



British Society for Proteome Research Summer Newsletter

Editorial

by Karin Barnouin (BSPR newsletter editor)

Although self-isolation imposed by SARS-COV-2 has disrupted our daily routine it has not brought our working lives to a complete stop. Thanks to the internet many have been able to continue working (teaching, conducting research) during lockdown despite having limited or no access to labs, elderly parents to take care of, or young children at home to home school. Others, sadly, have not been so fortunate. Young scientists and research assistants have been furloughed or are being made redundant because grants are not being renewed. Scientists on fixed-term contracts have perhaps been the most negatively affected by the current situation.

For many scientists it was difficult to remain idle knowing we have the knowledge and means to unravel the biology of SARS-COV2. Around the world people working in academia, biopharma and biotech have temporarily changed their research focus to SARS-COV2, given up laboratory equipment and personnel for use in testing. Lockdown has given us more time to think and change how we work. Who, only six months ago, would have foreseen the increase in collaborations and researchers across the world sharing data prior to publication to help understand the biology of this virus and its effect on people so that existing medicines could potentially be redeployed or new ones developed to save people who become critically ill after infection? The speed at which quality data on SARS-COV2 has been generated has been truly remarkable. In our own research community, a COVID-19 Mass Spectrometry Coalition (<https://covid19-msc.org/>) has been formed that enables researchers to share their expertise in virology proteomics, sample preparation, MS and data analysis.



**COVID-19
Mass Spectrometry
Coalition**

For those who weren't able to do SARS-COV2 research, the London Proteomics Discussion group, led by young scientists, have organised a fantastic series on COVID-19 proteomics research to inform the proteomics community. For more information see page 12.

It will take some time before things will go back to normal. We must remain careful to avoid another wave. But hopefully we will be able to hold the 2021 BMSS-BSPR super meeting in person.

BSPR Annual Meetings

At the beginning of the lockdown, the BSPR took the difficult decision to cancel the BSPR annual meeting that was to be held 6-8 July, 2020 in Oxford in St. Anne's College. This conference will now take place in 2022. We are pleased to announce that in September 2021, we will be organising a BSPR-BMSS super-meeting. Date and venue are still to be determined and will only take place in person if it is safe for us to attend.

BSPR2020 – cancelled
BSPR2021: BMSS- BSPR super-meeting
BSPR 2022 – Oxford University – St Anne's College

Bursaries and Fellowships during COVID-19

Several bursaries and fellowships are awarded each year to BSPR members that are either students (MSc and Ph.D.), post-docs, or technical staff to attend proteomics-related conferences or workshops. During the COVID-19 pandemic, most face-to-face conferences have been cancelled and several of them have moved them on-line. The BSPR has therefore decided to offer bursaries (up to £250) for students, technical staff and post-docs to attend virtual proteomics-related conferences and workshops that have a registration fee. Only one bursary will be awarded per person each calendar year.

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 (if applicable) to Karin Barnouin (kbarnouin@bioapicem.com) and John Timms (john.timms@ucl.ac.uk). Only members of the BSPR can 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.

BSPR Student Membership



The BSPR are proud to announce

**FREE* Student Membership*

From the 1st January 2019

See BSPR.org for further information and how to apply

British Society for Proteome Research BSPR
www.bspr.org @UKBspr

The graphic features a stylized purple protein ribbon structure in the background. The BSPR logo is in the top right corner, and the text is centered. The word 'BSPR' in the first line is accompanied by a small icon of a protein ribbon.



