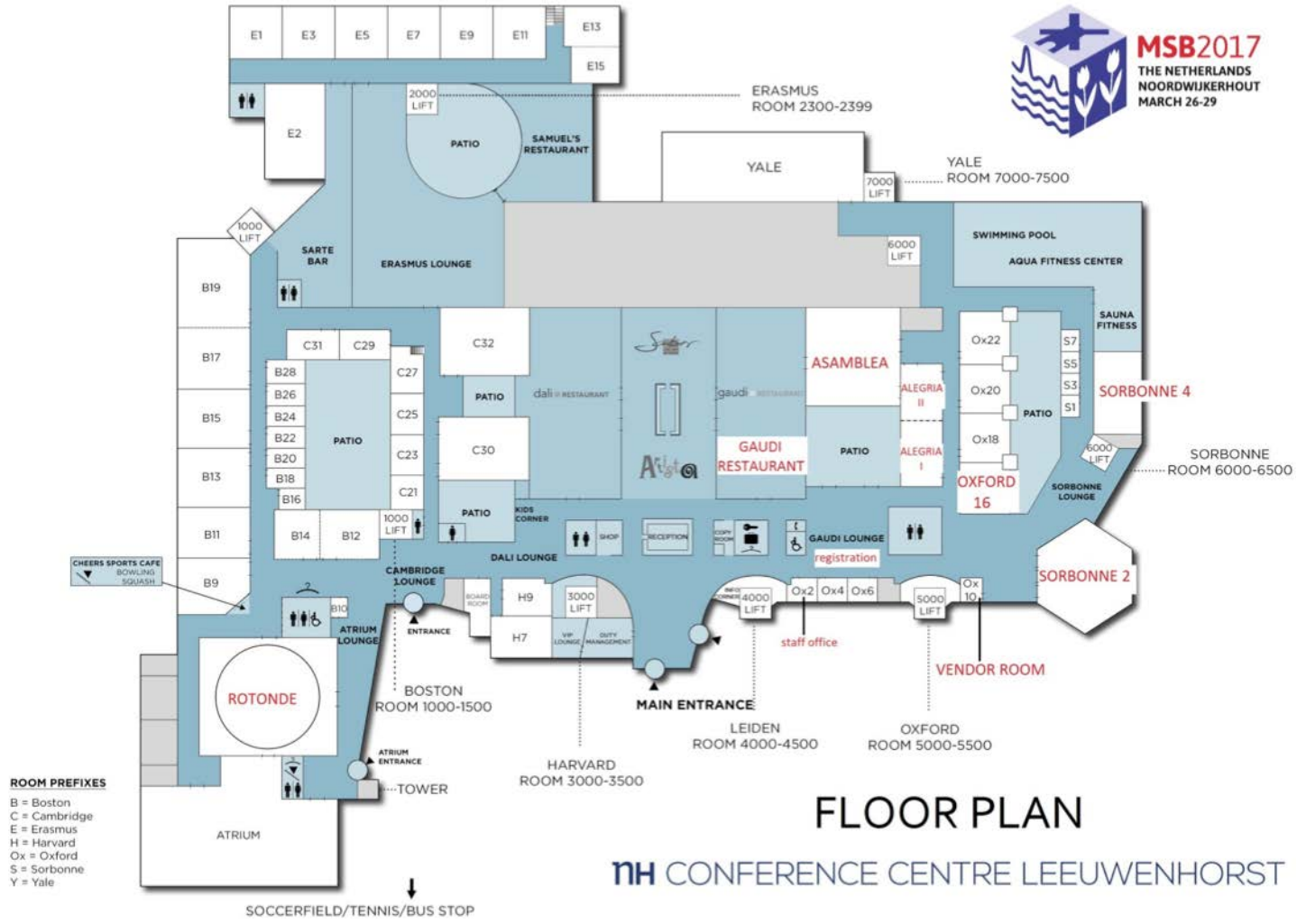
2016 Bohuslav Gaš
2015 Gyula Vigh
2014 Barry Karger
2013 Stellan Hjertén
2012 Pier Giorgio Righetti

Venue

NH Hotel and Conference Centre Leeuwenhorst
Langelaan 3
2211 XT Noordwijkerhout
The Netherlands
website: https://www.nh-hotels.nl/hotel/nh-noordwijk-conference-centre-leeuwenhorst

All symposium meeting rooms are located on the ground floor.

- The opening plenary session on Sunday will take place in room Rotonde.
- The plenary lectures on Monday, Tuesday and Wednesday will be in room Sorbonne 2.
- The oral sessions are in rooms Sorbonne 2, Sorbonne 4, and Oxford 16.
- Poster sessions, exhibitor table tops, and coffee breaks are in rooms Asamblea and Alegria I&II.
- Science Café seminars will be in Sorbonne 2.
- The Symposium Registration Desk is located in the Gaudi Lounge.



General information

Time zone
The Netherlands are in the Central European Time Zone, one hour later than GMT. The Netherlands switches to Daylight Saving Time (Summer Time) in the night from the 25th to the 26th of March 2017; the clock springs one hour forward.

Badge
The official symposium name badge must be worn by each registered participant in order to gain admittance to the meeting, symposium rooms and social gatherings. Badge sharing is not permitted.

Registration and information desk
The symposium registration desk is located in the Gaudi Lounge.
Opening hours:
Sunday 12:00 - 19:00
Monday 7:30 - 18:00
Tuesday 7:30 - 17:00
Wednesday 7:30 - 16:00

Exhibitors
Visit the exhibitors' table tops in the Asamblea and Alegria I&II rooms. Take the time to thank them for their generous support of the symposium by letting them share their latest services and products with you.

Shuttle bus
There will a shuttle bus service for MSB delegates for the transfer from Sassenheim Station to the NH Hotel & Conference Center Leeuwenhorst and vice versa.
Service times:
Sunday March 26, 10:00 - 17:00 hrs
Wednesday March 29, 17:00 - 19:00 hrs

WiFi
WiFi will be made available to all delegates. Passwords are indicated throughout the Conference Center.

Short Courses

MSB 2017 offers four stimulating and highly informative short courses for symposium participants. The short courses are lectured by recognized experts in the field and run in parallel on Sunday, March 26 from 13:00 to 16:00. The course fee is 80 Euro. Registration is possible until March 25 by writing an email to msb2017@caos.nl.

Two-dimensional liquid chromatography (Room Oxford 16)
presented by Dr. Andrea Gargano and Bob Pirok MSc, Centre for Analytical Sciences Amsterdam (a.gargano@vu.nl)
This short course will describe theory and operative principles of two-dimensional liquid chromatography (LC×LC), focusing in particular on recent developments of on-line approaches. Applications of LC×LC will be presented demonstrating the characterization of complex samples from diverse research areas, such as proteomics, food science, lipidomics and polymer analysis.

Ion mobility-mass spectrometry (Room Oxford 18)
presented by Dr. Albert Konijnenberg, University of Antwerp (albert.konijnenberg@uantwerpen.be)
Recent advances in ion mobility-mass spectrometry (IM-MS) have uniquely positioned the technique for the analysis of complex samples. Ultra-fast electrophoretic gas-phase separations on the basis of three-dimensional molecular structure are offered by IM, while accurate mass data is provided by MS. This short course will focus on principles and emerging instrumental configurations of IM-MS, and the application of IM-MS methods in biosciences and beyond.

Bioactivity screening analytics (Room Oxford 22)
presented by Dr. Jeroen Kool, Vrije Universiteit Amsterdam (j.kool@vu.nl)
During this course modern analytical screening techniques for activity & affinity profiling of biologically active mixtures will be discussed. Focus will be on state-of-the-art miniaturized analytics for the characterization of bioactives in complex samples. These techniques will be treated in relation to their application in drug discovery & ADME, metabolic profiling, screening of natural extracts (e.g. venoms), and environmental analysis (toxicant detection).

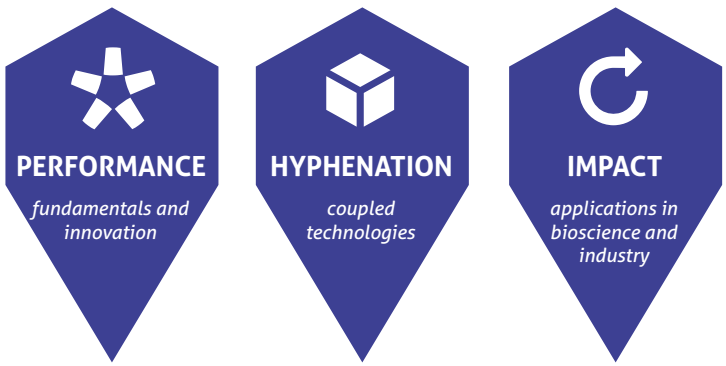
Robust capillary electrophoresis (Room Oxford 20)
presented by Dr. Cari Sänger - van de Griend, Kantisto BV (cari.sanger@kantisto.nl)
After a short repeat of the fundamentals of capillary electrophoresis (CE), approaches to development and optimize robust and precise methods will be discussed. Attention will be paid to the influence of key operating parameters and to good working practices. Many practical examples and applications from the pharmaceutical and biotechnology industry will be discussed. Although the focus is on pharmaceuticals, the principles apply for most quantitative CE methods.

Scientific Programme

Sunday, March 26

13:00	**Short course 1** room: Oxford 16 **Two-dimensional liquid chromatography** Andrea Gargano and Bob Pirok *(Center for Analytical Sciences Amsterdam)*	**Short course 2** room: Oxford 18 **Ion mobility-mass spectrometry** Albert Konijnenberg *(University of Antwerp)*	**Short course 3** room: Oxford 20 **Bioactivity screening analytics** Jeroen Kool *(Vrije Universiteit Amsterdam)*	**Short course 4** room: Oxford 22 **Robust capillary electrophoresis** Cari Sänger *(Kantisto)*
	Opening Plenary Session room: Rotonde co-chairs: Govert Somsen *(Vrije Universiteit Amsterdam)* and Rawi Ramautar *(Leiden University)*			
17:00	**Opening ceremony**			
17:15	PL1 - Vaccine development and bioanalysis: an industry perspective Jerome Custers *(Janssen Vaccines & Prevention)*			
18:00	PL2 - High-power one-, two-, and three-dimensional liquid-chromatographic separations Peter Schoenmakers *(University of Amsterdam)*			
18:50	**Welcome Reception** room: Atrium Lounge			
21:00				

Main themes oral presentations



YS = Young Scientist

Monday, March 27

Plenary Session
room: Sorbonne 2
chair: Maarten Honing *(DSM Resolve)*

8:30 PL3 - Microfluidics in biotherapeutic development: enhancing throughput and allowing for heightened characterization
Nathan Lacher *(Pfizer)*

	(Bio)Pharma-meets-microscale-separations Session 1 **room: Sorbonne 2**	**Metabolomics & Biomarker Analysis Session** **room: Sorbonne 4**	**Microfluidic Separations & Lab-on-a-Chip Session** **room: Oxford 16**
9:25	**Introduction by the session chair** Cari Sänger *(Kantisto)*	**Introduction by the session chair** Oleg Mayboroda *(Leiden University Medical Center)*	**Introduction by the session chair** Jörg Kutter *(University of Copenhagen)*
9:30	KN3 - **Why analytical science is ever more needed to develop biopharmaceuticals in the 21st century** Marta Germano *(Janssen Vaccines & Prevention)*	KN2 - **Robust CE-MS methods for metabolomics: achieving greater throughput, lower costs and better data comparability** Philip Britz-McKibbin *(McMaster University)*	KN1 - **One- and two-dimensional chip-HPLC coupled to MS** Detlev Belder *(University of Leipzig)*
10:00	Or11 - **Glycosylation of recombinant antigens from Mycobacterium tuberculosis: analytical challenges in a glycovaccine development** Caterina Temporini *(University of Pavia)*	Or6 - **Metabolic profiling of biomass-limited samples from a mouse model of polycystic kidney disease by sheathless CE-MS** Elena Sánchez-López *(University of Alcala)* YS	Or1 - **Microfluidic sample preparation combined with ultrasensitive nanoLC-MS for deep proteome analysis of 10–140 cells** Ryan Kelly *(Pacific Northwest National Laboratory)*
10:20	Or12 - **CE-MS for intact mass analysis of antibodies and antibody-drug-conjugates** Aran Paulus *(Thermo Fisher Scientific)*	Or7 - **Anion chromatography coupled to high resolution mass spectrometry: a powerful tool for targeted and non-targeted metabolomics** Michaela Schwaiger *(University of Vienna)* YS	Or2 - **MicroTAS for IMAC preconcentration, separation and detection of phosphorylated biomarkers** Myriam Taverna *(Université Paris-Sud)*
10:40	**Coffee break** in Asamblea and Alegria I&II		
11:00	Or13 - **Characterization of Fc receptor biotinylation under controlled reaction conditions by MS and ligand binding analysis** Karin Lubbers-Geuijen *(Synthon Biopharmaceuticals)* YS	Or8 - **Analytics in microbiome: investigating quorum sensing peptides** Nathan Debunne *(DruQuaR)*	Or3 - **Low-cost environmental diagnostics enabled by novel hybrid microsystems** Vincent Remcho *(Oregon State University)*
11:20	Or14 - **Improving the sensitivity for LC-MS quantitation of biologics in plasma using trap-and-elute microLC-MS** Remco van Soest *(Sciex)*	Or9 - **Metabolomics approach towards understanding rare cardiovascular diseases** Renata Wawrzyniak *(Medical University of Gdansk)* YS	Or4 - **Orthogonal charge- and size-based separations of polymer microparticles in non-uniform microfluidic channels** Sergio Fernandez-Posa *(University of Groningen)*

