British Society for Proteome Research Winter Newsletter

We are pleased to announce this year's BSPR conference on **Next Generation Proteomics**. It will be hosted by Shabaz Mohammed and Roman Fisher of the University of Oxford.

This year's meeting is a celebration 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 using the technologies to go well beyond traditional proteome analyses. Proteomics experiments can now capture not only quantitative data or PTM data but also protein interaction, spacial, structural and temporal data. In addition, proteomes synergistic links with the other main cellular systems such as the metabolome and transcriptome area being unravelled. The rapid development of proteomics technologies is leading to rapid proteome analyses at ever lower cell counts. Such work has led to clinical studies being performed on thousands of samples and generating stronger medical insight. Moreover, fragmentation technologies and bioinformatics have made crosslinking studies almost routine and contributed to the rapidly expanding number of posttranslational modifications and protein classes that can be characterised. The 2020 meeting will celebrate these next generation technologies and how they are transforming basic research and the medical sciences.

We have an excellent line-up of confirmed plenary speakers:

- Carol Robinson, University of Oxford, UK
- Perdita Barran, University of Manchester, UK
- Manuel Mayr, King's College London, UK
- Mike Gillette, Broad Institute, USA
- Ben Davis, University of Oxford, UK
- Josephine Bunch, National Physical Laboratory, UK
- Evangelina Petsalaki, European Bioinformatics Institute, UK
- Claire Eyers, University of Liverpool, UK
- Matthew Collins, University of Cambridge, UK
- Alfredo Castello, University of Oxford
- Christopher Tape, UCL Cancer Institute, UK
- Bernhard Kuster, Technical University of Munich

The remaining speakers (established scientists, post-doctoral scientists, and students) will be selected from the submitted abstracts. This year we will have two bioinformatics workshops taking place in parallel on the 5th July. Skyline will be run by Brendan MacClean, Ben Collins and Birgit Schilling. The EBI workshop on "Accessing freely available proteomics resources at EMBL-EBI" is being organized by Sandra Orchard and Juan Antonio Vizcaino. A satellite conference on 'One Health' organised by Rainer Cramer will also take place on 5th July. Please see 'Save the Date' section for more information.

Key Information and Dates

Abstract deadline – TBD

Registration deadline – 17 April 2020

Student BSPR member (*free BSPR membership for students*) £100

Student non-member £150

Non-Student (Other) BSPR member £250

Non-Student, Non-Member £300

Conference Dinner (optional) £50

Skyline Workshop (5 June 2020)

£130 (max 35 people)

EBI – data analysis and PRIDE workshop

£130 (max 35 people)

'One Health' Satellite Conference

£20

Student and technical staff travel bursaries and post-doctoral MJ Dunn Fellowships

Students (MSc and Ph.D.) and technical staff awarded a bursary will receive £250 to help cover meeting registration, accommodation and travel expenses for the BSPR 2020.

MJ Dunn Fellowship awards will be given to post-docs to cover registration, accommodation and travel expenses for the BSPR 2020 conference. Applicants must be within 6 years of completing their Ph.D. and be paid up members of the BSPR.

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 (kbarnouin@bioapicem.com) and John Timms (jtimms@ucl.ac.uk) no later than Monday 17 April 2020. Applicants must be 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 webpages.

For more information please visit: https://www.bspr.org/ and https://www2.bioch.ox.ac.uk/bspr2020/

BSPR Sponsors 2020

St Anne's College
University of Oxford

6th - 8th July
2020
BSPR Annual Scientific Meeting

Exhibition and Sponsorship Announcement

We cordially invite interested parties to participate in the exhibition and sponsor events for this prestigious meeting.

www.bspr.org @UKBspr

We thank all the companies that have already agreed to sponsor this meeting. If you are interested in sponsoring us, please contact Chris Sutton (C.W.Sutton@bradford.ac.uk).

Proteomics Network

by Harry Whitwell, BSPR Proteomics Network coordinator.

The BSPR Proteomic Map has now got 59 groups registered including 40 research group, 8 facilities 8 groups from industry and 3 proteomics meetings, including 2020 BSPR meeting next July. The map allows you to search for groups by key words, allowing people to identify areas of expertise across the country. The UK proteomic capabilities are broad, ranging forensics, cancer, PTMs, bioinformatics, quantitative analysis and clinical assays. We hope the map is useful to BSPR members and non-members, indeed, a number of people have mentioned what a useful feature this is.

If you are not registered but would like to, please do so by visiting:
https://www.bspr.org/proteomics/map
Registration takes 5 minutes!