BSPR Annual Scientific Meeting

Southampton

1-3rd July 2019

Integrative Proteomics
Protein Function,
Cellular Systems and
Big Data

About one year ago we were in Southampton attending the BSPR Annual Scientific meeting hosted by Paul Skipp and Rob Ewing from the University of Southampton. The thematic streams for that conference were:

- Cellular Dynamics
- Interactomics and Functional Proteomics
- Post-translational Modifications and Chemical Modification
- Emerging Technologies
- Computational Proteomics and Big Data /Modelling
- Health and Clinical Cancer Proteomics

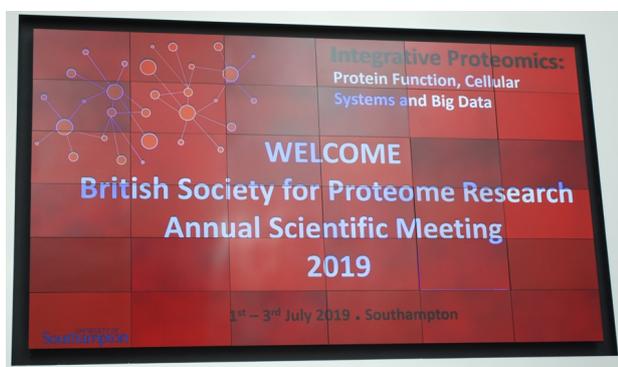
We had an excellent line-up of speakers:

- Angus Lamond, University of Dundee, UK
- Benedikt Kessler, Oxford University, UK
- Jyoti Choudary, Institute of Cancer Research, London, UK
- Luis Mendoza, Institute for Systems Biology, Seattle, USA
- Mike Snyder, Stanford University, USA
- Luis Beltrao, European Bioinformatics Institute - EMBL-EBI
- Rob Benyon, University of Liverpool
- Sara Zanivan, CRUK Beatson Institute
- Tim Elliott, University of Southampton
- Tiziana Bonaldi, Istituto Europeo di Oncologia

The remaining speakers were (established scientists, post-doctoral scientists, and students) selected from the submitted abstracts. The bioinformatics workshop on the Trans-Proteomic Pipeline was run by Luis Mendoza.

The conference was enjoyed by all. The relatively small size of the conference ensured that everyone had a chance to talk and exchange ideas and establish new collaborations.

Here are some photos to remind us of last year... Can you spot yourself in the next pages?



Solent conference centre

**Congratulations to 2019 Bursary, Mike Dunn Fellowship awardees,
Best poster presentations and young investigator talk.**



Best young investigator presentation



Mike Dunn Fellows

Bursary awardees



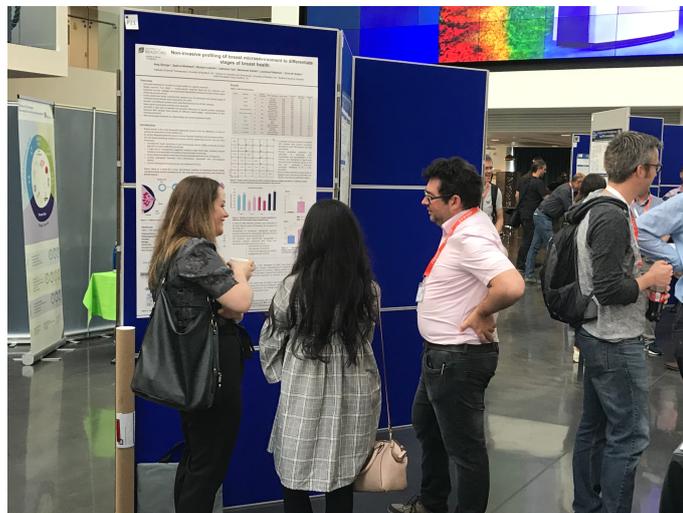
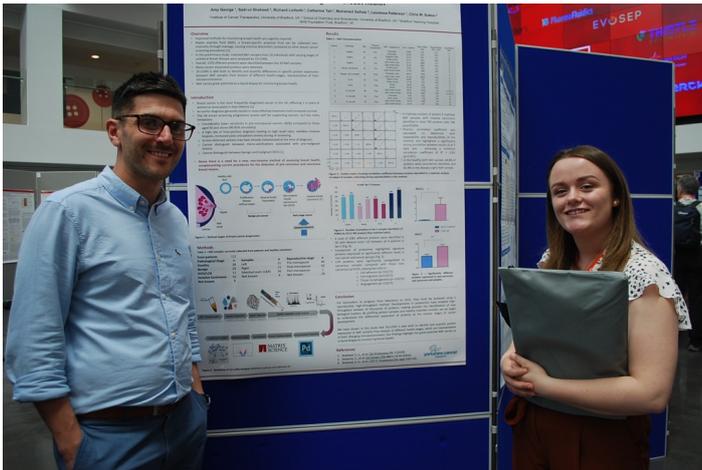
Best poster awards sponsored by Bruker



Thanks to our speakers for the great talks



Great participation in poster sessions



Excellent interaction with our sponsors....