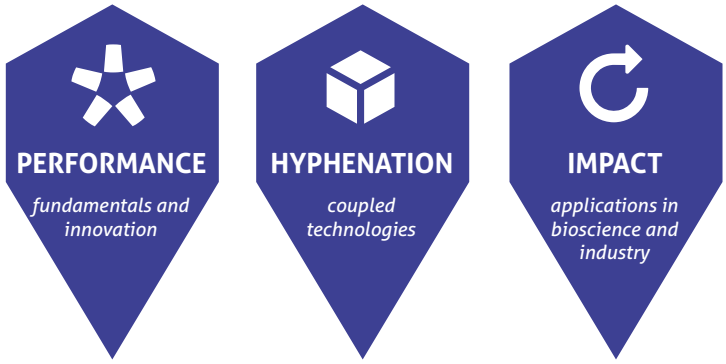
Monday, March 27

11:40	Or15 - **Forced degradation comparability of an AQbD-developed adenovirus quantification CZE method** Lars Geurink *(Janssen Vaccines and Prevention)* YS	Or10 - **Using metabolomics approach to investigate biochemical mechanisms involved in ultra-weak photon emission** Rosilene Rossetto Burgos *(Leiden University)* YS	Or5 - **Magnetic bead-based immunoassays coupled with isoelectric focusing of Aß peptides: towards microfluidic droplet manipulation** Thanh Duc Mai *(Institute Galien Paris-Sud)* YS
12:00			
12:15	**Science Café lunch** room: Sorbonne 2 presented by SCIEX		
13:15			
13:30	**Poster Pitches** room: Sorbonne 2 chair: Peter Schoenmakers *(University of Amsterdam)*		
14:00	**Poster Session 1** rooms: Asamblea and Alegria I&II		
15:15			
	(Bio)Pharma-meets-microscale-separations Session 2 **room: Sorbonne 2**	**Glycomics & Protein Analysis Session** **room: Sorbonne 4**	**Microcolumn Technologies & Separation Media Session** **room: Oxford 16**
15:25	**Introduction by the session chair** Michel Eppink *(Synthon/Wageningen University)*	**Introduction by the session chair** Herbert Lindner *(Innsbruck Medical University)*	**Introduction by the session chair** Gerard Rozing *(Rozing.com Consulting)*
15:30	KN6 - **Where industry meets academia in biopharma** Marc Eggink *(Synthon)*	KN5 - **Characterizing glycan and glycopeptide isomers derived from biological systems by LC-MS/MS** Yehia Mechref *(Texas Tech University)*	KN4 - **Impact of column diameter and flow rate on sensitivity and resolution in LC-UV and LC-MS separations** Monika Dittmann *(Agilent Technologies)*
16:00	Or26 - **N-glycosylation analysis of erythropoietin therapeutic formulations and bioprocess samples by MALDI-TOF-MS** David Falck *(Leiden University Medical Center)*	Or21 - **Glycan analysis by temperature gradient capillary electrophoresis. Some like it hot** Andras Guttman *(University of Debrecen)*	Or16 - **From analytical to nano flow LC-MS: high robustness and sensitivity to answer complex biological questions** Remco Swart *(Thermo Fisher)*
16:20	Or27 - **Ultra-fast pH-gradient ion exchange chromatography for the separation of monoclonal antibody charge variants** Robert van Ling *(Thermo Fisher Scientific)*	Or22 - **Sialic acid derivatization strategies for MALDI-TOF-MS profiling of glycans and glycopeptides in complex samples and tissues** Noortje de Haan *(Leiden University Medical Center)* YS	Or17 - **Benchmarking pillar array columns optimized for high peak capacities** Wim De Malsche *(Vrije Universiteit Brussel)*
16:40	**Coffee break** in Asamblea and Alegria I&II		

Monday, March 27

	(Bio)Pharma-meets-microscale-separations Session 2 (continued) **room: Sorbonne 2**	Glycomics & Protein Analysis Session (continued) **room: Sorbonne 4**	Microcolumn Technologies & Separation Media Session (continued) **room: Oxford 16**
17:00	**Panel discussion** **Two sides of Science** room: Sorbonne 2 chair: Martin Donker *(Isogen)*	Or23 - **Analysis of proteins, protein complexes, and proteomes using sheathless CZE-MS under native conditions** Alexander Ivanov *(Northeastern University)*	Or18 - **Development of microfluidic chip technology to achieve unprecedented separation performance** Jelle De Vos *(Vrije Universiteit Brussel)* YS
17:20		Or24 - **Glycosylation analysis of prostate specific antigen – towards improved diagnosis of prostate cancer** Guinevere Kammeijer *(Leiden University Medical Center)* YS	Or19 - **High sensitivity and selectivity in analysis of drugs in plasma using 4D micro-UHPLC-MS enabling enhanced sample loadability** Ronald de Vries *(Janssen Pharma)*
17:40		Or25 - **Characterization of Isomeric Glycans In Pancreatic Diseases by GRIL and ZIC-HILIC-MS combined with Exoglycosidase Digestion** Estela Gimenez *(University of Barcelona)*	Or20 - **3D-print of planar separation media** Gertrud Morlock *(Justus Liebig University)*
18:00			
19:00		**Conference dinner** Restaurant Gaudi	
21:00			

Main themes oral presentations



YS = Young Scientist

Tuesday, March 28

Plenary Session
room: Sorbonne 2
chair: James Landers *(University of Virginia)*

8:30 **Presentation of Arnold O. Beckman Medal**
Jeff Chapman *(Sciex)*

8:45 PL4 - **Lecture of Beckman Medal awardee TBA**

9:15

	Multidimensional Separations & Lipidomics Session room: Sorbonne 2	**Young Scientists Session room: Sorbonne 4**
9:25	**Introduction by the session chair** Michael Lämmerhofer *(University of Tübingen)*	**Introduction by the session chair** Rob Haselberg *(Vrije Universiteit Amsterdam)*
9:30	KN7 - **Microscale online comprehensive two-dimensional LC – second thoughts on speed, efficiency and selectivity** Thorsten Teutenberg (Institute of Energy- and Environmental Technology)	KN8 - **Pushing the boundaries of lipid research (and your own boundaries)** Jurre Kamphorst *(University of Glasgow)* YS
10:00	Or28 - **Toward high-throughput & high-resolution comprehensive 2D HPLC analysis of intact proteins: a parallel 2nd-D column approach** Shaorong Liu (University of Oklahoma)	Or33 - **Development of an ion chromatographic microfluidic chip platform integrating separation, suppression, and detection** Sam Wouters *(Vrije Universiteit Brussel)* YS
10:20	Or29 - **Online 2DLC meets top-down MS: WCX/a×m/RPLC UVPD-HRMS analysis of histone isoforms, a method with a long name and many forms** Andrea Gargano (Center for Analytical Sciences Amsterdam) YS	Or34 - **Novel CZE method for the quantification of intact adenovirus particles – QbD method development and implementation** Ewoud van Tricht *(Janssen Vaccins and Prevention)* YS
10:40	**Coffee break** in Asamblea and Alegria I&II	
11:00	Or30 - **Hyphenating IC and CE: The Development of a comprehensive system and its application to arsenic speciation analysis** Andrea Beutner *(University of Regensburg)* YS	Or35 - **Longitudinal plasma metabolic changes associated with cortical spreading depression in a transgenic mouse model of migraine** Isabelle Kohler *(Leiden University)* YS
11:20	Or31 - A laminar flow interface for efficient coupling of CE to capil**lary array electrophoresis for multidimensional separations** John Chin *(Concordia University)*	Or36 - **Glucose Unit calculation for CE analysis without the use of the maltooligosaccharide ladder** Gabor Jarvas *(University of Pannonia)* YS
11:40	Or32 - **A novel structure elucidation strategy of bacterial Lipid-A applying HPLC-MS/MS for future vaccine adjuvant bioanalysis** Agnes Dörnyei *(University of Pécs)*	Or37 - **A CE-based Method for the analysis of hIAPP oligomers involved in Type 2 Diabetes and the screening of aggregation inhibitors** Corentin Berardet *(Institut Galien Paris Sud)* YS
12:00		

Tuesday, March 28

12:15	**Science Café lunch** room: Sorbonne 2 presented by AGILENT TECHNOLOGIES	
13:15		
13:30	**Poster Pitches** room: Sorbonne 2 chair: Peter Schoenmakers *(University of Amsterdam)*	
14:00	**Poster Session 2** rooms: Asamblea and Alegria I&II	
15:15		
	Advanced Detection Strategies Session **room: Sorbonne 2**	**Forensic Analysis Session** **room: Sorbonne 4**
15:25	**Introduction by the session chair** Christopher Birch (University of Virginia)	**Introduction by the session chair** Marina Tavares *(University of Sao Paulo)*
15:30	KN9 - **Nanoscale measurements of vesicle content in solution, in cells, and in varicosities** Andrew Ewing *(Chalmers University & University of Gothenburg)*	KN10 - **The potential and challenges of rapid chemical and toxicological analysis in forensic science** Arian van Asten *(Netherlands Forensic Institute/University of Amsterdam)*
16:00	Or38 - **Analysis of polyvinyl alcohol microbubbles with different detectors** Leila Josefsson (KTH - Royal institute of Technology) YS	Or40 - **CZE automated fraction collection for the analysis of sexual assault evidence** Sarah Lum *(University of Notre Dame)* YS
16:20	Or39 - **Development of multi-parametric surface plasmon resonance for living cell sensing** Teemu Suutari (University of Helsinki/Vrije Universiteit Amsterdam) YS	Or41 - **Separation of organophosphate nerve agents by CE and microchip CE** Xi Cao *(Tyndall National Institute)* YS
16:40		
17:00	All-participant Excursion Keukenhof & Dinner	
21:00		

Wednesday, March 29

Plenary Session
room: Sorbonne 2
chair: Michael Ramsey *(University of North Carolina)*

8:30 PL5 - **A mass spectrometry view into diverse aspects of glycobiology**
Albert Heck *(Utrecht University)*

9:15

	CE-MS & Advanced MS Techniques Session room Sorbonne 2	**Sample Preparation Session: room: Sorbonne 4**
9:25	**Introduction by the session chair** Jeff Chapman *(Sciex)*	**Introduction by the session chair** Julie Schappler *(University of Geneva)*
9:30	KN11 - **CE-MS as a robust routine tool in clinical diagnosis** Harald Mischak *(Mosaiques-diagnostics/University of Glasgow)*	KN12 - **Microextraction through supported liquid membranes - Tuning the extraction chemistry for biomedical and pharmaceutical applications** Stig Pedersen-Bjergaard *(University of Oslo)*
10:00	Or42 - **Thiol-ene micropillar electrospray ionization platform for zeptomole level bioanalysis** Risto Kostiainen *(University of Helsinki)*	Or47 - **Microsampling and micropreparation of biological fluids for sensitive quantitation of estetrol by LC-(Chip)-MS/MS** Marianne Fillet *(University of Liege)*
10:20	Or43 - **Investigation of a multiply post-translationally modified brain protein by CE-MS** Betina Sarg *(Innsbruck Medical University)*	Or48 - **From hours to minutes: fast and sensitive profiling of the human tissues and biofluids** Irena Dapic *(University of Amsterdam)* YS

10:40 Coffee break in Asamblea and Alegria I&II

11:00	Or44 - **CE-MS for the assessment of protein conformers** Elena Dominguez-Vega *(Vrije Universiteit Amsterdam)* YS	Or49 - **Novel capillary isoelectric focusing device increases the depth of proteomics analysis** Roman Zubarev *(Karolinska Instutet)*
11:20	Or45 - **The application of capillary electrospray ionization to the detection of neuropeptides** Stephen Lock *(Sciex)*	Or50 - **Electroextraction coupled to CE-MS: a new tool for metabolomic profiling of biomass-limited samples** Amar Oedit *(Leiden University)* YS
11:40	Or46 - **Combining native ion mobility and top-down mass spectrometry for conformational footprinting of heterogeneous protein ensembles** Albert Konijnenberg *(University of Antwerp)* YS	Or51 - **Automated enzyme microreactor fabrication in a CE instrument for proteomics applications** Karen Waldron *(University of Montreal)*

