



British Society for Proteome Research Newsletter



The theme of the 2022 BSPR annual meeting is **Next Generation Proteomics**. The preparation of the scientific programme is well underway. Provided it is COVID-safe to do so, the meeting will return to our usual format i.e., an in-person conference. This year's meeting is an acknowledgement of how far proteomics has travelled. We are now in the era where generating multiple comprehensive proteomes in a day is becoming routine. The field is now utilising the underlying technologies to go well beyond traditional proteome analyses. Proteomic experiments can now capture not only quantitative data or PTM data but also protein interaction, spacial, structural, and temporal information. Whilst proteomes are becoming more granular, their synergistic links with the the metabolome and transcriptome are also being unravelled. Proteomics technologies continue to develop leading to ever more rapid proteomic analyses from ever lower amounts of starting material. Such work has led to studies being performed on thousands of samples, enabling large scale cohort analyses for medical research, while advances in fragmentation technology have made crosslinking studies almost routine and have rapidly expanded the number of post translational modifications and protein classes that can be characterised.

The 2022 meeting will celebrate these next generation technologies and how they are transforming applications from scientific research to commercial quality control and civil security.

We are excited to announce that all the keynote speakers have already been lined-up. They include Perdita Barran, Alfredo Costello, Matthew Collins, Sabine Flitsch, Michael Gillette, Anne-Claude Gingras, Manual Mayr, Evangelina Petsalaki, and Nobel prize winner Peter Radcliffe. Registration and abstract submission are now open. To avoid disappointment, participants wanting onsite accommodation should also book their onsite accommodation rapidly because the numbers of rooms are limited. Other options are available. Do visit the BSPR website for my information and if you have any questions, please email Shabaz Mohammad (shabaz.Mohammad@chem.ox.ac.uk).

We are inviting sponsors to come forward if they would like to sponsor the meeting. Please contact our vendor liaison Paul Skipp (pjss@soton.ac.uk) for more information.

Session Topics

- Native/ Structural Proteomics
- Systems Biology/Networks
- Towards P5 Medicine
- Chemical Biology
- Bioinformatics
- Imaging and Spatial Proteomics
- One Health Research
- Next Generation Technology

Organizing committee

- Rainer Cramer
- Roman Fisher
- Make Langini
- Shabaz Mohammed
- Paul Skipp
- Iolanda Vedrell

Scientific Committee

- Shabaz Mohammed
- Karin Barnouin
- Jyoti Choudhary
- Rainer Cramer
- Roman Fischer
- Sandra Orchard

In Memoriam Prof. John Timms 1969-2021

By Rainer Cramer, Reading University and Harry Whitwell, Imperial College

After being awarded a first-class honours degree from the University of Oxford, Dr John Timms completed a PhD at the same institution where he also met his future wife, Kate. In 1995, he moved to Boston in Massachusetts, USA, accepting a post-doctoral position at the Beth Israel Deaconess Medical Center, Harvard Medical School. In 1999, he returned to the UK, pursuing a second post-doctoral position at the Ludwig Institute for Cancer Research. He became Group Leader of Cancer Proteomics in 2003 and was awarded a lectureship at UCL in the Department of Biochemistry and Molecular Biology. In 2006, he moved to the Institute for Women's Health (UCL) and was promoted to Reader in Cancer Proteomics in 2015. The diagnosis of mesothelioma did not deter John from academic success. In his final years, John was promoted to Head of Women's Cancer at the Institute for Women's Health and was awarded a major CRUK grant. He had also applied for promotion to professor, a promotion that sadly came too late for John and he passed before being awarded this accolade.

John was a vivid supporter and member of the BSPR since he started working in proteomics back in the UK. He was a member of the BSPR's Board of Directors and for many years the society's secretary. Many BSPR members will fondly remember his wittiness and refreshing sense of humour, being an excellent scientist with a down-to-earth approach.

Colleagues and collaborators often became close friends and will miss his company, from the legendary poker nights to the intriguing and stimulating after-work drinks at the local pub.



Late Professor John Timms, University College

In memory of John the BSPR has created two new prestigious awards that acknowledge his dedication to the society and his support of students and colleagues: a travel bursary and a mentoring award. Please see next section for more details.