Fantastic dinner in a fabulous setting. Kathryn Lilley's quiz was, as always, a great success....

The evening ended in glory for the winners (awarded chocolate) and in shame for the losers (given a wooden spoon)!



The winners!

BSPR Lecturer 2019-20

Dear Angus,

On behalf of the BSPR I would like to thank you very much indeed for serving as the BSPR lecturer in 2019-2020. Your lecture tour taking in the length and breadth of the UK (as below) has been extremely impressive. We are delighted that you have given very varied groups of young and well-established researchers fantastic insights into the field of proteomics. Based on our experience at the BSPR annual meeting in July last, it is evident that these groups will also have had opportunity to hear about the fabulous work that you and your research group are doing to further develop and apply proteomics methodologies. We are hugely grateful - thank you.

With kindest regards,

Steve Pennington,
BSPR President

BSPR Lecturer Tour - Angus Lamond

2019

24 April	University of St Andrews (BMS Seminar Series)
1 May	University of Cambridge (Dept. of Chemistry)
6 June	Barts Cancer Institute, London
19 June	Proteomics Methods Forum (PMF) University of St Andrews
1-3 July	Keynote Speaker, BSPR Annual Conference, Southampton Solent University
25-26 Sept.	Edinburgh, SULSA Disruptive Technologies Conference
11 Nov	Babraham Institute, Cambridge

2020

13 Jan	Newcastle University
22 Jan	University of Glasgow
30 Jan	University of Hull

BSPR Lecturer 2020-21

The 2020 BSPR Lecturer is Professor Claire Evers 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:

1. The Expanding Landscape of Human Protein Phosphorylation
2. The Top to Bottom of phosphorylation-mediated signaling with mass spectrometry

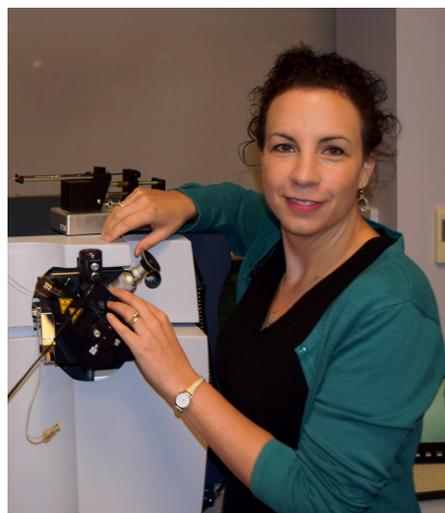
Inaugural Lecture

London Proteomics Discussion Group webinar chaired by Prof. Kathryn Lilley on 7th August, 2020.

"The Expanding Landscape of Human Protein Phosphorylation"

The lecture can be viewed on youtube:

<https://www.youtube.com/watch?v=D6UldshbEc4&feature=youtu.be>



To invite Claire Evers to give a lecture please email her
cevers@liverpool.ac.uk AND Amanda.penney@liverpool.ac.uk

EUPA – YPIC Club



The **Young Proteomics Investigators Club**, or **YPIC** for short, was initiated by the European proteomics association (EuPA) General Council in 2015 and officially launched as a “blank paper” in 2016. A group of **early career researchers** (ECR), nominated by the EuPA associated organisations, has worked hard on building the foundation of YPIC. Many ECR joined on the way and helped shape YPIC’s mission. Now, three years later YPIC proudly fights for ECR within EuPA and frequently joins forces with similar groups, for instance HUPO ECR, EuBIC and LPDG. Through various activities **YPIC aims to promote the exchange of knowledge, discussions, network growth and collaboration among ECR on a world-wide scale.**



Working atmosphere observed during “Meet the expert” sessions, here at Proteomic forum/EUPA 2019 in Potsdam, Germany.