12:00

12:15 **Science Café lunch**
room: Sorbonne 2
presented by ISOGEN LIFE SCIENCE

13:15

Wednesday, March 29

	Electrodriven Separations Session room: Sorbonne 2	Affinity, Bioactivity and Bioanalysis Session room: Sorbonne 4
13:25	**Introduction by the session chair** Sergey Krylov *(York University)*	**Introduction by the sesion chair** Jeroen Kool *(Vrije Universiteit Amsterdam)*
13:30	KN13 - **Some thoughts on electrodriven separations: Fields, friction, fluids, and free energy** Stephen Weber *(University of Pittsburgh)*	KN14 - **Simultaneous analysis of enzyme structure and activity by kinetic CE-MS** Maxim Berezovski *(University of Ottawa)*
14:00	Or52 - **Solid state electrophoresis** Rosanne Guijt *(University of Tasmania)*	Or56 - **Playing the ACE card for ligand binding assays** Herman Wätzig *(University of Braunschweig)*
14:20	Or53 - **An integrated, centrifugally-driven microdevice for the electrophoretic separation of DNA** Brandon Thompson *(University of Virginia)* YS	Or57 - **Fraction collection of full GC separations in 384-well plates with parallel MS detection for bioactivity screening** Willem Jonker *(Vrije Universiteit Amsterdam)* YS
14:40	Coffee break in Asamblea and Alegria I&II	
15:05	Or54 - **Organelle fractionation for subpopulation analysis** Daihyun Kim *(Arizona State University)* YS	Or58 - **Getting more with less: Improving sensitivity and reducing sample consumption with micro-LC/MS assays in bioanalysis** Eric van Beelen *(Waters)*
15:25	Or55 - **CE-C4D method development and validation for the determination of azithromycin, clarithromycin and clindamycin** Prasanta Paul (KU Leuven) YS	Or59 - **Quantitative profiling of endocannabinoids and related N-acylethanolamines in human CSF using nano LC-MS/MS** Vasudev Kantae *(Leiden University)* YS
15:45		
	Closing Plenary Session room: Sorbonne 2 co-chairs: Govert Somsen (Vrije Universiteit Amsterdam) and Rawi Ramautar (Leiden University)	
16:00	PL6 - **Microfabricated technologies for accomplishing liquid phase separations and mass spectrometry** Michael Ramsey (University of North Carolina)	
16:45	**Presentation of Best Poster Awards** Monika Dittmann (Chair Poster Award Jury)	
16:55	**Presentation of Young Scientist Award** Philip Britz-McKibbin (Chair Young Scientist Jury)	
17:00	**Invitation to MSB 2018, Sao Paulo, Brazil** Marina Tavares (chair)	
17:05	**Closing ceremony**	
17:15	**Farewell Reception** room: Gaudi Lounge	
18:00		

Science Cafe

Attend the Science Cafe seminars at MSB 2017 in room Sorbonne 2 on Monday, Tuesday, and Wednesday at 12:15, and find out about the latest advances in commercial separation technology. Lunch will be served. The seminars are presented by SCIEX, Agilent Technologies, and Isogen Life Science, respectively. Visit each vendor at office room Oxford 10 at the designated day for information, private meetings and presentations. Hours are 8:30 to 17:00.

Science Cafe Seminar presented by SCIEX
Monday March 27, 12.15-13.15
room: Sorbonne 2

Advances in the Separation of Post-Translational Modifications using CE-MS
Prof. Herbert Lindner *(Innsbruck Medical University, Austria)*

In this talk we show how CESI-MS, has been used to detect challenging post-translational modifications including deamidation in crude protein fractions. We will demonstrate how CESI-MS can be used to detect citrullination in intact and digested proteins and in combination with MS/MS and electron transfer dissociation (ETD) fragmentation, locate the presence of deiminated Arginine. Finally, we will discuss how CESI-MS can be used to separate and quantify individual positional isomers of isobaric mono-phosphorylated peptides obtained in the course of a kinase activity study.

Fast Glycan Labeling and Analysis: High-Resolution Separation and Identification in Minutes
Prof. Andras Guttman *(SCIEX, USA)*

There is a growing demand in the biopharmaceutical industry for rapid N-glycosylation profiling of biologics. We will present a fast glycan labeling and analysis approach using a novel magnetic bead-mediated process and a CE gel-buffer separation system to quickly profile glycoprotein N-linked carbohydrates. The rapid CE-LIF separation gave excellent yield, high reproducibility, supported large scale 96-well plate sample processing and was easy to automate. A triple-internal standard method significantly speeded up the glycoinformatics tasks and enabled precise glucose unit (GU) assignment of human IgG glycans (relative standard deviation ≤1.07%).

Science Cafe Seminar presented by Agilent Technologies
Tuesday March 28, 12.15-13.15
room: Sorbonne 2

Solutions for Orthogonal Separations using Electrophoresis and Chromatography and 2D-LC
Dr. Monika Dittmann and Dr. Martin Greiner (Agilent Technologies, Germany)

Analytical tasks in Biopharma are manifold and complex. In example for characterization of Antibodies trust in a single technique would have a high risk to miss details of the compound structure and quality. One approach to have a more complete view of the analyzed compound is to use different separation principles like Electrophoresis and Chromatography. Due to its different separation modes (separations based on compound mobility or on adsorption/desorption characteristics) scientists can expect real different results for the same complex mixture analyzed. The seminar provides some examples of peptide mapping by comparing CE/MS separations to LC/MS separations.
Another way using orthogonal effects with the same separation principle is Two-dimensional liquid chromatography (2D-LC). Here different stationary phases and selectivity's are used for complex mixtures to improve resolving power over conventional one-dimensional liquid chromatography. The seminar provides a basic overview on 2D-LC techniques and some separation examples of Biopharma relevant compounds.

Science Cafe Seminar presented by Isogen Life Science
Wednesday March 29, 12.15-13.15
room: Sorbonne 2

Whole Column-Imaged Capillary Iso-Electric Focusing for Protein Analysis
Dr. Martin Donker *(Isogen Life Science B.V., the Netherlands)*

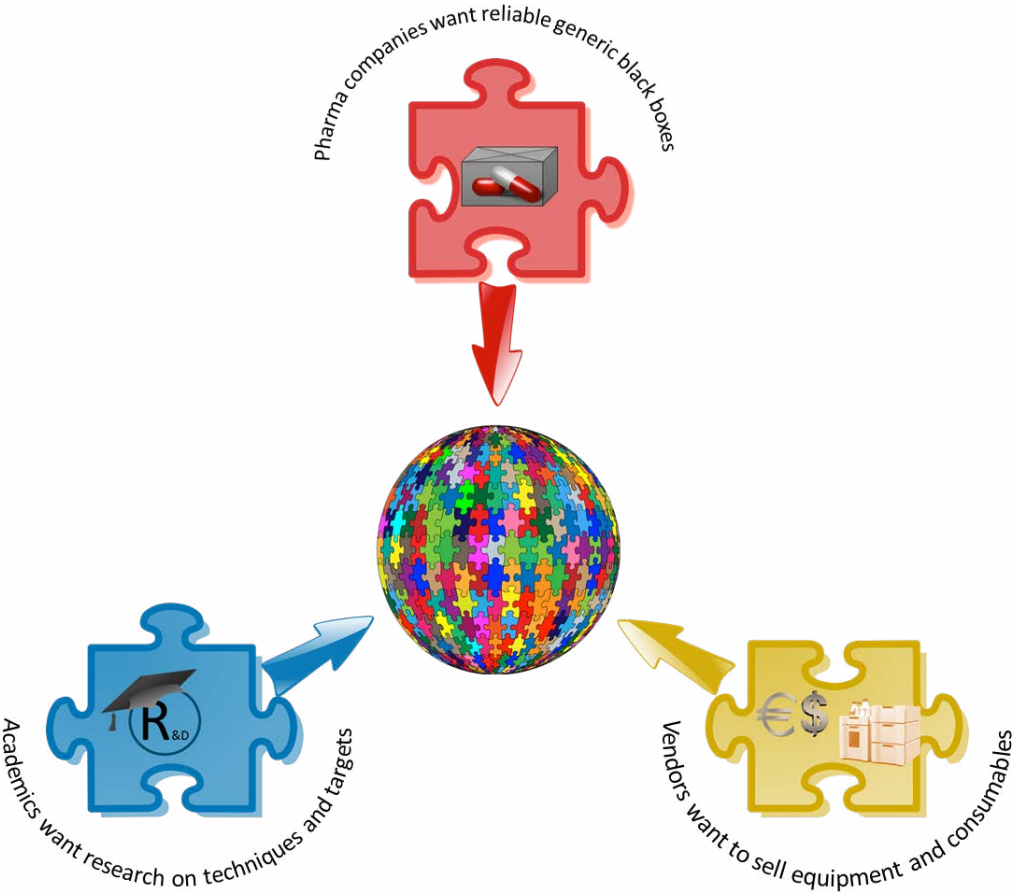
From unknown to having a charge based separation of your protein in only half a day is already common knowledge. But getting MS data from your charge based separation results is now available. The lunch session will be about the latest developments in whole column-imaged capillary IEF (WC-iCIEF).

Panel Discussion

Two Sides of Science

"It is harder to crack a prejudice than an atom." - Albert Einstein

Both academia and industry are fascinated in analytical sciences, but each has a different focus. Are these two sides of the same coin? Whereas analytical methods in Academia need to represent new science, in Biopharma these should address specific needs, e.g. product quality, process understanding, and to be reliable, reproducible and robust. Where and how can these two sides of science meet, and how can we ensure meeting in the middle? What is the role of vendors in all this? And, ultimately, how do we learn from each other?



Plenary speakers Abstracts & Biographies

PLENARY LECTURE 1 > Back to schedule
Opening Plenary Session

Sunday 17:15
Room: Rotonde

Vaccine development and bioanalysis: an industry perspective

Jerome Custers
Janssen Vaccines & Prevention

Short Biography

Jerome heads the research department responsible for design and development of prototype vaccine candidates against a series of viral infectious diseases. In addition, the department is involved in vaccine platform technology development and in supporting product development programs. The department consists of more than 60 scientific staff members. Jerome joined Janssen Vaccines in 2002 as a research scientist to work on the development of vaccines against a variety of infectious diseases based on adenoviral vectors. In 2004 he and his team switched to the product development group to fully support the development of several adenovector-based vaccine candidates for testing in clinical trials. Here he was involved in several pre-IND and IND processes. After a few years the team moved back to join vaccine research. Besides his work on adenoviral vectors, he now broadened his scope to work on whole inactivated vaccines like IPV and influenza, and to implement alternative viral vector systems (paramyxovirus) for vaccine development. Before joining Janssen Vaccines, Jerome worked as a molecular biologist in the plant biotechnology industry (Syngenta) for 8 years. He obtained his PhD from the University of Wageningen in 2007.

PLENARY LECTURE 2 > Back to schedule
Opening Plenary Session

Sunday 18:00
Room: Rotonde

High-power one-, two-, and three-dimensional liquid-chromatographic separations

Peter Schoenmakers
University of Amsterdam

Liquid-phase separations remain indispensable – together with mass spectrometry – to study the detailed composition of very complex mixtures. Especially in the life sciences many samples are so complex that we need all the separation power currently available – and more.

Liquid chromatography, which is the dominant liquid-phase separation technique, has progressed to a point where peak capacities up to 1,000 can be reached, be it at the expense of long analysis times (typically in excess of 10 hours). The most powerful one-dimensional separations are achieved on very long, narrow columns operated at low flow rates. Comprehensive two-dimensional liquid chromatography (LC×LC) offers much better separations (peak capacities of 5,000 or more) in a much shorter time (about 1 peak per second). LC×LC also offers a much-desired additional selectivity, allowing complex mixtures to be separated according to two very different "orthogonal" separation mechanisms. LC×LC puts requirements on (the speed of) mass-spectrometric

detection and on data-handling software, but it is experimentally rather straightforward and increasingly used in research and in industry.

However, for very complex samples a peak capacity of 5,000 may still be grossly inadequate. Comprehensive three-dimensional "spatial" LC promises unprecedented separation power, which estimated peak capacities approaching 1,000,000 in an overnight run. In this lecture, the principles of LC×LC and of spatial LC×LC×LC are reviewed. Some of the obstacles and possible ways to overcome these are discussed in this lecture.

Short Biography

Peter Schoenmakers has been a full-time professor in Analytical Chemistry (including its applications in forensic science) at the University of Amsterdam since 2002. His research focuses on analytical separations in general and on multi-dimensional liquid chromatography in particular. He obtained a Masters Degree in chemical engineering from the Technical University of Delft, The Netherlands and performed his PhD research with Professor Leo de Galan in Delft and with Professor Barry Karger in Boston, MA, USA. Thereafter he worked for Philips in Eindhoven (The Netherlands) and for Shell in Amsterdam and in Houston, TX, USA. While at Shell became a part-time professor in Polymer Analysis at the University of Amsterdam in 1998.
Peter Schoenmakers is also director of the van 't Hoff Institute of Molecular Science (HIMS) of the University of Amsterdam, an editor of the Journal of Chromatography A and the Education Director of COAST, The Netherlands' public-private-partnership organization on analytical chemistry. In 2016 he was awarded an ERC Advanced grant for the project STAMP (Separation Technology for A Million Peaks). Recent international awards include the CASSS Award (2015), the Csaba Horváth Memorial Award (2015), the John H. Knox Medal of the RSC (Belgium, 2014), the Martin medal of the Chromatographic Society (2011), and the EAS Award for Excellence in Separation Science (2010).
Peter Schoenmakers is a member of the Permanent Scientific Committee of the HPLC series of conferences and he was the chairman of HPLC2013 Amsterdam.

PLENARY LECTURE 3 > Back to schedule
Plenary Session

Monday 08:30
Room: Sorbonne 2

Microfluidics in biotherapeutic development: enhancing throughput and allowing for heightened characterization

Nathan Lacher
Pfizer

In biopharmaceutical development, there is a strong desire to enhance throughput to allow an organization sufficient bandwidth to support all process and formulation development activities that may simultaneously occur. There are many options available to the analytical lab but robustness is imperative for adoption of the technology. Technology that may not provide the level of quality expected from instrumentation within the quality control laboratory can be adopted within the development space if it is fit for purpose.