London Proteomics Discussion Group

by Harry Whitwell, London Proteomics Discussion Group Committee Member.

The LPDG is a local proteomic discussion group established and run by early career researchers throughout the South East. Having started at the beginning of this year, we have run two meetings welcoming speakers from Industry and Academia. The last meeting, held at the new MSRH building in White City and kindly sponsored by Sciex had talks from Holger Kramer (MRC), Gina Eagle (University of Liverpool/Sciex) as well as PhD students and post-docs. Unique to these meetings, we also run a themed challenge through the meetings, where participants can network and present ideas to the group over pizza and drinks. This format was really well received, with a challenge set by Prof. Rob Beynon (University of Liverpool).

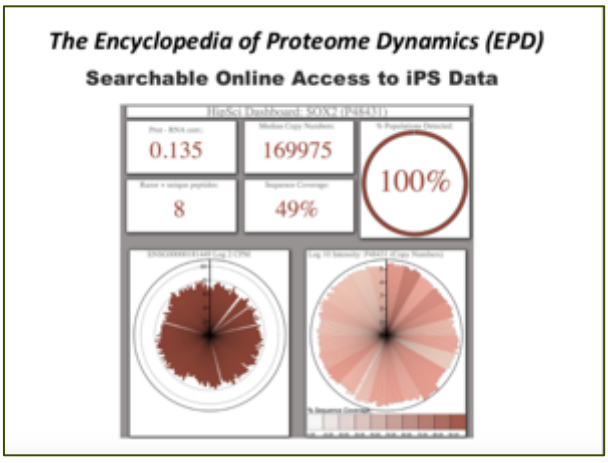
The next meeting will be held in March, for details, please visit our Facebook page (https://www.facebook.com/groups/471642630311490/) or find us on LinkedIn (https://www.linkedin.com/groups/13722087/). The meetings are free to attend, and run thanks to sponsorship, if you are interested in presenting, sponsoring or have a venue suggestion – please get in touch!

BSPR 2019-20 Lecturer

by Angus Lamond, BSPR Lecture, University of Dundee.

I am a Professor of Biochemistry at the University of Dundee. My co-workers and I have used quantitative, mass spectrometry-based methods for many years to study cell proteomes at a multidimensional level. Our work integrates data on protein isoform expression, subcellular localisation, post-translational modifications, protein complex formation and protein turnover, to characterise cellular phenotypes and biological response mechanisms in both human cells and model organisms. To meet the growing 'Big Data' challenges in the proteomics field, we have also developed new computational tools to aid data management, analysis and integration. This includes the 'Encyclopedia of Proteome Dynamics' (EPD), an integrated analytics repository that provides a searchable, open access data sharing tool.

During the past year, I have been the BSPR Lecturer. This has provided me with an opportunity to visit University departments and research institutes around the UK and describe how we apply proteomics methods to address biological problems. In 2019 I have presented seminars at the University of St Andrews, University of Cambridge, Barts Cancer Institute and Babraham Research Institute. As part of this series I also gave keynote lectures at the 2019 BSPR Annual Conference in Southampton and at the annual UK Proteomics Methods Forum. I have already planned further BSPR lectures, scheduled for early 2020, at the Universities of Newcastle, Glasgow, Hull and Keele.
In my BSPR seminars, I chose to focus on work we have done, together with our collaborators, that has pioneered high throughput, quantitative studies on the proteomes of large numbers of human induced pluripotent stem cell lines. These iPS cells are derived from both healthy donors and from disease cohorts with specific genetic disorders (see; www.hipsci.org). This project has integrated deep proteome data, mostly generated using multiplex, TMT labelling, with parallel transcriptome RNA expression data and exome sequence data from the same cell lines. The resulting data provide a detailed picture of how gene expression is coordinated in pluripotent, induced human stem cells and how gene and protein expression vary across individuals within the population. I have also used these iPSC data to illustrate how large-scale, complex poly-omics data sets can be integrated and interactively explored and shared with the community, using our online, EPD database.



Angus Lamond lecturing at the University of Newcastle on 13 January 2020.

An important role for the BSPR Lectures is to highlight to a wide audience the opportunities now provided by modern proteomics technologies for advancing research in many areas of biology and clinical research. As such, my lectures were designed to be accessible to a wide general audience. It is clear from the feedback I have received and from my experience in meeting with a wide range of researchers across the UK, that there is huge and growing interest in proteomics. A clear take home message is that many groups who have not previously used proteomics in their own research are increasingly aware of the opportunities proteomics now provides to generate valuable new data. I found there was widespread interest from many life scientists in how they can address major questions in their respective fields using experimental strategies that employ quantitative proteomics methods. Perhaps the most common question I encountered has been, 'How can I get help to carry out these types of experiments?"