New Awards in memory of John Timms

John Timms Memorial Travel Bursary

This bursary will be awarded to one any-stage career researchers for attendance and participation (poster or oral presentation) in a Proteomics meeting. Priority will be given to researchers presenting cancer proteomics. The bursary will cover registration, travel and accommodation or other eligible costs. To apply please submit a proposal (max 500 words) explaining how the conference would be of value including presentation abstract by 1st May to Karin Barnouin (Karin.Barnouin@ucb.com), Sarah Hart (s.r.hart@keele.ac.uk) and Harry Whitwell (h.whitwell@imperial.ac.uk). The award can cover registration, travel, and accommodation (other eligible expenses by prior agreement) up to £1000. By accepting the award, the Society will expect to receive a report on the meeting for inclusion in the Society's newsletter and webpages. Please include acknowledgement of funding on slides/poster.

John Timms Mentoring Award

This prestigious award has been created to recognise the effort, time, and commitment to mentoring proteomics researchers (e.g., early career, technical staff, colleagues). It will be a personal lifetime award: medal and £1000 for personal use. One cannot get renominated. Suggestions can be made by BSPR committee and members at any time. The nominations will be considered at the next selection committee meeting. The award will be presented at the following annual meeting. This year the deadline is 1st May 2022. The nomination must include a proposal explaining how the nominated scientist supported the wellbeing, development, of one or more people. Provide evidence of impact on mentees research, development, time, and commitment regardless of career stage. Max. 500 words. Nominators can also be at any career stage/position e.g., post-doc, core facility head and work in academia or industry. Nominators will receive recognition for putting forward a nomination.



John Timms (right) together with his former member mentees of staff John Sinclair (left) and Stephane Camuzeaux (middle) at a BSPR conference.

BSPR Bursaries, Fellowships, and Travel Awards

Student and Support Staff Bursaries

Students (MSc and Ph.D.) and support staff awarded a bursary will receive £250 to help cover meeting registration, accommodation, and travel expenses for the BSPR annual meeting or another proteomics conference such as HUPO. To apply, please send a brief CV, a statement saying why you wish to attend the meeting and an abstract of the work that you plan to present to Karin Barnouin (Karin.Barnouin@ucb.com), Sarah Hart (s.r.hart@keele.ac.uk) and Harry Whitwell (h.whitwell@imperial.ac.uk). To apply for BSPR 2022 student bursary, please apply no later than Monday 1st May 2022. For other conferences please apply at least two months prior to the meeting. Students must be members of the BSPR to apply. By accepting the award, the Society will expect to receive a report on the meeting for inclusion in the Society's newsletter and webpages.

MJ Dunn Fellowship

MJ Dunn Fellowship awards will be given to cover registration, accommodation, and travel expenses for the BSPR 2022 conference. To apply, please send a brief CV together with a statement saying why you wish to attend the meeting, including an abstract of the work that you plan to present to Karin Barnouin (Karin.Barnouin@ucb.com, Sarah Hart (s.r.hart@keele.ac.uk) and Harry Whitwell (h.whitwell@imperial.ac.uk) no later than 1st May 2022. Applicants must be within six years of completing their Ph.D. and be paid-up members of the BSPR. By accepting the award, the Society will expect to receive a report on the meeting for inclusion in the Society's Newsletter and webpages.

Travel Bursary to Regional Meetings

These travel bursaries will be awarded to students and support staff who are members of BSPR. The purpose is to support students and technical staff with travel cost to their nearest local meetings e.g., London Proteomics Discussion group, London Biological Mass Spectrometry Discussion Group, Midlands's mass spectrometry group. Maximum value is £50 per year. To apply, please provide evidence to Karin Barnouin (Karin.Barnouin@ucb.com, Sarah Hart (s.r.hart@keele.ac.uk) and Harry Whitwell (h.whitwell@imperial.ac.uk) they are travelling to their closest local meeting. Applications can be submitted any time but at least two weeks prior to the meeting.

European Summer School Travel Bursary

One BSPR member will awarded a Travel award which will cover registration, accommodation, and travel expenses for the 14th European Summer School (<http://www.proteomic-basics.eu/>). To apply, please send a brief CV together with a statement saying why you wish to attend the course, including an abstract of the work that you plan to present to Karin Barnouin (karin.barnouin@ucb.com), Sarah Hart (s.hart@) and Harry Whitwell (h.whitwell@ic.ac.uk) no later than 31 May 2022. By accepting the award, the Society will expect to receive a report on the meeting for inclusion in the Society's Newsletter and webpages.