Throughout the year YPIC organises webinars on non-proteomics topics, such as the ECR fellowship programs, the important difference between PI/mentor/supervisor, how a good mentor can make an ECR’s professional life easier, what qualities to look for when choosing a mentor/supervisor/PI/collaborator, career planning, and much more. The webinars are interactive, free of charge, and freely available after the webcast (1, 2). During EUPA annual conferences, YPIC organises Educational/Mentoring day, Career, and Meet the expert sessions, as well as ECR networking hubs. All our events are planned with the purpose to help ECR on their individual professional paths. **Instead of the usual activities at the HUPO World Congress, this year we hope our joint effort with the HUPO ECR will result in a series of virtual meetings in fall 2020.**

In 2017, YPIC initiated the Challenge; a proteomics game which helps ECRs practice teamwork, cooperation and leader skills as well as manuscript writing, next to first real experience of the peer-review procedure from the position of a corresponding author. Until now two YPIC Challenges have been successfully completed with help of the Leibniz-Institute for Analytical Sciences (ISAS) and Polyquant, resulting in a scientific publication for each participating team, a one of a kind trophy for the respective winning team and lots of fun for all participants (3, 4). **The Challenge no. 3 is in preparation, and its launch is planned for fall 2020.**



The winner of YPIC’s Challenge no. 2, Lili Niu holding her trophy (centre) with several YPIC board and core members: (from left to right) [Christian Moritz](#), [Viviana Greco](#), [Dina Rešetar](#) and [Florian Wiesenhofer](#)

If you want to learn more about YPIC or would like to join, you can contact us via ypic16@gmail.com, subscribe as a member at <https://eupa.org/ypic/> and/or follow us on social media (Facebook, LinkedIn and Twitter). And best of all, becoming a YPIC member is free of charge if you are a member of a national society linked to EuPA!

Neither of our activities would be possible without the continued support of senior researchers, scientific companies, national proteomics societies, EuPA, HUPO and most of all the ECR organising and participating at YPIC events. Thank you all!

Maike Langini, YPIC secretary

Medicines Discovery Catapult, Discovery Science & Technology, Alderley Edge, United Kingdom

Dina Rešetar Maslov, YPIC president

University of Rijeka, Department of Biotechnology, Rijeka, Croatia

- (1) YPIC YouTube Channel:
<https://www.youtube.com/channel/UCgJ5yXiKIFCZ0kNxMrlRcMw>
- (2) EUPA YPIC webinar page: <https://eupa.org/ypic/webinar/>
- (3) (3) YPIC Challenge no 2. on Nonlinear dynamics blog: <http://blog.nonlinear.com/2018/03/19/ypic-challenge/>
- (4) (4) <https://www.sciencedirect.com/journal/eupa-open-proteomics/vol/22/suppl/C>

BSPR committee member Kathryn Lilley awarded EMBO membership

Kathryn Lilley is one of 63 scientists elected to become EMBO members this year. Membership is awarded to scientists who have made significant contributions to their field of research in Europe and the rest of the world. Kathryn uses mass spectrometry, RNA-seq and computational tools to study spatial proteomics and transcriptomics, RNA interactome, multifunctional proteins and the structural dynamics of the proteome.

EMBO members influence the direction of the organisation, promote talented researchers and strive for excellence in the life sciences. EMBO plays a role in science policy, particularly in biotechnology, research integrity and scientific publishing. EMBO members are actively involved in organizing workshops, courses and conferences, award funding to talented young scientists (e.g EMBO post-doctoral fellowship and young investigator awards) and conference or lecture travel grants.

The BSPR congratulates Kathryn for this amazing achievement.