Conventional CE Instrumentation (Beckman and ProteinSimple) have been the workhorse for the biotherapeutic development and quality control laboratories. Microfluidic technologies including the GXII (Perkin Elmer), Bioanalyzer (Agilent), HPLC-chipLC (Agilent), and ZipChip (908 Devices) have been evaluated for potential replacement of conventional instrumentation based on expected throughput enhancements, ease of use, and

data quality. Applications that have been transferred to a microfluidic format include size heterogeneity (CE-SDS), charge heterogeneity (CZE), glycan analysis, and RNA/DNA analysis.

The general separation profiles achieved with microfluidic technology were consistent with profiles generated using conventional instrumentation. Minor differences in the profile and quantitation were evident in some cases that appear to be related to the molecular substrate. Despite minor differences in some cases, the technology has been applied within Pfizer to rapidly characterize process development design space. The technology was also successfully applied to support development of a non-mAb vaccine conjugate. More recently, the ZipChip has been utilized for analysis of intact and proteolytic mapping of monoclonal antibodies (mAbs) and antibody-drug conjugates (ADCs) offering CE-MS capability that did not previously exist within our organization.

Although data was generated using microfluidic technology that showed promise for adoption in the biotherapeutic development space, our organization has been slow to transition. This is mainly due to expectations for data quality to be on par with conventional systems which in our experience has not always been the case and seems to be dependent on the molecule being analyzed. An additional drawback may be the reduced flexibility that users may have with developing new applications within the provided framework. There are however areas where microfluidic technology does have a niche such as CE coupled to MS detection.

Short Biography

I am a Senior Principal Scientist in Pfizer BioTherapeutics Pharmaceutical Sciences in Chesterfield, MO. My background and training are in analytical chemistry. After obtaining a B.S. degree (Chemistry) from Buena Vista University (Storm Lake, IA) in 1999, I received a Ph.D. (Pharmaceutical Chemistry) in 2004 from Kansas University (Lawrence, KS) under the direction of Dr. Susan Lunte.

In 2004, I joined Pfizer working at the La Jolla Laboratories (La Jolla, CA) on the development of small molecule pharmaceuticals for ophthalmology and oncology in Analytical R&D. One of the first projects I worked on was the development of the initial FIH analytical package for Xalkori. Since 2005, I have worked on the development of biotherapeutic candidates covering a wide range of indications at the St. Louis Laboratories in Chesterfield, MO. I currently lead a group within Analytical R&D supporting development of prophylactic vaccines, therapeutic vaccines, and mAbs.

PLENARY LECTURE 4 > Back to schedule
Plenary Session

Tuesday 08:45
Room: Sorbonne 2

Lecture of the Arnold O. Beckman Medal awardee

Winner to be announced

The Arnold O. Beckman Medal and Award for Outstanding Achievements in the Field of Electrodriven Separations.

A mass spectrometry view into diverse aspects of glycobiology

Albert Heck
Utrecht University

Around for more than a century the analytical technique of mass spectrometry is blooming more than ever, and applied in nearly all aspects of the natural and life sciences. In the last two decades mass spectrometry has become routine for the high-throughput analysis of peptides and glycans, and to a lesser extent glycopeptides. However, also intact proteins and even complete protein complexes can nowadays be analyzed. In this lecture, I will describe the emerging role of mass spectrometry with its different technical facets in molecular and structural biology, focusing especially on the analysis of intact glycoproteins. Moreover, I will describe how we use native mass spectrometry to study dynamic protein assemblies, especially those involved in complement activation.

Recent developments in mass spectrometry technology have allowed us to analyze intact native glycoproteins and protein complexes using Q-ToF and Orbitrap mass analyzers with very high sensitivity and mass resolving power, enabling us to profile the quality and biosimilarity of protein biotherapeutics, in their native state without requiring much sample preparation. In detail, I will demonstrate how native mass spectrometry can be combined with middle-down proteomics to profile complex structures of various glycoproteins, focusing on mAbs, plasma derived factor P, and Erythropoietin.

Furthermore, I will describe how native mass spectrometry has evolved into a tool that can provide unique structural and functional information about the assembly and topology of protein assemblies involved in complement activation, analyzing complexes of more than 40 subunits, when associated together exhibiting molecular weights over 2 million Da in mass. These data have provided new insight in how the complement pathway may be specifically activated by hexameric IgGs.

Short Biography

Albert J.R. Heck (1964) is professor at the Science Faculty of Utrecht University. He is scientific coordinator of the Netherlands Proteomics Centre and the European large-scale proteomics infrastructure PRIME-XS. A large emphasis of Heck's group is on the development and applications of advanced mass spectrometry based proteomics technologies. A specific highlight in this area involves the development of new methods to enrich a complex mixture of proteins/peptides for specific post-translational modifications. Heck introduced in 2004 enrichment of phosphopeptides using TiO2 material. The Heck-lab also introduced the use of a protease named LysN that in conjunction with ETD provides unique sequence ladders that are straightforward to interpret and allow facile de novo sequencing and improve the analysis of protein phosphorylation. More recently we introduced for large-scale proteomics a simple and cost-effective stable isotope labeling by using reductive dimethylation, and an effective combination of the peptide fragmentation methods HCD and ETD termed EThcD.
Heck's proteomics research focuses for a large part on (embryonic and adult) stem cells and immunology. Most of these studies are aimed at the understanding of embryonic, adult an induced pluripotents stem cell differentiation, which may eventually lead to these cells being used for regenerative purposes. Complementary to the proteomics efforts, the group of Albert Heck is also known for its specific expertise in the mass spectrometric analysis of intact proteins and protein complexes. They developed therefore unique and dedicated instruments, with most recently a new modified Orbitrap that can be considered a serious breakthrough for top-down proteomics. Research in native mass spectrometry focuses on virus assembly,

therapeutic antibodies, transcription complexes and CRISPR related protein assemblies.
Heck's is council member of Human Proteome Organization (HUPO) and was chair of the HUPO Conference in Amsterdam in 2008. He received the Gold Medal of the Dutch Royal Chemical Society in 2001, the Descartes-Huygens Award in 2007, the Life Science Award of the German Mass Spectrometry Society in 2010, the HUPO Discovery Award in 2013 and the EuPA Pioneer in Proteomics Award in 2014. In 2014 he was elected member of EMBO and elected member of the Royal Netherlands Academy of Sciences (KNAW). He accepted in 2010 a Guest professor-ship in Systems Biology at the ETH Zurich, and was a visiting scientist at The Scripps Research Institute, in 2011.

PLENARY LECTURE 6 > Back to schedule
Closing Plenary Session

Wednesday 16:00
Room: Sorbonne 2

Microfabricated technologies for accomplishing liquid phase separations and mass spectrometry

Michael Ramsey
University of North Carolina

We have pioneered the development of a sensitive, stable, and efficient microchip electrospray interface that enables the integration of MS detection with rapid and highly efficient microfluidic separation methods. The separative performance of these devices is near the theoretical diffusional limit for cationic species. This performance is achieved through the use of novel surface modification strategies that result in highly homogeneous surface characteristics. These devices yield electrospray ionization (ESI) sensitivity commensurate with commercial nanoESI emitters without sacrificing separative performance. Compared to CE-MS performed using fused silica capillaries, microchip CE-MS can achieve greater separation efficiency in shorter analysis times as the integrated injection and ESI functional elements greatly reduce extra-column band broadening. Microchip CE-ESI-MS has been used for challenging applications such as the characterization of intact biopharmaceuticals and antibody-drug conjugates, where achieving optimal separation efficiency is crucial for the success of the analysis. Moreover, light and heave chain analysis and peptide mapping can also be performed rapidly with high coverage. Most of these separations are completed in less than three minutes and most samples require minimal sample preparation. We have used the same technology to address bioanalytical assays such as metabolomic and clinical assays. Our group has also developed the technique of high-pressure mass spectrometry (HPMS) that enables very compact mass spectrometry platforms. As a natural progression of development we have also integrated these two miniaturized platforms. Various elements of the above will be described in this presentation.

Short Biography

Dr. J. Michael Ramsey holds the Minnie N. Goldby Distinguished Professor of Chemistry Chair at the University of North Carolina - Chapel Hill. In addition, he is a member of the faculty in the Departments of Biomedical Engineering and Applied Physical Sciences, and the Carolina Center for Genome Sciences. He is a member of the National Academy of Engineering and a Fellow of the Optical Society of America, the American Chemical Society, and the American Institute for Medical and Biological Engineering. Dr. Ramsey is the scientific founder of Caliper Technologies (NASDAQ:-CALP), renamed Caliper Life Sciences and acquired by PerkinElmer in 2011. He is also the scientific founder of the venture backed companies 908 Devices Inc., a company developing revolutionary compact mass spectrometry and separations-based products, and Genturi Inc., a genomics tools provider. Prof. Ramsey has published over 300 peer-reviewed papers and presented over 500 invited, plenary, or named lectures. In addition, he has over 100 issued patents.

Keynote speakers Abstracts & Biographies

KEYNOTE LECTURE 1 > Back to schedule
Microfluidic Separations & Lab-on-a-Chip Session

Monday 09:30
Room: Oxford 16

One- and two-dimensional chip-HPLC coupled to MS

Detlev Belder
University of Leipzig

There is significant progress in the research field of chip-based separation devices, which is also reflected by the increasing commercial activities in the field of HPLC on chip. HPLC on microfluidic chips enables a seamless integration of various functionalizes on a single device avoiding swept and dead volumes and associated band broadening. By the use of appropriate chip and interface technology high performance Chip-HPLC MS with more than 160.000 plates /m is feasible. When slurry packed columns are integrated in high pressure resistant glass devices any commercial particulate HPLC-Phase material can be used which facilities method transfer from classical HPLC.

The seamless interconnection of two columns on a single device enables two dimensional chip-HPLC/MS. By the combination of two different columns packed with reversed-phase and chiral stationary phase the enantiomeric purity of compounds in complex mixtures can be assessed applying two-dimensional heart-cut liquid chromatography.

Beside ESI-MS detection optical detection can be implemented straightforwardly due to the optical transparency of the glass chips. This is demonstrated for Raman (CARS) and fluorescence detection in chip-HPLC.

Recent results on high temperature chip-HPLC will be presented as well. HT chip-HPLC allows to generate high speed temperature gradients which is an attractive alternative to common solvent gradient elution.

Short Biography

Curriculum Vitae

1991 Diploma in Chemistry, Philipps-University Marburg
1994 Dr. rer. nat, Philipps-University Marburg / MPI für Kohlenforschung, Mülheim
1994 Postdoctoral Fellow at SmithKline-Beecham (England)
1995-2006 Head of the Chromatography group at the MPI für Kohlenforschung, Mülheim
2003 Habilitation at the University of Wuppertal
2006-2007 Professor of Analytical Chemistry at the University Regensburg
Since 2007 Chair of Analytical Chemistry at the University of Leipzig

Research Areas

Miniaturization in chemistry (chip-Laboratories, Lab-on-a-Chip): microfluidics, microsystem technology, surface chemistry, mass spectrometry, chip electrophoresis, chip HPLC, catalysis on chip, Raman microscopy, fluorescence microscopy, integrated sensors, integrated devices, time and space resolved imaging and detection, capillary electrophoresis.

Official Functions

Since 2008 Director of the institute of analytical chemistry at the University Leipzig
Since 2009 Member of the extended Board of Governors of the Separation Science group of the Gesellschaft Deutscher Chemiker (GDCh)
Since 2012 Member of the Board of Governors of the Analytical Chemistry division of the GDCh
Since 2012 Elected Review Board Member of the DFG (Analytical Chemistry)
Since 2012 Vice Dean of the Faculty of Chemistry and

Mineralogy of the University of Leipzig
2013-2016 Dean of the Faculty of Chemistry and Mineralogy of the University of Leipzig

Member of the International Advisory Board of ABC
Member of the Editorial Board of Journals such as Electrophoresis, Micro Chimica Acta

Awards & Distinctions
2011 Fresenius Lecture
2015 Gerhard Hesse Award

KEYNOTE LECTURE 2 > Back to schedule
Metabolomics & Biomarker Analysis Session

Monday 09:30
Room: Sorbonne 4

Robust CE-MS methods for metabolomics: achieving greater throughput, lower costs and better data comparability

Philip Britz-McKibbin
McMaster University

Capillary electrophoresis-mass spectrometry (CE-MS) is widely perceived as a promising microscale separation platform that ultimately lacks robustness for large-scale metabolomic studies due to migration time variations and conditions that are difficult to reproduce in other laboratories or comparable with previously validated methods. Much of these problems stem from inadequate method validation during assay development, the lack of standardized operating conditions and quality assurance protocols and poor support by vendors in terms of training with software tools that are customized to the unique separation principles of CE relative to LC methods. Recent efforts in our laboratory towards enhancing sample throughput, data fidelity and quality assurance will first be discussed as a way to accelerate biomarker discovery in metabolomics using multiplexed CE-MS technology as applied to population health and precision medicine. For instance, aminolysis of the outer polyimide coating of the fused-silica capillary and incidental capillary fractures when using alkaline ammonia-based buffers will be first discussed as a simple way to improve method robustness for anionic metabolite profiling under negative ion mode conditions that has long been associated with poor reliability.

Also, temporal signal pattern recognition using multiplexed separations coupled to high resolution, accurate MS will be presented as a novel strategy for high throughput screening, unambiguous identification and reliable quantification of biomarkers associated with in-born errors of metabolism in asymptomatic neonates from a dried blood spot, such as galactosemia.