BSPR Interact 2021 - review

In 2021 the BSPR annual meeting was held for the first time due to the COVID-19 pandemic online over three days in the morning. The conference organizing committee was led by post-doctoral fellow Maïke Langini. Together with James Waddington, Harry Whitwell, Kathryn Lilley, Sara Zanivan, Phil Green, and Kareena Adair, they put together a fantastic programme containing distinguished proteomics scientists from across the world. Each oral session had two chairs: a senior and an early career researcher who took turns to moderate questions and help stimulate discussions. As is the custom in our conference, early career researchers (ECR) were also invited to present their work either as an oral presentation or poster format. All ECR and poster presenters were contenders for a prize. Wael Kamel and Marko Noerenberg both received the ECR award for their presentation entitled "Global analysis of protein-RNA interactions in SARS-COV-2 infected cells". Two people were selected for the ECR award as the work was from Wael Kamel, but Marko Noerenberg stepped in to do the presentation because he could not attend the conference. It was a great team effort! The poster award went to David Newman for his presentation on "Developing the concept of quantotypicness for protein quantitation in proteomics". The winners have been awarded free registration to BSPR2022 and a £100 Amazon voucher. The winner of Kathryn Lilley's quiz gamification was Iliyana Kaneva. She received a £75 Amazon voucher. Congratulations to all the winners! We are grateful to all the sponsors. Without them we could not have organized such a fantastic meeting.



INTERACT 6-8th July 2021

www.bspr-interact.com
 @UKBspr
 @UKBspr
 @BSPR - British Society for Proteome Research

Abstract submission* and registration are open!

Student: £35 | BSPR Member: £65 | BSPR Non-member: £120

The British Society for Proteome Research (BSPR) annual conference features prominent and upcoming scientists from the UK and across the globe, presenting the latest research and methodology in the field of proteomics, as well as participating in round table discussions.

Day 1	6 th July	Day 2	7 th July	Day 3	8 th July
Break, Poster Viewing and Networking	09:00	Break, Poster Viewing and Networking	09:00	Break, Poster Viewing and Networking	09:00
Session 1		Session 3 - ECR Session		Session 5 - Single Cell and Clinical Proteomics	
Welcome	09:30	Vendor Talk 2	09:30	Vendor Talk 4	09:30
Plenary 1 Paola Picotti Structural proteomics Proteomes in 3D	09:45	ECR 1 Title TBA	09:35	Speaker 8 Erwin Schoof Characterizing heterogeneity within hematopoietic cell hierarchies using quantitative Single-Cell Proteomics approaches	09:35
Q&A	10:30	ECR 2 Title TBA	09:47	Speaker 9 Tami Geiger Proteomic analysis of cancer internal heterogeneity	09:50
Speaker 1 Covaris Sponsored Talk Jereen Krijgsveld Automated sample preparation for reproducible proteomics in biology and the clinic	10:30	ECR 3 Title TBA	09:59	Speaker 10 Christoph Messner Ultra-high-throughput proteomics and its clinical applications	10:05
Q&A	10:50	ECR 4 Title TBA	10:11	Discussion	10:20
Break, Poster Viewing and Networking	11:00	Discussion	10:23	Break, Poster Viewing and Networking	11:00
Session 2 - Cell Signalling and Emerging Technologies		Break, Poster Viewing and Networking	11:00	Session 6	
Vendor Talk 1	11:30	Session 4 - Computational Proteomics		Vendor Talk 1 ProDomics What's your key concern, sample prep or the MS analysis? Time to look for a streamlined process	11:30
Speaker 2 Helan Cooper Native ambient mass spectrometry: Mass spectrometry imaging of intact proteins and protein complexes	11:35	Vendor Talk 3	11:30	ECR Talk & Poster Prizes	11:35
Speaker 3 Maria Robles Daily cycles of protein and phosphorylation abundance regulating rhythmic physiology	11:50	Speaker 5 Mischa Savitski Understanding post-translational regulation using biophysical proteomics	11:35	Plenary 2 Bernhard Küster Cancer drug interaction with the proteome Watching drug action in cancer cells through the proteomic burning glass	11:45
Speaker 4 Aeshaa Coon New mass spectrometry technology for proteome analysis	12:05	Speaker 6 Oliver Crook Uncertainty and choices in mass spectrometry data science	11:50	Q&A	12:20
Discussion	12:20	Speaker 7 Mike MacCoss Can we put Humpty Dumpty back together again? What does protein quantification mean in bottom-up proteomics?	12:05	Closing	12:45
Poster Presentations	13:00	Discussion	12:20	Kathryn Lilley Quiz!	13:15
		Poster Presentations	13:00	Meet the Experts Confirmed participants: Claire Evers, Joshua Coon, Christoph Messner, Olly Crook, Helan Cooper, Maria Robles, Erwin Schoof & Tami Geiger	16:00
		BSPR Annual General Meeting (AGM)	14:15		



YPIC "Meet-the-experts" session:
This is your chance as an ECR to have your proteomics questions answered by experts in our field! All of us constantly have several questions running through our head but it is not always easy to find someone to answer them. This session will allow you to ask experts in our field your proteomics related questions in an informal setting. Make sure to register in advance as spaces are limited!