London Proteomics Discussion Group

SARS CoV-2/CoVID-19: What role can proteomics play? – An LPDG Webinar Series ***By Harry Whitwell***

With support from the BSPR, EuPA, YPIC and Imperial College London, the London Proteomic Discussion Group (LPDG) have been running a webinar series with speakers and audiences from around the world (see map!) discussing their work on the CoVID-19 pandemic. When we initially conceived this series, we planned on a monthly webinar, but it was quickly apparent that with the rapidity of proteomics research being done, we would need a fortnightly meeting to maintain the value of reporting the most recent science. It has been truly impressive the speed in which proteomics research has been performed including generating lab-models of infection, bioinformatic insights into viral protein structures and interactions, and high-throughput analysis of clinical samples. This has only been possible through open and highly collaborative research and it is a testament to how science done this way, can rapidly yield results for a common goal.

In our first webinar, on the 3rd April, Dr Christian Münch presented work, from their pre-release publication in March (<https://www.researchsquare.com/article/rs-17218/v1>, data available here: <https://biochem2.com/research-group/protein-quality-control#coronavirus>), in which they studied the proteomic changes in cells during infection with SARS CoV-2, reporting both protein and protein expression rates (using mePROD proteomics) during an infection. This work showed that the virus did not effectively shut off host translation as other viruses do, but competed for the translational machinery, thus they may be very susceptible to translational inhibitors. Through analysis of transcription rates, they identified proteins whose transcription matched the trajectory of viral protein expression, revealing increases in pathways for nucleotide synthesis and the use of ribovarine, which inhibits guanosine nucleotide synthesis, as a potential CoVID-19 antiviral.

Also pre-released in March, was Prof Krogan's publication on the SARS-CoV-2-Human Protein-Protein Interactions map (<https://www.biorxiv.org/content/10.1101/2020.03.22.002386v3>). This impressive publication, achieved in a very short space of time, in which expressed viral proteins and host interactions were quantified from immunoprecipitation (IP) and was the combined work of 100 co-authors. Dr Pedro Beltrao from EMBL-EBI presented his contribution to this tour de force. This work revealed 69 FDA-approved drugs that could potentially target 67 different viral-host protein interactions, including, as Dr Münch observed, ribovarine, which is currently in clinical trials for treating SARS CoV-2 infections. The research also showed that many of the host-proteins identified by IP are preferentially expressed in the lung with known differences in expression of these proteins in males and females, although they did not yet explore if this contributes to the apparent differences in infectivity rates.

Infection of the virus into host cells depends on the interaction between the viral S-protein and host ACE2 receptor. Dr David Matthews (University of Bristol) used proteomics informed by transcriptomics to investigate the proteins expressed by the virus (<https://www.biorxiv.org/content/10.1101/2020.03.22.002204v1>). With evidence at both transcriptomic and proteomic levels, a significant proportion of the S-protein contains a genetic-deletion, this has subsequently been confirmed by other groups from the virus in both cell culture and clinical samples. The deletion results in loss of a furin cleavage site from the glycoprotein, which is specific to SARS CoV2 (compared to SARS CoV1) and is thought to be important for enhancing viral maturation. He noted that this deletion may be artificially selected for by cell culture – particularly when using primate-derived cell lines, and this should be carefully monitored when grown for vaccine challenge studies. The S-protein is of interest not only for its biological role in mediating viral entry into host cells, but also for its potential antigenicity for vaccine generation. This protein is heavily glycosylated and research into this was presented by Prof Max Crispin (University of Southampton), who compared it to other viral S-proteins. He observed that the density of glycosylation was much lower than virus (e.g. HIV), this low degree of shielding should assist the generation of vaccines against the virus.