An inter-method comparison of validated isotope-dilution flow injection analysis-tandem MS derived from an accredited clinical laboratory with CE-MS results will be evaluated in terms of screening performance for unambiguous confirmatory testing of a diverse array of presumptive/screen-positive diseases. The development of faster, less expensive yet more reliable CE-MS methods that provide quality assurance is critical to biomarker discovery in metabolomics, as well as quantitative biomarker measurements in clinical medicine that is ideally suited to the analysis of volume-restricted and bio-banked specimens.

Short Biography

Philip is a Professor in bio-analytical chemistry at the Department of Chemistry and Chemical Biology at McMaster University (Hamilton, Canada), and he is a Cystic Fibrosis Canada Researcher. He is also an affiliate member of the Metabolomics Innovation Centre (TMIC) – Canada's national laboratory for metabolomics analytical services and technology

development while also serving as a founding member of the North American Metabolomics Chapter. Philip's research contributions include the design of novel analytical strategies to quantify and identify metabolites in biological samples, as well as characterization of their interactions with protein for drug discovery. Philip is a leading proponent of metabolomics research and major innovator in capillary electrophoresis-mass spectrometry-based technology development. His multidisciplinary research program involves both fundamental studies and clinically relevant applications of metabolite profiling relevant to advancing clinical diagnostics, personalized health and population health with a focus on chronic disease prevention. Philip's research contributions have been recognized by several prestigious provincial, national and international awards of merit from Cystic Fibrosis Canada (2015), American Chemical Society (2010), Japan Society for Promotion of Science (2009), Petro-Canada Young Investigator Award (2007) and Premier's Research Excellence Award (2004-2010).

KEYNOTE LECTURE 3 > Back to schedule
(Bio)Pharma-meets-microscale-separations Session 1

Monday 09:30
Room: Sorbonne 2

Why analytical science is ever more needed to develop biopharmaceuticals in the 21st century

Marta Germano
Janssen Vaccines and Prevention

It is generally acknowledged that biopharmaceutical companies regularly work together with university medical centers when discovering new medicines and carrying out clinical trials. On the other hand, collaboration between academia and the biotech industry in other fields of science may be less common. Yet, in the 21st century, I expect that such collaborations will be intensified for four main reasons:
(i) regulatory agencies such as the FDA have long expressed the need for using state of the art analytical technology in support of development of biopharmaceuticals;
(ii) with the spread of Quality-by-Design approaches, biopharmaceutical development is expected to be more and more science-based;
(iii) the pharmaceutical industry has defined as its general objective to enable global access to medicines, meaning that efforts are being made towards innovative manufacturing technologies, which in turn require innovative analytical technologies; and
(iv) with the advent of biosimilars, the product knowledge that was traditionally generated by clinical trials is shifting to in-depth physicochemical and biochemical knowledge, gathered by as diverse as possible analytical methods.

Successful biopharmaceutical development in the context described above will depend on effectively leveraging the analytical (bio)chemistry knowledge and technological developments that are created in academia. In this presentation I will share some of the needs of analytical sciences in support of biopharmaceutical development in the 21st century which in my view can be best fulfilled by collaborating with university. I will also share some examples of such collaborations and which aspects of biopharmaceutical product knowledge they can address.

Short Biography

Dr. Marta Germano is a principal scientist within the analytical development department of Janssen Vaccines and Prevention. She holds an MSc in Chemistry from the Technical University of Lisbon, Portugal and a PhD in Biophysics from the University

of Leiden, The Netherlands. She has worked in analytical development of biopharmaceuticals for over 13 years, both in small biotech and in big pharma. She has experience in development and registration of therapeutic recombinant proteins and, since August 2012, she is head of product characterization at Janssen Vaccines. In her current role, she is responsible for characterization of virus based vaccines and she leads the implementation of Quality-by-Design approaches to vaccine development. In addition, she was recently appointed associate director of CASSS.

KEYNOTE LECTURE 4 > Back to schedule
Microcolumn Technologies & Separation Media Session

Monday 15:30
Room: Oxford 16

Impact of column diameter and flow rate on sensitivity and resolution in LC-UV and LC-MS separations

Monika M. Dittmann
Agilent Technologies

UHPLC in combination with mass spectrometry has proven robust and widely applicable for high sensitivity analyses of many types of chemical compounds. The majority users employ narrow bore columns with 2.1 mm internal diameter (ID). Sample limited applications often use reduced diameters down to capillary- (ID ≤ 0.5 mm) or even nano-column formats. Capillary or small-bore columns (ID ≤ 1 mm) can be a good compromise between system robustness and enhanced sensitivity. Modern ion sources are developed to reduce the sensitivity gap between nano-spray and ESI. This brought up the question whether it was time to rethink the setup for high sensitivity experiments, especially when developing methods for routine applications.

Data will be shown comparing chromatographic performance as well as detection sensitivity obtained with columns that only varied in ID (0.3, 0.5, 1 and 2.1 mm) but otherwise were of the same length and packed with identical stationary phases. Columns were operated in gradient mode at the same linear flow velocities. Low molecular weight compounds were used for assessment. Injection volumes were kept at 0.5 µL, the sample concentration was kept constant. Detection was done with A) an UV-detector using an ultra-low dispersion flow cell and B) a quadrupole mass spectrometer operated in multiple reaction monitoring and positive electrospray ionisation mode. The ion source used incorporates several measures to support drying and thus promote ionisation efficiency at higher mobile phase flow rates. Further experiments compared column loadability and the influence of matrix upon MS sensitivity when injecting Yangtze river and sewage water.

In summary, our findings suggest that use of modern ion sources could allow application of larger ID columns in LC/MS without having to sacrifice the sensitivity that is required for sample limited applications and the detection of low abundant species. In addition, use of larger ID allows for higher column loading and can have a positive influence on MS results obtained with real samples, which is most likely due to on column dilution of the matrix.

Short Biography

Dr. Monika Dittmann currently holds the position of a Principal Scientist in Research and Development in the Life Sciences and Applied Markets Group of Agilent Technologies in Waldbronn, Germany. After obtaining her PhD from the University of Paderborn she spent two years as a post-doc in the department of Chemical Engineering at UC Berkeley working on theoretical aspects of phase-equilibrium thermodynamics. In 1988 Monika Dittmann joined HP (now Agilent Technologies) as an R&D scientist. During her career she has been involved in the design and

development of instruments and technologies in the fields of HPLC and UHPLC, Capillary Electrophoresis, Capillary Electro-Chromatography and Lab-on-a-chip systems as a research scientist and project manager. Her current work is focused on applied and fundamental aspects of (U)HPLC and the design and development of next generation HPLC systems. In 2012, she received the Silver Jubilee Medal of the Chromatographic Society of the UK.

KEYNOTE LECTURE 5 > Back to schedule
Glycomics & Protein Analysis Session

Monday 15:30
Room: Sorbonne 4

Characterizing glycan and glycopeptide isomers derived from biological systems by LC-MS/MS

Yehia Mechref
Texas Tech University

Glycosylation, as one of the most common post-translational modification (PTM), plays critical roles in various biological processes. Development of quantitative glycomics/glycoproteomics profiling methods is essential for understanding the biological attributes of glycans. Although high-resolution mass spectrometry facilitates accurate sequential identification of glycans, identification of glycan isomers is not readily attainable without LC separation. Moreover, the interpretation of isomeric microheterogeneity associated with the glycosylation sites of proteins is one of the major technical challenges of glycoprotein and glycopeptide analysis. Here, isomeric separation of released N-glycans and glycopeptides on the porous graphitic column at elevated temperatures will be described and discussed.

Permethylation of glycans enhances ionization efficiency, stabilize sialic acid and eliminates fucose rearrangement. However, the isomeric separation of permethylated glycans is always not satisfactory due to the increased intramolecular interaction after permethylation. In this study, we have achieved efficient isomeric separation of permethylated glycans by using PGC-LC at 75 oC. Similarly, isomeric separation of glycopeptides was also achieved using PGC column at elevated temperatures. Base peak isomeric separation of glycopeptide mixture was attained at 75 oC. We are reporting here for the first time, the ability to attain isomeric separation of released N-glycans and glycopeptides on PGC columns at elevated temperatures. Accordingly, comprehensive characterization of the isomeric microheterogeneity of the glycosylation sites of proteins is readily achieved by interfacing PGC columns to mass spectrometry.

We are reporting here for the first time the efficient isomeric separation of glycans and glycopeptides on PGC column at elevated temperatures. Accordingly, comprehensive characterization of the isomeric micro heterogeneities of the glycosylation sites of proteins is readily achieved by LC-MS/MS analysis on PGC column at elevated temperature.

Short Biography

Yehia Mechref is a professor in the Department of Chemistry and Biochemistry at Texas Tech University, Lubbock, TX. He received his B.Sc. in chemistry from the American University of Beirut (Beirut, Lebanon) and his PhD with an honorable mention from Oklahoma State University (Stillwater, Oklahoma). Dr. Mechref's research focus is on the development of sensitive biomolecular mass spectrometry methods enabling qualitative and quantitative assessments of the roles of proteins, glycoproteins and glycans in biological systems. Thus far, Dr. Mechref has published 22 review articles, 14 book chapters and 156 peer-reviewed research papers. Currently, Dr.

Mechref Scopus H-index is 46 with 6115 citations. He received 11 US patents. He has organized and co-organized numerous symposia and conferences. Dr. Mechref is the recipient of Barnie E. Rushing JR. Faculty Distinguished Research Award in 2016 and Barnie E. Rushing JR. Faculty Outstanding Research Award in 2015.

KEYNOTE LECTURE 6 > Back to schedule
(Bio)Pharma-meets-microscale-separations Session 2

Monday 15:30
Room: Sorbonne 2

Where industry meets academia in biopharma

Mark Eggink
Synthon

Developing and producing monoclonal antibodies and antibody drug conjugates is a challenging job. In this process a lot of analytics is involved to support lead discovery, process development support up to final product release. During this development difficult analytical questions needs to be answered; to make this possible specialized equipment and/or knowledge could be necessary which is not always directly available within the company. This is a perfect opportunity for industry to meet with academia and vice versa.

Questions like developing specific screening or characterization tools for post translational modification, identification of host cell proteins and supporting in multi attribute method development academia can help out. New technologies or the extensive knowledge can be of great help by solving the specific questions. Multiple new technologies are initiated in academia due to extensive knowledge to study the proof of principle, when successful; these technologies need to be tested on useful application to show the real value. Here academia could use industry to supply them with the urgent needs and material.

The biggest challenge is to asses if these technologies can be directly or easily implementable in the analytical labs of biopharma and if not what is needed to meet the industry standards. A commonly used strategy nowadays is to develop a product based on Quality by Design (QbD) approaches. Continues risk assessments are performed to generate a production process as efficient as possible. This also counts for answering analytical question or the development of analytical assays, authorities are asking more and more for QbD like approaches.

Short Biography

Mark Eggink is a lead scientist/group leader Bioanalytics at Synthon Biopharmaceuticals involved in extended protein characterization and assay development of therapeutic proteins such as antibodies and antibody drug conjugates. He obtained his Ph.D. in Analytical Chemistry at the Vrije Universiteit Amsterdam before joining Synthon. He has a strong background in analytical separations techniques in combination with mass spectrometry. The past 8 years he extensively focused on in-depth characterization and method development of therapeutic proteins. His main focus is glycosylation, primary and secondary structure characterization and method development up to validation. Furthermore he is involved collaborations with academia and tech transfers of analytics to external partners.

Microscale online comprehensive two-dimensional liquid chromatography – second thoughts on speed, efficiency and selectivity

Thorsten Teutenberg
Institute of Energy- and Environmental Technology Duisburg

Two-dimensional liquid chromatography (2D-LC) is said to be far superior in terms of peak capacity than 1D-LC. There are different variants of 2D-LC like e.g. LC - LC, sLC x LC, LC x LC and LC + LC, which can be executed either offline or online. In this presentation the potential and limitations of online LC x LC are discussed with an emphasis on miniaturization. Moreover, the possibility to separate isobaric compounds that are difficult or impossible to distinguish by mass spectrometry is evaluated when using LC x LC, 1D-LC and ion mobility spectrometry (IMS).

The experiments have been carried out on a microscale 2D-LC system using nano-LC and micro-LC in the first and second dimension. A set of low molecular weight isobaric compounds has been used as model analytes. The kinetic plot method has been used to gain information about the peak capacity when very fast gradient times are applied in the second dimension. Ion mobility spectrometry and 1D-LC were employed as reference methods.

A very fast analysis cycle for online LC x LC has been developed, where the efficient gradient time in the first dimension was reduced to 12 minutes with a cycle time of 34 minutes. The efficient gradient time for the second dimension separation was reduced to 17 seconds with a cycle time of 30 seconds. Although this system yielded a higher peak capacity production rate than the 1D-LC reference method, the absolute peak capacity was not sufficient to adequately resolve the isobaric compounds either in the first or second dimension. Although ion mobility spectrometry is said to be very suitable for a separation of structurally related compounds, the majority of peak pairs could not be separated by IMS. In order to design a better 2D-LC system, the kinetic plot theory was used to determine the minimum peak capacity that is necessary for a chromatographic separation of the isobaric species. In this context, a concept that was recently introduced by Schmitz et al. and is termed LC + LC could be interesting to overcome some limitations of the "classical" LC x LC approach.