Proudly sponsored by...







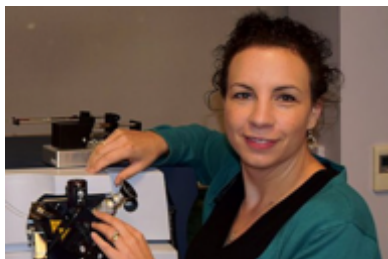







*Abstract submission closes on the 25th May 2021.

BSPR Lecturer – Claire Eyres



Professor Claire Eyres, University of Liverpool

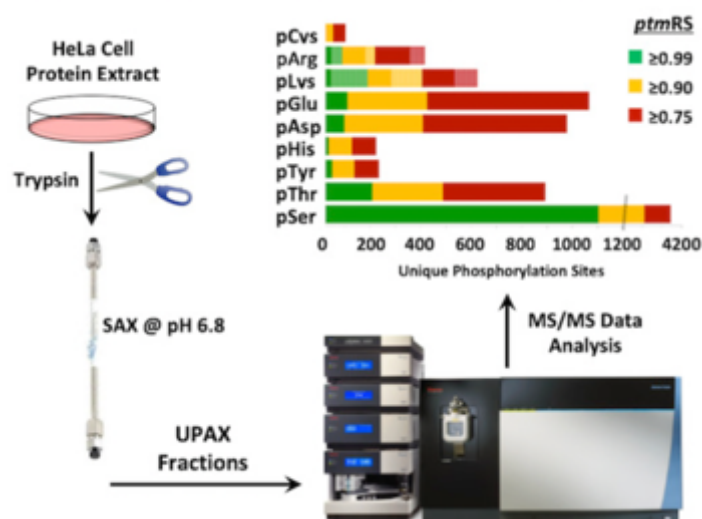
By Kathryn Lilley, Cambridge University

The 2020 BSPR Lecturer is Professor Claire Eyres from the Institute of Integrative Biology (IIB) at the University of Liverpool. She is also Director of the Centre for Proteome Research (CPR), and Research and is impact lead for the Institute of Integrative Biology and Deputy APVC for the Faculty of Health and Life Sciences. Her research employs biophysical and biochemical methodologies to elucidate the structure and function of post-translational modifications regulating cell signalling in health and disease. Her lab has developed LC-MS-based methods, including ion mobility MS to investigate the structure of proteins and the effects of PTM's and ligand binding. Claire is offering the following lectures:

- The Expanding Landscape of Human Protein Phosphorylation
- The Top to Bottom of phosphorylation-mediated signalling with mass spectrometry

Prof Eyres Inaugural lectures, hosted by the London Proteomics Discussion Group webinar and chaired by Prof. Kathryn Lilley on 7th August, 2020, entitled “The Expanding Landscape of Human Protein Phosphorylation” can be viewed on [youtube](#). Claire will now also offer in-person lectures.

To invite Claire Eyres to give a lecture, please email her: ceyers@liverpool.ac.uk and Amanda.penney@liverpool.ac.uk



Overview of the comprehensive phosphopeptide analysis workflow

Sarah Hart Proteomics Scientist Show Case

Proteomics characterization of Leishmania and Neural cells stroke model

By Sarah Hart, Keele University School of Medicine

I was lucky enough to be exposed to proteomics as an undergraduate student whilst at Bristol University– I had the fortune of being a Year in Industry student at a Thermo group company making MALDI-ToF instruments in Hemel Hempstead, carrying out a research project with samples generated by Mike Dunn's group under Chris Sutton's supervision.

That early experience gave me a first insight into the exciting world of biological mass spectrometry and proteomics, and I returned to my undergraduate studies keen to follow this up. I was fortunate to find a PhD studentship at the then UCL branch of the Ludwig Institute for Cancer Research, housed at that time in the Courtauld Building on Middlesex Street. I worked alongside more familiar BSPR names, Rainer Cramer, Karin Barnouin, the late great John Timms and Pedro Cutillas, and was

lucky to publish several papers on protein phosphorylation site analysis.