For many of us, it is not possible return to the lab – and even if we could, getting hold of clinical samples and establishing protocols for handling CoVID samples is not trivial. Dr Benjamin Orsburn (of the Proteomics News blog) discussed a great number of bioinformatics tools available online, and data sets for CoVID-19. He has produced *in silico* transition lists and methodology to aid the implementation of mass-spectrometry based virus diagnosis. Datasets for CoVID-19 are not limited to proteomeXchange; Alistair Bullward from NHS Digital presented what is available from the NHS – at the time this was mainly triage data (<https://app.powerbi.com/view?r=eyJrIjoiNzhiNTlhZmUtYmI1Zi00NWU1LTgzNWUtNGVlZTEwNzlhMGFklwiidCI6IjUwZjYwNzFmLWJiZmUtNDAxYS04ODAzLTY3Mzc0OGU2MjllMiIsImMiOj9>), however more population-level data about CoVID infections and transmission will be available soon.

The CoVID-19 Mass Spectrometry Coalition (established by Prof Perdita Barran, Prof Frank Sobott and Prof Konstantinos Thalassinou) is an excellent initiative aimed at pulling together and sharing proteomics resources globally. Prof Andrea Sinz (Martin-Luther University), a member of the coalition, has developed an MS-based protocol for the detection of SARS-CoV2 particles in gargle wash solution and discussed this methodology, along with her research colleagues at our webinar on the 15th May. In the last webinar, Prof Ray Iles (MAPSciences) and Dr Maarten Dhaenens (Ghent University) presented MALDI-TOF and MRM assays for high-throughput and sensitivity viral detection. Prof Iles demonstrated that the viral particles could be enriched very rapidly through tuning of acetone-precipitation and that using this technique, a number of different virus can be identified by MALDI-TOF. Dr Dhaenens presented an optimised cross-platform MRM workflow with transition ion selection directed by data-driven scoring, increasing the sensitivity and specificity of detection. Our webinar series has really highlighted the breadth of proteomics research in tackling CoVID-19. During the time the webinar has been running (from the 3rd April), we have seen the emphasis change rapidly from bench-top research towards clinical implementation. It has been really impressive how swiftly this transition is occurring and the capabilities of proteomics across the world. In our webinar on June 12th, Prof Markus Ralser (CRICK and Charité) will present his application of high-throughput serum proteomics for stratifying patients by severity of outcome.

If you have missed one of our webinars, they are available to watch on our YouTube Channel: <https://www.youtube.com/channel/UCFD0BC5gGMwOFx4yOqziYTO>. All information on our upcoming meetings can be found on our website: www.londonproteomics.co.uk



A global audience for LPDG webinars - based on 600 registered attendees on the 17th April 2020.

Sponsor showcase

Bruker News From ASMS: Further Innovations in CCS-Enabled 4D Proteomics on the *timsTOF Pro*

By Daniel Tome

Email: Daniel.tome@bruker.com

Bruker's revolutionary *timsTOF™ Pro* has been further enhanced by combining PASEF® with parallel reaction monitoring (PRM) for label-free quantitative proteomics. This unique mode of prm-PASEF takes advantage of the 4th dimension of separation using TIMS to improve selectivity and sensitivity, combined with the speed of PASEF to increase the number of precursor targets. Working closely with the Skyline team to enable prm-PASEF methods, Skyline software can now analyze the prm-PASEF data and produce quantitative reports.

New short-gradient methods have been developed using the **dia-PASEF workflow**, which is finding increasing use in many *timsTOF Pro* labs. Dia-PASEF can provide a meaningful advance in data completeness, and the dia-PASEF workflow is now supported by Bioinformatics Solutions Inc. *PEAKS* and Biognosys *Spectronaut* software.

With the launch of prm-PASEF, the growing success of dia-PASEF, and the trend towards shorter gradients that take advantage of the robustness, sensitivity and unmatched duty-cycle of PASEF, the *timsTOF Pro* provides the capabilities to make 4D-proteomics 'translational reality'. Furthermore, the unique MOMA feature of TIMS allows for targeting isobaric precursors at similar retention times for MS/MS acquisition. Having MOMA capability helps improve the depth of coverage using short gradients, and this is important to our translational research proteomics users who are running >50 samples per day per *timsTOF Pro*.