In order to facilitate ultra-fast gradients in the second dimension of an LC x LC system with gradient tines of less than 15 seconds, very small particles with a diameter of less than 1.5 µm at temperatures between 80 und 100 °C should be used. However, the requirements on valve technology will be very high in order to guarantee a robust operation of such a system that can be used for industrial applications.

Short Biography

Thorsten Teutenberg studied Chemistry at Ruhr University Bochum. He studied for a doctorate in Analytical Chemistry at this institution, submitting a thesis on 'High-temperature HPLC'. In 2004 his career took him to the Institut für Energie- und Umwelttechnik e. V. in Duisburg as a research associate. Since 2012 he has been in charge of the Research Analysis Department, mainly working on the various aspects of high-temperature HPLC, miniaturized separation and detection techniques, and multi-dimensional chromatography processes.

KEYNOTE LECTURE 8 > Back to schedule
Young Scientists Session

Tuesday 09:30
Room: Sorbonne 4

Pushing the boundaries of lipid research (and your own boundaries)

Jurre Kamphorst
University of Glasgow

Lipids make up an integral component of our physiology, and disruptions in lipid metabolism and signalling are implicated in a variety of diseases, including obesity and cancer. Despite their importance, our knowledge about lipids remains very limited. In particular, while the individual reactions of the major lipid metabolic pathways have been described, much still remains to be learned about actual pathway activity and regulation in cells in various conditions. Additionally, analytical coverage of the 'lipidome' is still poor, and approximately half of all lipids that can be detected remain uncharacterised. The limited progress in addressing these issues is in part due to a lack of adequate analytical methodology, and developing such methods has been a major focus of my new group. In this presentation I will describe the analytical platform we are developing for the analysis of lipids and their metabolism. It involves the use of stable isotope tracing and both GC-MS analysis of total fatty acids and cholesterol, and LC-MS analysis of intact lipids. In particular, I will highlight our approach to increase the coverage of the lipidome by combining extraction procedures and mobile phase setups and optimising gradients and data acquisition, and discuss the limitations that we face. Finally, as the keynote of the Young Scientists Session, throughout the presentation I will share my thoughts on the process of becoming independent and setting up a research group.

Short Biography

Jurre Kamphorst is a Cancer Research UK (CRUK) Career Development Fellow and Group Leader of the Cancer Metabolomics Laboratory of the CRUK Beatson Institute. He obtained his PhD from Leiden University in the Netherlands, and subsequently was a Hope Funds for Cancer Research Postdoctoral Fellow with Joshua Rabinowitz at Princeton University, USA. In his current work Jurre exploits lipidomics and stable isotope tracing to determine how aberrations in lipid metabolism and signaling contribute to disease.

KEYNOTE LECTURE 9 > Back to schedule
Advanced Detection Strategies Session

Tuesday 15:30
Room: Sorbonne 2

Nanoscale measurements of vesicle content in solution, in cells, and in varicosities

Andrew Ewing
Chalmers University / University of Gothenburg

Electrochemical cytometry and mass spectrometry imaging with NanoSIMS have been used to peer into the contents and even the substructure of single neurotransmitter vesicles in pheochromocytoma cells. Electrochemical cytometry involves isolating single nanometer vesicles stochastically, and measuring their contents via an electroporated opening, a process taking microseconds. NanoSIMS involves using a tightly focused ion beam to ablate material from a surface, in this case a fixed cell, and carrying out mass spectrometry on the ions ejected. This can be done with 40-50 nanometer resolution. Using electrochemical cytometry and

amperometry, we have discovered differences in neurotransmitter release with cisplatin, a chemotherapeautic drug that decreases cognition causing the "chemobrain" effect. We have also discovered that the learning supplement, zinc ion, the dietary supplement, curcumin, and the anaesthetic, lidocaine, all either change the amount of dopamine stored in vesicles, or the amount released during exocytosis. A key aspect to all these findings is the equilibrium between a proteinateous dense core in the nanometer vesicle and the solution around it. To understand this we have developed protocols with the NanoSIMS to get about 50 nm spatial resolution and determine the relative contents of these compartments in single vesicles observed in fixed cells. Additionally, we have used intracellular cytometry to measure the content of small synaptic vesicles (50-60 nm) in the nerve terminals of the living fruit fly larva and found the amount to be orders of magnitude higher than that measured during exocytosis release leading to the conclusion that release from an actual nerve cell is a very small fraction of the content in each vesicle. This model system is being used to make the transition from model cell systems to the living brain system and the complexity is remarkable.

Short Biography

Andrew Ewing received his BS degree from St. Lawrence University and a PhD from Indiana University. After a postdoc at the University of North Carolina he joined the faculty at Penn State University for 25 years. He is now Professor at Chalmers University of Technology and the University of Gothenburg, Sweden. His group has pioneered small-volume chemical measurements at single cells, electrochemical detection for capillary electrophoresis, novel approaches for electrochemical imaging of single cells, and new electrochemical strategies to separate individual nanometer vesicles from cells and quantify their contents. His 309 publications have been cited 17279 times with an H-index of 72. He has recently received the Charles N Reilley Award from the Society for Electroanalytical Chemistry (2013), the ACS Analytical Division Award in Electrochemistry (2013), the Norblad-Ekstrand Medal of the Swedish Chemical Society (2014), and the Pittsburgh Conference Award in Analytical Chemistry (2015). He is an Honorary Professor at both Nanjing University of Science and Technology and Beijing University of Science and Technology. He is a member of the Royal Swedish Academy of Sciences (2012) and the Gothenburg Academy of Arts and Sciences (2013).

KEYNOTE LECTURE 10 > Back to schedule
Forensic Analysis Session

Tuesday 15:30
Room: Sorbonne 4

The potential and challenges of rapid chemical and toxicological analysis in forensic science

Arian van Asten
Netherlands Forensic Institute / University of Amsterdam

Chemical analysis in forensic science is concerned with providing chemical information that assists with law enforcement, solving crime and the ultimate decision by the courts with respect to guilt and innocence. In some cases the identification of compounds can suffice for instance in cases involving the production, trade and possession of illegal substances such as drugs of abuse and explosives. For other situations the law dictates a quantitative analysis such as for instance alcohol levels in relation to driver impairment. With detailed chemical analyses including impurity profiling the forensic expert can assist in crime reconstruction and can establish chemical links in a criminal investigation. In any of these applications time is usually an important factor and sometimes even of crucial importance. Precious time, means and capacity can be saved in the criminal justice system when chemical analysis can be performed on the spot and provides answers in real time. The challenge is to maintain the high quality standards and generate results of lab-like robustness. In this presentation the

potential of rapid screening methods in forensic toxicology will be discussed. Latest results on the use of paper spray mass spectrometry (PS-MS) for the analysis of drugs of abuse in whole blood will be shown and a new framework for method selectivity will be introduced

Short Biography

Arian van Asten studied analytical chemistry at the University of Amsterdam (UvA) where he obtained his Master's degree with honors in 1991 and his PhD degree in 1995. After working for over 10 years in the chemical industry (Akzo Nobel and Unilever) he transferred to the Netherlands Forensic Institute (NFI) in 2006 and became involved in forensic science. In June 2012 Arian van Asten was appointed professor at the Faculty of Science of the University of Amsterdam on a special chair in Forensic Analytical Chemistry. Additionally, in 2013 he became the co-director of the Co van Ledden Hulsebosch Center, the Amsterdam Center for Forensic Science and Medicine (www.clhc.nl). Since his appointment at the UvA Arian van Asten has been involved in the Forensic Science Master program. In 2015 he joined the editorial board of Elsevier's peer reviewed journal Forensic Chemistry. The scientific interests of Arian van Asten include the chemical profiling of illicit drugs and explosives, forensic toxicological analysis in hair, fingermarks and biological traces, rapid chemical analysis in the laboratory, on site and point-of-care analysis with ambient mass spectrometry, chemical imaging in forensic science and the forensic application of comprehensive chromatography. He has authored/co-authored 32 peer reviewed scientific publications on (forensic) analytical chemistry.

KEYNOTE LECTURE 11 > Back to schedule
CE-MS & Advanced MS Techniques Session

Wednesday 09:30
Room: Sorbonne 2

CE-MS as a robust routine tool in clinical diagnosis

Harald Mischak
Mosaiques Diagnostics / University of Glasgow

Urinary peptides are produced either by the kidney, or a result of plasma filtration. In depth investigation has demonstrated that urinary peptides show very high stability, and significant association with specific pathologies. As such, these peptides have the potential of mirroring biology/pathophysiology, serving as biomarkers for specific diseases. To date, over 100000 urine peptides have been identified, over 3000 are sequenced. Urine has therefore emerged as a prime source for proteomic biomarkers, also due to its ease of collection. Large multicenter studies involving over thousand individuals suggested a significant added benefit of urinary proteomic biomarkers.

Among the technologies employed, capillary electrophoresis coupled mass spectrometry (CE-MS) has established itself as the leading technology employed for the analysis of low molecular weight proteins and peptides in urine. In comparison to other approaches, CE-MS has demonstrated superior reproducibility, and complete absence of carry over effects, both highly relevant in clinical application. More than 40000 samples have been analyzed to date in a comparative way using CE-MS, enabling the generation of a large urine peptidome database that serves as basis for the identification of biomarkers based on large numbers of independent samples, a prerequisite when aiming to identify valid biomarkers. Studies based on over 10000 subjects have been published, highlighting superiority of the CE-MS approach.

Based on first available data it became evident that single biomarkers are of limited value as a result of

moderate specificity and high variability. However, combining multiple biomarkers into specific classifiers has presented itself as the ideal approach to assess disease in a non-invasive way with high precision.
Since more than two thirds of the urine peptides appear to originate in the kidney, an obvious target for urinary clinical proteomics is the application in chronic kidney disease (CKD). CKD is a major health burden with associated costs exceeding 100 bio € per year in Europe. Urinary peptide biomarkers enable early and accurate detection of CKD (2-5 years prior to clinical diagnosis) and prognosis of future development. Specific urine collagen fragments show the highest predictive value at very early stage CKD. This opens a therapeutic window at an early point in time, possibly even enabling curative treatment. The results have led to the initiation of a first large, multicentric, randomised controlled clinical trial guided by proteome analysis, PRIORITY, aiming at preventing the development of diabetes-associated CKD by early intervention. Additional fields of clinical application are in the (early) detection of cardiovascular diseases (heart failure, and coronary artery disease) and in the detection and, in some cases, monitoring of malignancies like prostate or bladder, carcinoma.

Short Biography

Harald Mischak, born 1961 St. Pölten in Austria, received his PhD in technical science from the Technical University of Vienna, Austria, in 1986 (grade "excellent"). Between 1988 and 1993, after postdoctoral work on the Rhinovirus receptor at the University of Vienna (Institute for Biochemistry), he was on leave as an invited scientist on signalling by protein kinase C and Raf at the Laboratory of Viral Carcinogenesis (funded by the Fulbright Foundation) and as a Schroedinger and Fogarty Fellow at the Laboratory of Genetics of NIH National Cancer Institute in Bethesda, Maryland, USA. He continued his research on kinases as Group Leader at the GSF - National Research Center for Environment and Health, Munich, Germany from 1993-1998. He wrote his habilitation in clinical microbiology at the Technische Universität München on Protein Kinase C in Signal Transduction. After one year as a scientific group leader at Franz-Volhard Klinikum (MDC) at Berlin-Buch, he worked on the structure of kinases and related molecules at the NIDDK, Bethesda, Maryland, USA. In 1999 he took up a position at the Department of Nephrology at Medical School of Hannover. Here he founded Mosaiques diagnostics and therapeutics AG in 2002, which was started with the aim to identify disease-specific polypeptides. Currently, he holds a position as Professor for Proteomics and Systems Medicine at the University of Glasgow, and he is the chief scientific officer of Mosaiques AG as well as executive director of Mosaiques diagnostics GmbH and Mosaiques DiaPat GmbH. With more than 300 scientific publications on signaling and proteomics that have been cited over 20000 times, he is one of the leading experts worldwide in the field of proteome research and applied systems biology. In addition, more than 100 patent applications have been filed with Prof. Mischak named as inventor, the majority on proteomic biomarkers.
Based on his experience on proteomics in basic research, he initiated the use of urinary proteomics and CE-MS for clinical application, and is the leading authority in clinical proteomics and biomarker identification. Among his achievement in this field are the development of guidelines for clinical proteome analysis, where he led a large international and multidisciplinary group to develop clinically relevant proteomic biomarkers and the demonstration of successful application of CE-MS-based clinical proteomics in the diagnosis and prognosis of several diseases.

Wednesday 09:30
Room: Sorbonne 4

Micro-extraction through supported liquid membranes – Tuning the extraction chemistry for different biomedical and pharmaceutical applications

Stig Pedersen-Bjergaard
University of Oslo

The last two decades, substantial efforts have been devoted to the development of liquid-phase microextraction (LPME), and several different approaches have emerged. In all of these, analytes of interest are extracted from an aqueous sample and into a microliter volume (< 100 µL) of acceptor phase (liquid). The acceptor phase can be an aqueous solution, which can be injected directly into liquid chromatography systems (LC), mass spectrometers (MS), or instruments for capillary electrophoresis (CE). Alternatively, the acceptor phase can be an organic solvent, which can be injected directly into gas chromatography systems (GC). The major incentives for the LPME research have been to (1) reduce the consumption of organic solvents (green chemistry), (2) increase the analyte pre-concentration, (3) eliminate the need for solvent evaporation, and (4) to improve the compatibility of the sample preparation with micro-scale chromatography systems. Major LPME approaches include single-drop microextraction (SDME), hollow-fiber liquid-phase microextraction (HF-LPME), dispersive liquid-liquid microextraction (DLLME), electromembrane extraction (EME), and parallel artificial liquid membrane extraction (PALME).