Following my PhD I moved to Simon Gaskell's lab at Manchester's Michael Barber Centre, where I worked as a postdoc on proteomics characterisation of the African trypanosome, a parasite which causes African Sleeping Sickness, and worked with the Maternal and Fetal Health research cluster on preeclampsia biomarkers as part of an EPSRC Fellowship.

In late 2009 I secured a lectureship at Keele School of Medicine, where I have been since, where I work on projects related to parasites again, this time Leishmania, with my colleague Helen Price, and have worked on neuroscience and bioengineering with Divya Chari. In 2020 I responded to the call for new committee members to serve on the BSPR committee, which I was keen to do as an educator, member, and long-term practitioner of proteomics methods.

Current work in progress includes quantitative study of positional proteomics in Leishmania and data independent analysis of primary neural cells in a stroke model.



Dr. Sarah Hart, Keele University School of Medicine

Update on the COVID-19 Mass Spectrometry Coalition and Project Moonshot

By Professor Andy Pitt, The University of Manchester

In early 2020, as evidence grew that the SARS-CoV2 pandemic was going to be a global challenge, a small group of mass spectrometrists, led by Professor Perdita Barran from the University of Manchester, set up the COVID-19 Mass Spectrometry Coalition (<https://covid19-msc.org/>). Understanding the power of mass spectrometry, the aim of the consortium was to “use mass spectrometry to reduce the harm caused by the SARS-Cov2 virus”. The consortium grew rapidly and now has over 800 members across 18 countries. One of the outcomes of raising the profile of mass spectrometry for clinical research was the establishment of the DHSC Test & Trace funded COVID MS Moonshot project to harness the power of mass spectrometry for the diagnosis of COVID infection.

PCR-based methodologies, whilst considered the gold standard for COVID diagnosis, are also time-consuming and expensive and have limited capacity to test in parallel for emergent variants of concern and any other respiratory viruses that could cause symptoms similar to coronavirus. As such there is considerable scope for new tests. Modern clinical mass spectrometry is capable of very high sensitivity and good throughput, has unique capabilities for parallelization of assays and the ability to rapidly adapt to changing targets and the potential for relatively accurate quantification from a range of biofluids.

The challenges set by UK Test & Trace for the MS Moonshot took this to another level. The primary requirements were to develop an MS method that would at least compete with PCR in terms of speed, cost, sensitivity, and selectivity which could be rapidly translated directly to hospital clinical analysis laboratories, and to do this in 12 weeks. To take on a challenge of this magnitude during a period when many labs were closed due to stay at home orders and supply chains were highly disrupted was particularly demanding. Only through the establishment of a consortium of academic and hospital laboratories across the UK working very closely together, substantial input and investment from mass spectrometry and chromatography companies, rapid, flexible, and responsive investment by UK Test & Trace, and selfless commitment by research and other staff, was this achieved.

Some of the challenges were unexpected. The Manchester Institute of Biotechnology hub had to rapidly become a logistics and distribution centre for sampling packs, which as can be seen from the photograph, resulted in the foyer becoming a factory for sample pack preparation, and during the early stages, the demand for samples across the different UK activities was high and sample numbers were very limited, exacerbated by the drop in number of infections due to the lockdown. The variability in PCR data, especially quantitative Ct values, made the use of this as the comparator diagnostic data challenging.

Initial work within the consortium identified the optimum proteotypic tryptic peptides from the SARS-CoV2 nucleocapsid protein that were specific to the SARS nCoV-2 virus, validated initially using recombinant materials and then known positive swab samples that had been subject to PCR testing. Led by the input from the clinical labs, chromatography speed was increased to give sample run time < 5 min, and the sample processing was optimised so that it could be easily followed in a clinical biochemistry lab and automated. Increased sensitivity came from using the SISCAPA peptide level enrichment method developed by Anderson and Anderson.

The demands of the UK Moonshot have been met – the UK-wide network analysed swab and saliva samples, and successfully developed a methodology that was translated to NHS labs for accreditation. It was also shown that the methods could be used for variant analysis, and for discrimination between SARS-CoV2 and other winter respiratory viruses.

Some important lessons were also learned. For rapid and straightforward translation, it is important to take a “good enough” approach, which balances simplicity and robustness of the methods and equipment with what is needed for the assay. Mobilization of a consortium of academic, clinical and industry labs, properly funded, can achieve remarkable things in a short space of time. Consideration of robustness of supply chains is important. And, most importantly, mass spectrometry can provide the speed, sensitivity and accuracy needed for large scale population screening.