My experience to date as the 2019 BSPR Lecturer has highlighted both specific challenges and opportunities where the BSPR can help to make an important contribution to the future of biomedical research in the UK. The challenges include the need to provide our UK colleagues with training and education in how to design and implement effective proteomics workflows. We need to share and update our experience in how to achieve best practice across sample preparation, data acquisition and in data analysis and interpretation. A further challenge lies in coordinating access to facilities in the UK that can help biologists and clinical researchers to access proteomics technologies and instrumentation. As a result, I feel there is a great opportunity here for the BSPR to play a leading role in providing the requisite education and training that will help to widen access and successful application of proteomics methods. I suggest that an important task for the Society moving forward, therefore, is to coordinate a strategy to help achieve this goal.

I look forward now to delivering the future BSPR lectures scheduled for January 2020. If there are any other institutes in the UK or Ireland who would be interested to have me visit and present a BSPR lecture, please get in touch (a.i.lamond@dundee.ac.uk).

Why do I use Proteomics in my Research?

Understanding Proteome organization and variation

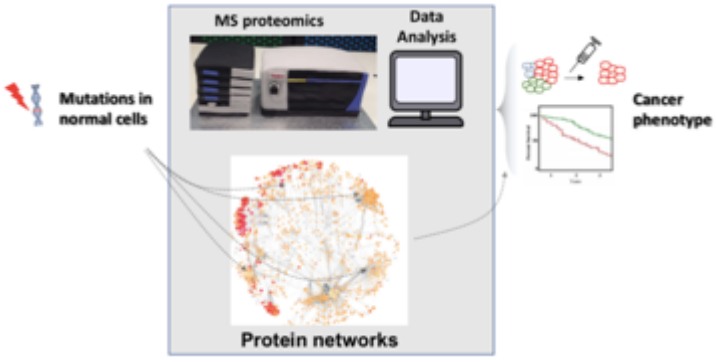
By Jyoti Choudhary, Group Leader at the Institute for Cancer Research, Fulham.

I became interested in mass spectrometry during my undergraduate degree and pursued this further by doing a PhD under the guidance of Professor Howard Morris (FRS) at Imperial College, London. My PhD and Postdoc were focused on developing techniques to study the turnover and regulation of membrane proteins in the Photosystem II complex, in collaboration with Professor James Barber (FRS FRSC MAE). In subsequent positions in pharma and biotech sectors, I expanded my expertise in applying mass spectrometry-based solutions to address biological and structural problems.

I became interested in using proteomics data to interrogate the genome. We were one of the first groups to report the use of the draft human genome for database searching, thereby exploring the use of proteomics for discovery of novel protein coding regions. Our group at GSK, the Cell Map Project, was one of the first to establish high throughput proteomics and we spun out a company.

I became a founding member of Cellzome UK, an internationally recognized biotech company that specialized in affinity and chemical proteomics. In 2004, I joined the Wellcome Trust Sanger Institute to start my independent research group in proteogenomics. Here, my group developed open access computational tools and pipelines to refine genome annotation as well as to integrate proteomics and genomics datasets. To enhance the functional annotation of the genome in a systematic manner we devised the endogenous Tandem Affinity Purification, eTAP, approach that uses recombineering or CRISPR to tag genes in stem cells. This technology enables the characterization protein interactions and primary structure in a range of cell types and tissues.

Moving to the ICR in 2017, my team develop computational and experimental quantitative MS proteomics approaches to study proteome features such as turnover, interaction and post-transcriptional regulation. We want to understand the impact of mutations and genetic variation on protein attributes and how these changes lead to remodelling of protein networks during cancer progression and resistance.



Revealing the impact of cancer mutations on proteome networks using quantitative Mass Spectrometry

Photo: Jyoti Choudhary's group at the ICR. From left to right: Theo Roumeliotis, Qiyun Zhong, Eve Hopkins, Michel Wanger, Angela Paul, James Wright, Mercedes Pardo, Jyoti Choudhary, Ernie So and Lu Yu.

Liquid Biopsies and P4 Medicine

By Christopher Sutton, University of Bradford

With the development of digital devices, and collection and assimilation of "big data" by AI systems, healthcare is undergoing a significant shift in direction in developed countries. Society, healthcare providers and governments are recognising that the economic burden of health management will be better dealt with by prevention rather than cure. Particularly, as an increasingly aging population requires a directly proportionate increase in medical support. The earliest detection of physiological changes that could lead to disequilibrium or loss of homeostasis associated with the first stages of disease, can be identified and appropriate action taken to intervene and possibly reverse perturbations back to a normal healthy state. This is particularly important for those maladies with a long incubation period before manifestation (e.g. neurodegenerative diseases, cancers such as breast and pancreatic).