This keynote lecture focus on PALME and EME, which are highly efficient techniques for extraction of drugs and peptides from biological fluids (such as blood plasma and urine). The operating principles of both techniques will be discussed, and examples of PALME and EME in 96-well and micro-chip systems will be given. The lecture will show how the extraction chemistry can be tailored to basic drugs, acidic drugs, non-polar drugs, polar drugs, and peptides, based on (1) careful selection of pH, (2) the composition of the SLM, and (3) the direction and magnitude of the electrical field (EME). Finally, the perspectives of both techniques will be discussed; PALME and EME are new approaches for sample preparation prior to liquid chromatography-mass spectrometry (and related techniques), and may be high-clean-up, high-throughput, and green chemistry alternatives to traditional techniques such as protein precipitation, solid-phase extraction, and liquid-liquid extraction. In addition, as highlighted at the end of the lecture, EME may be developed into a highly specific extraction system, and therefore it may be combined successfully with very simple detection systems such as a smartphone. Especially in the latter area, substantial research is expected in the future.

Short Biography

Stig Pedersen-Bjergaard is Professor at School of Pharmacy, University of Oslo (Norway), and Professor (part time) at Department of Pharmacy, University of Copenhagen (Denmark). He has specialized in analytical micro extraction technologies, on development and applications of artificial liquid membranes, and on electrokinetic separation methods. He has published more than 165 papers in international journals, is Contributing Editor of Trends in Analytical Chemistry (Elsevier), and Associate Editor of Journal of Pharmaceutical Analysis (Elsevier).

Wednesday 13:30
Room: Sorbonne 2

Some thoughts on electrodriven separations: Fields, friction, fluids, and free energy

Stephen Weber
University of Pittsburgh

Multicomponent separations in columns depend on differences in solute (analyte) velocity and the time- and space-dependence of that velocity. In the case of electrodriven separations, many factors control solute velocities. A given solute with a particular electrophoretic mobility and in a medium with a particular electroosmotic velocity may find its velocity altered by many types of noncovalent interactions including association with binding partners in the liquid phase and association with a chromatographic stationary phase. When the electroosmotic flow occurs in a porous medium, local medium properties can alter the local solute velocities. In cases where the kinetics are not rapid or where the concentrations of binding partners are not uniform and high compared to the solute, solutes will take on a distribution of velocities leading to complex, but informative, peak shapes. Related to these phenomena is the idea of electroosmotic sampling in tissue in which solutes undergo chemical reactions as well as alterations in their velocity based on local conditions in the medium (in this case, tissue). This presentation will try to illustrate the richness of this area with selected examples from nonaqueous affinity CE and electroosmotic push-pull perfusion in his lab and of powerful techniques developed by others.

Short Biography

Stephen Weber is currently Professor of Chemistry and Professor of Clinical Translational Science at the University of Pittsburgh, Pittsburgh, PA, USA. He received his BA with dual majors, Chemistry and Biology, from Case-Western Reserve University, in 1970. He did undergraduate research in gas chromatography with Dr. Irving Sunshine in the Forensic Toxicology group at the Cuyahoga County Coroner's Office. He then enlisted in the U.S. Navy. After Hospital Corps School at the Great Lakes Naval Station he was recruited to the clinical lab at the Naval Hospital there where he, among other things, helped to establish a drug analysis lab. He went to the University of Maryland in 1974 to work with Prof. William Purdy, an early pioneer in bioanalytical chemistry. He followed Prof. Purdy to McGill and he received his PhD in Chemistry in 1979 for theoretical work on the electrochemical detector and developing an electrochemical immunoassay using an electrochemical detector. He began his independent career in 1979 at the University of Pittsburgh in the Department of Chemistry. The research of Steve's undergraduate and graduate research students and postdocs has encompassed electroanalytical chemistry as well as separations including microextractions, molecular recognition, capillary electrophoresis and liquid chromatography. He has over 200 publications and has given nearly 250 invited presentations on his research group's work. He is on the Editorial Board of Analytical Chemistry for a second three-year term and is currently a Contributing Editor for Trends in Analytical Chemistry and on the Editorial Board of the Journal of Chromatography A. Recent awards include the Pittsburgh Award of the ACS (2008), the University of Pittsburgh Provost's Award for Excellence in Mentoring (2012), the Palmer Award from the Minnesota Chromatography Forum (2015), and the Dal Nogare Award of the Chromatography Forum of the Delaware Valley (2016).

Simultaneous analysis of enzyme structure and activity by kinetic CE-MS

Maxim Berezovski
University of Ottawa

To enable the detection of protein conformational isomers, their enzymatic activity and inhibition in a single experiment, we developed a method based on kinetic capillary electrophoresis, coupled on-line with UV detection and ion mobility mass spectrometry (CE-UV-IM-MS). Kinetic CE-UV separated protein conformers and monitored their interconversion dynamics in solution. Ion mobility mass spectrometry analysed conformer size, exact molecular weights and structures of an enzyme, its substrates, inhibitors and corresponding products. This coupled CE-UV-IM-MS system allowed the simultaneous, real-time observation of the effect of small molecule inhibitors on both the conformational distribution and enzymatic activity of human tissue transglutaminase TG2. By expanding mass spectrometry profiling of enzymatic reactions beyond proteins and substrates to include protein dynamics, CE-UV-IM-MS opens a new avenue for the modulation and regulation of cellular functions, drug development and protein engineering.

Short Biography

Maxim V. Berezovski is Associate Professor in the Department of Chemistry and Biomolecular Sciences and leads the Bioanalytical and Molecular Interaction Laboratory in University of Ottawa since 2009. His research focuses on bioanalytical chemistry, biological mass spectrometry and nucleic acid-based pharmaceutics. His research lab develops analytical methods for studying biomolecular interactions with kinetic capillary electrophoresis and mass spectrometry, discovers protein biomarkers of cancer and immune cells with DNA aptamers, makes biosensors for circulation tumor cells and pathogens. Berezovski published 67 articles, 4 book chapters, and 3 patents with >2700 citations and h-index of 28. His research funding has surpassed $15 million. He was awarded a University of Ottawa's Young Researcher of the Year Award (2015) and Early Research Award from Ministry of Research and Innovation (2012). Before academia, he served as CEO of a pharmaceutical company for six years. Currently, Berezovski manages two university core facilities: Cellular Imaging and Cytometry Facility and John L. Holmes Mass Spectrometry Facility, and teaches Analytical Chemistry course for 2nd year students and Modern Bioanalytical Chemistry and Analytical Biochemistry courses for 4th year and graduate students.

Posters

Poster instructions

- Posters should be up Monday-Wednesday during the entire symposium.
- Posters should preferably be mounted on Sunday afternoon March 26, but not later than Monday morning March 27 before 09:00.
- Poster presentations are assigned a number that will also be attached to the poster board; authors should mount their posters only at their assigned board.
- Poster boards have the following dimensions: 1.25 meter high x 1.50 meter wide. The poster does not necessarily have to fill the entire working area.
- The poster can be oriented in the "landscape" or "portrait" position (long dimension is horizontal).
- A banner displaying poster title, author name, and department should be positioned at top-center of the poster.
- Poster mounting material will be available.
- Two poster sessions are scheduled: Monday March 27 14:00-15:15 and Tuesday March 28 14:00-15:15.
- Presenters of a poster with an odd number should be at their poster during the poster session on Monday; presenters of posters with an even number should be at their poster during the poster session on Tuesday.
- Poster should be taken down on Wednesday March 29 between 15:00 and 15:30.
- Any posters left after the symposium closing session will be removed by the organisers and recycled.

Poster presentations

nr.	*Title*	*Presenter*	*Affiliation*
P01	Affinity capillary electrophoresis to assess the binding affinity of cholera toxin inhibitors	Oier Aizpurua Olaizola	*Utrecht University*
P02	A novel concept of chemiluminescence detection using nano-liter droplet microfluidics for a micro-HPLC system	Haider A.J. Al Lawati	*Sultan Qaboos University*
P03	Separation of synthetic Peptides and Proteins using specially designed OT-CEC column	Ashraf Ali	*Inha University*
P04	Rapid and highly sensitive mass spectrometry by SAWN	Alina Astefanei	*University of Amsterdam*
P05	Coupling RP-UPLC with High Resolution Intact Protein Mass spectrometry for Characterization of Complex Viral Vector Vaccines	Nadine Binai	*Janssen Vaccines via CLS*
P06	The development and integration of electrode materials for the separation of DNA	Christopher Birch	*University of Virginia*
P07	CE can evaluate the anti-amyloid activity of a new multifunctional tool for Alzheimer's disease treatment	Federica Bisceglia	*University of Pavia*
P08	Towards Novel Biomarker: Insight into Amyloid ß Oligomers in Alzheimer's Disease Based on Electrochemistry and CE	Dimitri Brinet	*Sahlgrenka Academy at Gothenburg University*
P09	Persistent Organic Pollutants in human breast milk	Timea Dergez	*University of Pécs*
P10	Development and evaluation of a new parallel-electromembrane extraction device	Nicolas Drouin	*University of Geneva*

P11	Application of a new parallel-electromembrane extraction device for the extraction of endogenous polar compounds	Nicolas Drouin	*University of Geneva*
P12	Generic Instrument Control of G7100 Agilent Capillary Instrument via Instrument Control Framework	Emde Ortrud	*Agilent Technologies*
P13	Analysis of Proteins Related to Osteoporosis and CRPS Using CE, nLC, ESI-MS and MALDI-MS	Åsa Emmer	*KTH Royal Institute of Technology*
P14	Application of CE-MS for the Quantification of Mono-phosphorylated Isobaric Peptides	Klaus Faserl	*Innsbruck Medical University*
P15	Evaluation of Mesoporous Silica Layers on Radially Elongated Pillars	Shunta Futagami	*Vrije Universiteit Brussel*
P16	Metabolomics of Human Neural Cells: an Untargeted HILIC-HRMS Approach Assisted by ANOVA Multiblock OPLS Data Analysis	Victor González-Ruiz	*University of Geneva*
P17	Isoelectric Focusing – A Comparison of Different Carrier Ampholytes for Monoclonal Antibody Charge Heterogeneity Analysis	Martin Greiner	*Agilent Technologies*
P18	Comparison of three CE-ESI-MS interfaces applied to organic acids in neg mode and to digested and intact proteins in pos mode	Oliver Höcker	*Aalen University*
P19	Automated Online Monitoring & QC Glycan Profiles of Antibodies Using FabRICATOR Enzyme & Subunit Separation plus UHR-QTOF MS	Patrick van Houts	*Bruker*
P20	A Fully Automated High Precision Glucose Unit Calculation Method Based on Three Internal Standards	Gabor Jarvas	*Horváth Csaba Memorial Institute of Bioanalytical Research*
P21	An Ionic Current Detection Technique in a Microfluidic Device for Cell Deformability Measurement and Microorganism Detection	Noritada Kaji	*Nagoya University*
P22	Validated HPLC method for determination of Nevirapine in human plasma	Maria Kasatkina	*Chemical Analyst*
P23	Characterization of a poly(dimethylsiloxane) microfluidic chip containing adsorbed trypsin for rapid protein digestion	Adam Kecskemeti	*University of Debrecen*
P24	Novel CE-MS Method to Profile the Toxic Phosphoglycolipid Part of Bacterial Endotoxins	Ferenc Kilár	*University of Pécs*
P25	Characterization of Bacterial Endotoxins Directly from a Few Bacterial Colonies by MALDI-TOF MS	Aniko Kilar	*University of Pécs*
P26	Quorum Sensing in the Environment	Anikó Kőnig-Péter	*University of Pécs*
P27	CE-TOF/MS Metabolic Fingerprinting in Renal Cell Carcinoma	Marta Kordalewska	*Medical University of Gdańsk*
P28	A Nanospray Liquid Junction Interfacing for Versatile CE-MS	Jana Krenkova	*Institute of Analytical Chemistry of the Czech Academy of Sciences*
P29	Long term groundwater monitoring – passive sampling of volatile pollutants and their degradation products	Zdena Křesinová	*Institute of Environmental Studies, Charles Universtiy*
P30	Characterisation of carcinoembrionic antigen site-specific glycosylation using CE-ESI-MS	Valeriia Kuzyk	*VU Amsterdam*
P31	Improved sample pre-concentration and separation by depletion zone isotachophoresis	Simon Leygeber	*Leiden University*