The article is based on presentations to the Midlands Mass Spectrometry Group Seminar Series by Dan Lane (a PhD student in the group of Don Jones at the University of Leicester) and Andy Pitt (University of Manchester). The Midlands Mass Spectrometry Group is supported by Midlands Innovation (<https://midlandsinnovation.org.uk/>) and the partner Universities and brings together the mass spectrometry community in the Midlands to advance the scientific use of mass spectrometry.



London Proteomics Discussion Group



The role of proteomics – LPDG Webinar series

by Suniya Khatun, UCL & *London Proteomics Discussion Group Committee Member* and Karin Barnouin, UCB Biopharma & *BSPR newsletter editor*

Our first LPDG webinar series on *CoVID-19/SARS-CoV2: What Role Can Proteomics Play?* Continued with Dr Christian Muench being invited back to present his exciting work on the activation of signalling pathways following SARS-CoV2 infection using the mePROD tool for quantification of translome. On the 10th of July, we had a break from our SARS-CoV2 series and explored the role of machine learning in proteomics with Prof. Lennart Martens. Prof Martens highlighted the tools MS²PIP and DeepLC for peptide retention time and peptide fragmentation spectrum prediction. He also discusses ionbot - a search engine for protein identification taking into consideration post-translational modification and single amino acid polymorphism. With an upsurge in machine learning and deep learning tools, the future of proteomics looks bright.

For our next few webinars, we continued with SARS-CoV2 research. Dr Jeroen Demmers presented mass spectrometry-based detection method for SARS-CoV2 while host-perturbation strategies of SARS-CoV2 were discussed by Prof Andreas Pichimair. The importance of glycopeptides and glycoforms in SARS-CoV2 virulence was investigated by Dr Rod Chalk and Dr Miloslav Sanda in our 11th webinar, describing methods for the identification of glycopeptides belonging to the spike protein. Prof Ray Kruse Iles returned on our 13th webinar to update us on the development of MALDI-ToF MS for SARS-CoV2 detection. Our final webinar on SARS-CoV2 was delivered on the 6th of

November, where we were joined by three speakers: Dr Vadim Demichev, Dr Pedro Beltro and Prof Perdita Barran, presenting their current research on SARS-CoV2 proteomics. The presentations were followed by group discussion and questions and answer session chaired by Dr Maarten Dhaenens to mark the end of this webinar series.

In August we got to hear about discussions on another exciting topic: Structural proteomics where Mark Skehel from The Francis Crick Institute explained how his team uses cyclic IMS to expand the utility of HDX to investigate the conformations of bovine mitochondrial complex I. Dr. Francis O'Reilly Berlin Institute of Technology Berlin, Germany gave an interesting presentation on his work on discovering the topology of protein complexes in situ using crosslinking-MS. In September we revisited COVID-19 research, a webinar chaired by Dr Markus Ralser, Herein, Dr. Wael Kamel University of Glasgow spoke about how global analysis of protein-RNA interactions in SARS-CoV-2-infected cells revealed key regulators of infection. Dr. David S. Roberts (University of Wisconsin Madison) how mass spectrometry can reveal the Structural O-Glycoform Heterogeneity of the SARS-CoV-2 Spike Protein Receptor-Binding Domain. The October webinar was focussed on Bioinformatics in Proteomics. Dr. Oliver M. Crook (University of Oxford) demonstrated how Bayesian statistics can be used to quantify uncertainty in mass-spectrometry-based spatial proteomics. Dr. Juan Antonio Vizcaino EMBL-EBI Cambridge, UK explained how the EBI is working on bringing proteomics data closer to biologists.

We are excited to see how our webinar series and in person meetings develop in 2022.

For YouTube links and more information about the webinars please visit

www.londonproteomics.co.uk. Please see also our Facebook page

(<https://www.facebook.com/groups/471642630311490/>) or find us on LinkedIn

(<https://www.linkedin.com/groups/13722087/>). The meetings are free to attend, and run thanks to sponsorship, if you are interested in presenting, sponsoring or have a venue suggestion – please get in touch!

A Tree for Chris Sutton



Chris Sutton retired and stepped down from the BSPR committee in summer 2021. He was a long-standing and very active member of the society, frequently participating in scientific programme organization as well as liaising with our sponsors. In July 2018, Chris hosted and co-organized a very successful meeting in Bradford in July 2018. He is currently pursuing his dream of cultivating an orchard. To help him in his endeavour and in thanks to all the work he has done, the BSPR has given him a tree!