Large-Scale, High-Precision Peptide CCS Measurements for Deep Learning

Peptide collisional cross sections (CCS) measured at large scale and with high precision by the unique TIMS technology deliver added dimensionality for increased confidence of identification in 4D proteomics. A new study by Florian Meier et. al., entitled '*Deep learning the collisional cross sections of the peptide universe from a million training samples*', and submitted to bioRxiv, (2020.05.19.102285; doi: <https://doi.org/10.1101/2020.05.19.102285>), uses a deep learning training set of 570,000 CCS values measured in 360 LC/MS runs of fractionated digests of five organisms, run on a *timsTOF Pro* system.

New application notes released at ASMS, and posters will all be made available at:

<https://www.bruker.com/events/2020/asms-2020-reboot.html>

Bruker TimsTOFPro



Save the Date



HUPO 2020 World Congress (HUPO 2020 Stockholm), originally scheduled for October 18-22, 2020 in Stockholm, Sweden has been postponed to October 24-28, 2021. To keep HUPO members and friends connected, you are invited to participate in the first-ever international HUPO virtual experience: **HUPO Connect 2020**.

We are delighted to inform you that all members of EuPA proteomics societies, including the BSPR, can register for HUPO Connect 2020 (<https://hupo2020.org>) at the "HUPO member" rate. When you register just use the country-specific registration discount code: **GB**

During the registration process you will be asked the following questions:

1. Are you a member of the European Proteomics Association (EuPA)?
2. If yes, please enter your EuPA Member discount code. i.e. **GB**

If you enter their code correctly, you will receive the HUPO member rates. If not, you will receive an error message.

With the GB code you will be able to register for the conference at the 'HUPO member' rate of 100\$. AND, if you attend any of the three pre-congress webinars that are scheduled in July, August and September, during the registration for the webinars you will be offered an additional discount code for 25% off the congress registration bringing registration to 75\$

Note: registration is inclusive of all HUPO Connect 2020 events and registrants will have the opportunity to submit a poster. These are excellent options for participation in HUPO Connect 2020 and we hope that BSPR members will take advantage of these special conditions.

So, included in registration is:

Pre-Congress Webinars (July 21, August 24, Sept 24)

Connect with colleagues and opinion leaders on proteomics research hot-topics including Proteomics in COVID-19, Proteomics in Precision Medicine, New Innovations in Proteomics. Free registration for HUPO members! Watch the webinar to receive a time-limited discount code for HUPO Connect 2020 registration.

HUPO Pre-Congress Training Course is also included in your registration! Training topics selected from HUPO 2019 delegate feedback include proteogenomics, PTM analysis, and bioinformatics tools for functional analyses.

Main Congress Program (Oct 19-22)

Three days of scientific sessions, including posters, industry seminars, early career researcher mentoring and manuscript competition, student poster competition, HUPO awards, Human Proteome Project day.

Scientific sessions include: • Cellular Proteomics; • Impact of Proteomics on COVID; • New Technologies/Innovations (MS and non-MS); • Precision Medicine in Wellness and Disease; • Protein Structures and Complexes; • Proteogenomics; • Proteoforms; • Spatial Proteomics; • Systems Biology

Open Positions

Postdoctoral Research Associates Mass Spectrometry, Separations and Chemical Biology

The Rosalind Franklin Institute (the Franklin) is a new national Research Centre, funded by the UK government through UK Research and Innovation, dedicated to bringing about transformative changes in life sciences through interdisciplinary research and technology. We are currently expanding our Proteomics team and are looking for several Postdoctoral Research Associates specializing in Mass Spectrometry, Separations and Chemical Biology. Further information can be found by following the link:

<https://opportunities.rfi.ac.uk/vacancies.html>

For informal enquiries please email Shabaz Mohammad: shabaz.mohammed@rfi.ac.uk.

If you would like us to send any job, meeting or course adverts to the BSPR mailing list, please email Roz Jenkins (r.jenkins@liverpool.ac.uk).

BSPR members, if you wish to contribute an article, advertise jobs, meetings or courses in the next newsletter, please email Karin Barnouin (kbarnouin@bioapicem.com).