P32	Online bioassay based on immobilized enzyme reactor to target human nucleoside diphosphate kinase b	Juliana Maria Lima	*University of São Paulo*
P33	Papain-functionalized Gold Nanoparticles as Heterogeneous Biocatalyst for Bioanalysis and Biopharmaceuticals Analysis	Siyao Liu	*University of Tübingen*
P34	The study of intact casein as a model system for the separation of intact phosphorylated proteins by CESI-MS	Stephen Lock	*Sciex*
P35	Charge heterogeneity analysis of intact monoclonal antibodies using CESI-MS	Stephen Lock	*Sciex*
P36	Improving Identification and Quantification of Polar Herbicides by CESI-MS	Stephen Lock	*Sciex*
P37	Screening and identification of plasmin inhibitors and metalloprotease in snake venoms	Morwarid Mayar	*VU Amsterdam*
P38	Sample preconcentration using vision-controlled droplet evaporation for high-throughput LC-MS-based metabolomics	Paul Miggiels	*Leiden University*
P39	A Validated Assay to Determine Monomethyl Fumarate in Human Plasma	Daria Nikitina	*Analytical chemist, BIOCAD*
P40	Modifications of sequential injection protocol in CIEF analysis of proteins with MS detection	Csilla Páger	*University of Pécs*
P41	Application of Polar Organic Compound Integrative Sampler for Screening of Micro-pollutants	Klara Petru	*Institute for Environmental Studies, Charles University*
P42	Towards robust and sensitive doping control analysis of human growth hormone by CE-MS – an integrated approach	Angela ten Pierick	*VU Amsterdam*
P43	Development and Validation of a Quantitative Method for Measuring of Endocannabinoid and Related Compounds	Viktoria Poor	*University of Pécs*
P44	Analysis of Antibody Charge Variants by Isoelectric Chromatofocusing Coupled to Native Mass Spectrometry	Susanna Pot	*Vrije Universiteit Amsterdam*
P45	Integrated determination of hydrodynamic radii in separation techniques	Nicklas Poulsen	*University of Copenhagen*
P46	High throughput lipidomics by UHPLC methods combined with a novel linear retention index system for identification purposes	Francesca Rigano	*Chromaleont Srl*
P47	Apocarotenoids determination in Habanero, by supercritical fluid chromatography-mass spectrometry	Francesca Rigano	*Chromaleont Srl*
P48	Separation Technology for a Million Peaks	Liana Roca	*University of Amsterdam*
P49	Streamline iCIEF Protein Separation and Characterization	Gerard Rozing	*ROZING.COM Consulting*
P50	An HPLC Method with Monolithic Column for Quantification of Rivaroxaban in Human Plasma	Ahmet Olcay Sagirli	*Istanbul University*
P51	Online Heart-Cutting Liquid Chromatographic Analysis of Linezolid in Human Serum	Ahmet Olcay Sagirli	*Istanbul University*
P52	Identification of N-glycans using Synthetic Standards	Javier Sastre Toraño	*Utrecht University*
P53	Study of Virus-Like Particles of Human Papillomavirus and their Interaction with Soluble Receptor Fragment in CE	Anne-Catherine Servais	*University of Liège*
P54	Development of a Novel Cellulose Acetate-Based Decoupler for Electrochemical Detection in Microchip Electrophoresis	Joseph Siegel	*University of Kansas*

P55	Analysis of Intact Monoclonal Antibodies Using Microflow LC and Time of Flight Mass Spectrometry	Remco van Soest	*Sciex*
P56	The Involvement of Microbial Degradation During the Remediation of Pharmaceuticals and VOCs by Photo-Oxidation and Aeration	Kamila Šrédlová	*Institute for Environmental Studies, Charles University*
P57	Immobilized enterokinase bioreactor: a powerful tool for the cleavage of fusion proteins	Sara Tengattini	*University of Pavia*
P58	BChE Immobilized Capillary Enzyme Reactor on flow Ion Trap-Mass Spectrometer: versatile tool assay for screening ligands	Adriana Ferreira Lopes Vilela	*University of São Paulo*
P59	Quantification of 2-hydroxypropyl-ß-cyclodextrin in human gastric and intestinal fluids by LC-MS/MS	Matthias Vink	*Vrij Universiteit Amsterdam*
P60	Development and application of microfluidic thermoplastic chips in high-performance liquid chromatography	Jelle de Vos	*Vrije Universiteit Brussel*
P61	Isomeric separation of positively labeled N-glycans by CE-ESI-MS	Sander Wagt	*Leiden University Medical Center*
P62	Evaluation of Microchip HT capillary electrophorsis assays for QC testing - a multi-site ring trial	Friederike Winkhaus	*Roche Diagnostics GmbH*
P63	Feasibility study for the application of immobilised-enzyme-reactors for degradation of various macromolecules	Bert Wouters	*Universiteit van Amsterdam*
P64	Development of a Microfluidic Platform for Ion Chromatography Integrating Separation, Suppression, and Detection	Sam Wouters	*Vrije Universiteit Brussel*
P65	Enabling metabolomics of biomass-limited samples by capillary electrophoresis-mass spectrometry	Wei Zhang	*Leiden Academic Center for Drug Research - Leiden University*
P66	Liquid-chromatographic nanofractionation with parallel mass spectrometry for screening of CYP450 inhibitors in mixtures	Barbara Zietek	*Vrije Universiteit Amsterdam*
P67	Miniaturizing a Metabolic Platform for the Analysis of Inflammatory Mediator Levels in the Interstitial Fluid of Cell Models	Adja Zoumaro-Djayoon	*Leiden Academic Center for Drug Research - Leiden University*
P68	Understanding Aqueous SEC-MS Elution and Ionization Behavior of Biomacromolecules	Iro K. Ventouri	*Vrije Universiteit Amsterdam*
P69	Deep and reproducible human proteome profiling with novel nano-flow LC technology and HRAM mass-spectrometry	Remco Swart	*Thermo Fisher Scientific*
P70	Improved sensitivity and robustness with capillary flow LC-MS targeted protein quantification	Remco Swart	*Thermo Fisher Scientific*
P71	Development of a HTS coagulation assay for assessment of heamotoxic snake venoms	Kristina Still	*Vrije Universiteit Amsterdam*
P72	Challenges encountered using CE-LEDIF/ high throughput DNA sequencing for G quartet aptamer selection	Francois Couderc	*Universite Paul Sabatier*
P73	Coupling capillary electrophoresis with surface plasmon resonance for the affinity assessment of protein mixture components	Elena Dominguez-Vega	*Vrije Universiteit Amsterdam*
P74	Development of a Comprehensive Lipidomics Platform	Sergey Tumanov	*The Beatson Institute for Cancer Research*

P75	Glycoproteomic Analysis of Intact Prostate Specific Antigen with CE-ESI-MS	Tamás Pongrácz	*University of Pécs*
P76	A miniaturized LC-MS/MS platform for in-depth quantitative profiling of endocannabinoids in human cerebrospinal fluid	Vasudev Kantae	*Leiden Academic Center for Drug Research - Leiden University*
P77	Real-time Label-free Monitoring of Nanoparticle Cell Uptake	Teemu Suutari	*University of Helsinki / Vrije Universiteit Amsterdam*
P78	Novel CZE Method for Quantification of Intact Virus Particles in Complex Matrices – Quality by Design method development	Ewoud van Tricht	*Janssen Vaccines and Prevention*
P79	Surface Plasmon Resonance – Application driven assessment of feasibility and applicability	Robert Voeten	*Vrije Universiteit Amsterdam*
P80	An Ultra-Rapid DNA Analysis System with Sample-to-Answer Capability	Brandon Thompson	*University of Virginia*
P81	Deeper Proteomics using Actively Modulated Online HILIC×nRPLC-HRMS	Andrea Gargano	*Center for Analytical Sciences Amsterdam*
P82	Linkage-specific sialic acid derivatization for MALDI-TOF-MS profiling of IgG glycopeptides	Noortje de Haan	*Leiden University Medical Center*
P83	Neuraminidase enzyme microreactor as a tool for screening inhibitors from compound library and Tradition Chinese Medicine	Yumei Zhao	*Jinan University*
P84	Development of double chain phosphatidylcholine functionalized polymeric monoliths for IAM chromatography	Wang Xiangyu	*Jinan University*
P85	On-line CE Preconcentration Methods for the Quantification of Alzheimer's Disease Biomarkers in Cerebrospinal Fluid	Thanh Duc Mai	*Université Paris-Sud*
P86	High resolution N-glycan analysis by temperature gradient capillary electrophoresis	Andras Guttman	*University of Debrecen*
P87	Fast Glycan Labeling and Analysis of N-linked glycans of Biopharmaceutical Interest	Andras Guttman	*University of Debrecen*
P88	Separation of Organophosphate Nerve Agents by CE and MCE	Xi Cao	*Tyndall National Institute*
P89	Search for multiple myeloma glycobiomarkers by CE-LIF	Zsuzsanna Kovács	*University of Debrecen*
P90	Development Of Immobilized Metal-Chelate (IMA) Monolith Incorporated Microfluidic Device For Plasma Proteomics	Ashish Khaparde	*CBST-Vit University*
P91	Influenza Virus proteins CGE method development; the effects of the injection mode and gel buffer dilution	Lars Geurink	*Janssen Vaccines and Prevention*
P92	Dynamic Constriction Insulator-Based Dielectrophoresis for Particle Manipulation	Daihyun Kim	*Arizona State University*
P93	Separation of proteoforms under native conditions at semi-preparative scale, using free-flow electrophoresis (FFE)	Michiel Akeroyd	*DSM Biotechnology Center*
P94	Streamlined workflow to discover antibiotics	Gertrud Morlock	*Justus Liebig University Giessen*
P95	Office Chromatography - do it yourself!	Gertrud Morlock	*Justus Liebig University Giessen*

Poster pitches

A select number of poster presenters have been nominated for a short pitch on Monday or Tuesday at 13:30-14:00 in room Sorbonne 2. They will present their research in a maximum of 5 min using a maximum of 3 informative slides.

Poster Pitch Session, Monday March 27, 13:30, room Sorbonne 2

Time	Presenter	Title
13:30	Federica Bisceglia *(University of Pavia)*	CE can evaluate the anti-amyloid activity of a new multifunctional tool for Alzheimer's disease treatment
13:35	Nicolas Drouin *(University of Geneva)*	Application of a new parallel-electromembrane extraction device for the extraction of endogenous polar compounds
13:40	Marta Kordalewska *(Medical University of Gdańsk)*	CE-TOF/MS metabolic fingerprinting in renal cell carcinoma
13:45	Siyao Liu *(University of Tübingen)*	Papain-functionalized gold nanoparticles as heterogeneous biocatalyst for bioanalysis and biopharmaceuticals Analysis
13:50	Nicklas Poulsen *(University of Copenhagen)*	Integrated determination of hydrodynamic radii in separation techniques

Poster Pitch Session, Tuesday March 28, 13:30, room Sorbonne 2

Time	Presenter	Title
13:30	Christopher Birch *(University of Virginia)*	The development and integration of electrode materials for the separation of DNA
13:35	Oliver Höcker *(Aalen University)*	Comparison of three CE-ESI-MS interfaces applied to organic acids in neg mode and to digested and intact proteins in pos mode
13:40	Csilla Páger *(University of Pécs)*	Modifications of sequential injection protocol in CIEF analysis of proteins with MS detection
13:45	Joseph Siegel *(University of Kansas)*	Development of a novel cellulose acetate-based decoupler for electrochemical detection in microchip electrophoresis
13:50	Adriana Ferreira Lopes Vilela *(University of São Paulo)*	BChE immobilized capillary enzyme reactor on flow ion trap-mass spectrometer: versatile tool assay for screening ligands

MSB 2017 Young Scientist Award

The MSB 2017 Young Scientists Award is intended to give talented young scientists extra encouragement. It will be presented to a young researcher whose outstanding work sets an example for other scientists. All presenters of an oral contribution who are less than 35 years of age at the time of their lecture are eligible for consideration. An international jury of scientists will judge the qualified presentations and choose a winner. The price consists of a certificate and a cash amount (**sponsored by Janssen Biologics**). The winner will be announced and awarded at the Closing Ceremony on Wednesday.

MSB 2017 Poster Awards

All posters presented at MSB 2017 will be considered for a MSB 2017 Best Poster Award. The posters will be reviewed by an international panel of scientists. Posters will be up during the entire symposium. Presenters of a poster with an odd number should be at their poster during the poster session on Monday; presenters of posters with an even number should be at their poster during the poster session on Tuesday. Poster awards comprise cash prizes (**sponsored by Janssen Biologics**) for the four best posters. Runners-up 5-10 will receive a book voucher (**made available by Springer-Verlag**) or a one-year free subscription to Analyst, Analytical Methods or Lab-on-a-chip (**made available by the Royal Society of Chemistry**). Poster prize winners will be presented and awarded at the Closing Ceremony on Wednesday. All nominees will receive a certificate to acknowledge their achievement.

Social Program

MSB recognizes that good science is all about strong interaction between people. Therefore, next to a comprehensive scientific program with active discussion, MSB 2017 will provide ample opportunities to build up and strengthen social networks. All social events are included in the registration and open for each delegate. So join us and take the occasion to meet up with old friends and make new friendships.

Welcome Reception
Sunday March 26, 18:45 – 21:00 @Atrium Lounge
Refreshments and full buffet just after the Opening Plenary Session.

Symposium Dinner
Monday March 27, 19:00 – 21:00 @Gaudi Restaurant
Enjoy the Chef's three-course buffet with your fellow participants.

Symposium Excursion
Tuesday March 28, 17:00 – 19:00 @Keukenhof Holland Park
A 10-min bus transfer will bring us to the world-famous Keukenhof gardens with millions of bulb flowers blooming. Watch 800 varieties of tulips. A unique and unforgettable experience!

Green House Dinner
Tuesday March 28, 19:00 – 21:00 @Arendshoeve
Buses will take us from the Keukenhof into the Dutch countryside for an exceptional sit-down dinner in a surprisingly green environment.

Farewell Reception
Wednesday March 29, 17:15 – 18:00 @Gaudi Lounge
A last drink before returning home.

All symposium participants and accompanying persons are kindly welcome to all social events.

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