Thank you, Chris for all your contributions and enjoy your retirement!

Save the Date



EUOPA
EUROPEAN PROTEOMICS ASSOCIATION



Deutsche Gesellschaft für
Proteinforschung e.V.



Abstract deadline: 15 November 2021

PROTEOMIC FORUM | EuPA 2022

XIV Annual Congress of the European Proteomics Association

3–7 April 2022 | Leipzig/Germany

www.proteomic-forum.com

GENERAL INFORMATION

Conference venue
Kongresshalle am Zoo Leipzig
Pflaendorfer Strasse 31 | 04105 Leipzig

Date
3–7 April 2022

Hosting society
German Society of Proteome Research (DGPF e.V.)
www.dgpf.org

In cooperation with



European Proteomics Association (EuPA)
www.europa.org

About DGPF
The German Society of Proteomic Research (DGPF) sees itself as a platform to bring together the proteomics activities that have been started at different locations and within the framework of different programmes in Germany and in addition, to advance proteomics research through nationally and internationally coordinated initiatives. The aim is to bring about a bundling and optimal utilisation of national research capacities through overarching coordination in order to be able to hold a leading position in global competition.

Congress chair
Prof. Dr. Uwe Völker
University Medicine Greifswald
Interfaculty Institute for Genetics and Functional Genomics
Greifswald, DE

Organising committee

Bettina Warscheid (DE)	Hans-Peter Braun (DE)
Stefanie Hauck (DE)	Matke Langenil (UK)
Eva Cosoz (HU)	Nico Jehmlich (DE)
Uwe Völker (DE)	Marius Ueffling (DE)

Important dates

Deadline abstract submission	15 November 2021
Notification of abstract authors	January 2022
Deadline early bird registration	11 January 2022

Congress organiser
Conventus Congressmanagement & Marketing GmbH
Andreas Lelle | Felix Schüller
proteomic-forum@conventus.de

CALL FOR ABSTRACTS

All abstracts for oral or poster presentations are to be submitted online and in English only via www.proteomic-forum.de. Abstracts can be submitted to all fields of proteomics and should be assigned to one of the categories below:

Abstract submission categories

- Single cell proteomics
- Structural proteomics and protein complexes
- Systems biology and medicine
- Subcellular and spatial proteomics
- Computational proteomics and big data | Modelling
- Proteomics in cell biology
- Proteomics meets virology – Viral proteomics | Viral infection proteomics
- Precision medicine in wellness and disease | Deep proteomic phenotyping in cohorts
- Top-down proteomics
- Plant and nutrition
- Animal and veterinary medicine
- Metaproteomics and the microbiome
- Human disease: Cancer, neuro, cardio, rare, immunology
- Pharmacoproteomics, chemical proteomics
- Glycoproteomics
- Bioinformatics | Data processing
- Signalling proteomics | PTMs
- Clinical applications
- Microbial pathogens and host-pathogen-interactions
- Emerging technologies
- Native mass spectrometry
- Imaging meets mass spectrometry & cytometry
- Immunoproteomics

Abstract submission deadline 15 November 2021

Awards and prizes
Each society awards a poster prize. Please mark during the abstract submission, if you would like to be considered for the award.

SCIENTIFIC PROGRAMME AND REGISTRATION

Confirmed speakers

Michal Bassani-Sternberg (CH)	Kathrin Marcus (DE)
Pedro Beltrao (CH)	Lennart Martens (BE)
Justin Benesch (UK)	Karl Mechtler (AT)
Julia Chamot-Rooke (FR)	Harvey Millar (AU)
Sarah Cianferani (FR)	Matthias Munschauer (DE)
Beana Cristea (US)	Gary Nolan (US)
Maarten Dhaemens (BE)	Jesper V. Olsen (DK)
Richard R. Drake (US)	Markus Ralser (DE)
Leonard Foster (CA)	Juri Rappolber (DE)
Albert Heck (NL)	Paola Roncada (IT)
Ron Heeren (NL)	Michail Savitsky (DE)
Henning Hermjakob (UK)	Matthias Selbach (DE)
Connie Jimenez (NL)	Andrea Sinz (DE)
Neil Kelleher (US)	Nikolai Slavov (US)
Jeroen Krijgsveld (DE)	Michael P. Snyder (US)
Claudia Langenberg (DE)	Bernhard Spengler (DE)
Janna Lehtio (SE)	Jennifer van Eyk (US)
Kathryn Lilley (UK)	Tim van den Bossche (BE)
Matthias Mann (DE)	Bernd Wolfschlag (CH)

Check out the constantly updated online programme via www.proteomic-forum.com/programme/scientific-programme.

Conference registration fees

	Early bird * registration (until 11 Jan)	Regular registration (from 12 Jan)	Late registration (from 8 March)
DGPF/EuPA member*	450 EUR	550 EUR	600 EUR
Non member	600 EUR	650 EUR	700 EUR
DGPF/EuPA member Student**	200 EUR	250 EUR	300 EUR
Non member student**	350 EUR	400 EUR	450 EUR

* Including presenting abstract author.
** Proof of status needs to be provided.

Please register online via www.proteomic-forum.de. State of printing

Become part of the
PROTEOMIC FORUM 2022!



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Save the Date

HUPO 21ST HUMAN PROTEOME ORGANIZATION WORLD CONGRESS

MEXICO

CANCUN

2022.HUPO.ORG DECEMBER 4 - 8, 2022

HUPO 21ST HUMAN PROTEOME ORGANIZATION WORLD CONGRESS

MEXICO

CANCUN

2022.HUPO.ORG DECEMBER 4 - 8, 2022

<https://2022.hupo.org/>

Open Positions

PhD Studentship in (micro)biological mass spectrometry @ Reading University

Project title: Advancing LAP-MALDI mass spectrometry profiling/biotyping for the analysis of microbes and their pathogenicity
Department of Chemistry / School of Chemistry, Food & Pharmacy (University of Reading)

Supervisors: Prof Rainer Cramer, Prof Ian Jones

Project Overview: MALDI mass spectrometry (MS) biotyping has become the method of choice in identifying bacterial pathogens of infectious diseases and therefore in clinical microbiology (<https://www.gov.uk/government/publications/smi-tp-40-maldi-tof-ms-test-procedure>). Preliminary data from an earlier EPSRC-funded PhD studentship indicates that liquid atmospheric pressure (LAP)-MALDI MS provides an excellent alternative to current clinical (solid) MALDI MS biotyping for advanced microbial speciation/characterisation and the detection of antimicrobial resistance (AMR). Based on this data and aligned with a current EPSRC-funded project (<https://gow.epsrc.ukri.org/NGBOViewGrant.aspx?GrantRef=EP/V047485/1>), this PhD studentship project will explore the advantages of greater analytical speed, superior structural characterisation (by MS/MS), the liquid sample environment and simpler sample preparation that LAP-MALDI MS can provide with respect to microbial biotyping in the health sciences. The supervisory team also includes industrial and clinical (NHS) experts in mass spectrometry, analytical chemistry, biochemistry, clinical microbiology and infectious diseases.

Eligibility:

- Applicants should hold or expect to gain a minimum of a 2:1 bachelor's degree or equivalent in the Physical or Life Sciences.
- Due to restrictions on the funding this studentship is open to UK applicants.

Funding Details:

- Starts September/October 2022
- 3-year award
- Funding covers full tuition fees plus UKRI stipend

How to apply:

To apply click

at https://www.risisweb.reading.ac.uk/si/sits.urd/run/siw_ipp_lgn.login?process=siw_ipp_app&code1=P_ADM&code2=0001

create your account and use the link sent by email to start the application process. During the application process please select the PhD in Chemistry.

Important notes

1. Please quote the reference 'GS22-021' in the 'Scholarships applied for' box which appears within the *Funding Section* of your on-line application.
2. When you are prompted by the online application system to upload a research proposal, please omit this step as the project is already defined.

Application Deadline: 30th April 2022

Further Enquiries:

Please note that, where a candidate is successful in being awarded funding, this will be confirmed via a formal studentship award letter; this will be provided separately from any Offer of Admission and will be subject to standard checks for eligibility and other criteria.

For further details please contact Isaac Wilks (chem-pgadmin@reading.ac.uk).

For further project-specific details please contact Prof R. Cramer, Chemistry, University of Reading.

Application Scientist @ Thermo Fisher Scientific

Field-based Application Scientist.

https://jobs.thermofisher.com/global/en/job/198300BR/Application-Scientist-Proteomics-UK?utm_source=copy-link&utm_campaign=job-share&utm_medium=social-share

Proteomics lab based position in Hemel Hempstead:

https://jobs.thermofisher.com/global/en/job/195312BR/Lab-Application-Scientist-Proteomics-UK?utm_source=copy-link&utm_campaign=job-share&utm_medium=social-share

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