Those fortunate enough to attend the HUPO 2017 meeting in Dublin would have had the opportunity to hear Lee Hood (1,2,3) elucidate the concept of P4 medicine - Predictive (genomic information), Preventive (avoiding those factors that are known to cause poor health), Personalised (recognising that we are all individuals with unique physiologies) and Participatory (proactive volunteering to undertake self-examination and screening on a regular basis). At the BSPR meeting in Southampton this year, Mike Snyder, a living embodiment of the P4 principle, demonstrated the way digital devices and data monitoring can be used. The NHS, at the beginning of 2019, presented a long-term plan (https://www.longtermplan.nhs.uk/publication/nhs-long-term-plan/) to invest substantially on disease prevention by increasing personal responsibility and healthy aging.

So, where does proteomics fit into this paradigm shift in healthcare management? Although increasingly accessible, portable devices that continuously measure physical properties are optimal monitors for some diseases at a superficial level, many internal microscopic disorders are not detected with sufficient sensitivity and specificity using these monitors or imaging approaches. Hence, molecular diagnostics provides the potential to address these shortcomings. As proteins are one of the key groups of molecules active within the body, changes in their expression can correlate with specific tissue disease or damage. However, sampling tissues on a routine basis is not practical. Biofluids, of which there are more than 30 in the human body and many are tissue specific, represent an ideal source of information about normal and maligned body processes. Blood, urine, saliva and faeces are already collected as liquid biopsies in national health screening programmes or home-based testing kits. However, there is potential for even greater impact by using proteomics to identify new biomarkers in the various biofluids where there is an unmet clinical need to find better solutions. For any single type of liquid biopsy that can be linked to a particular disease, such an approach provides the prospect of using proteomics to explore normal healthy variation and longitudinal collection for individual variation. Changes in profile correlate with genuine emergence of the disease or confounding factors that are non-specific. This is a fantastic opportunity to take proteomics into the next generation of biomedical applications.

1. Hood and Friend, Nat Rev Clin Oncol. 8, 184-7 (2011)
2. Tian et al, J. Intern Med. 271, 111-121 (2012)
3. Hood and Tian, Genomics Proteomics Bioinformatics 10, 181–185 (2012)

Be a poster child for science communication!

By Rosie Maher (PhD student) and Rob Beynon (supervisor and BSPR committee member)
Centre for Proteome Research, University of Liverpool
www.liv.ac.uk/cpr
Twitter: @rosie_maher, @astacus @c4pr_liv

We really enjoy scientific conferences – the chance to hear about the greatest and (sometimes) latest developments, and the pleasure of talking science, life, the universe and everything with like-minded colleagues. An opportunity to let a just-starting postgraduate student share their work by presenting and talking through their poster…. what a fabulous way to break into the community!

Inevitably, in many conferences, there are relatively few speaking slots, and most science is communicated through the poster sessions. So, this medium of communication - is it effective? Ask that question of a student, or even a near-retirement academic, how it feels to stand by your poster for an hour and watch people avoid eye contact and swiftly pass by. Or, the poster session that has 200 people juggling plates of food and glasses, packed in a boxy, stuffy room with posters crammed up against each other, often in the herringbone 'zig-zag' arrangement that makes access, let alone discussion, nearly impossible. Then of course, we have the poster sessions where there is plenty of room

Figure 1: A poster session before the rush! Anyone who attends a poster hall like this should wear a pedometer and very comfortable shoes! Hard floors, exhausting and almost impossible to find anyone.

We have been thinking about ways to make posters more effective, and the behaviours that make a poster session more rewarding. There are so many interacting elements to this – the poster itself, the room design, the room layout and even the presence/absence of refreshments.

'*We need to talk about posters*'. Look at Figure 1 again. How many words on a typical poster there? We guesstimate about 500-1000 words per poster. There are several thousand posters in that meeting, which means that the room could have delivered several million words. We posit that of those posters, virtually none of them **will be read** fully. Nobody really wants to be told if you used 3mM or 6mM of a particular reagent, so why add it? - if they really needed to know, they'll find you and ask you. Posters are not research papers or thesis chapters, they are visual communication opportunities, and they should be eye catching, colourful and concentrate on the most important messages.

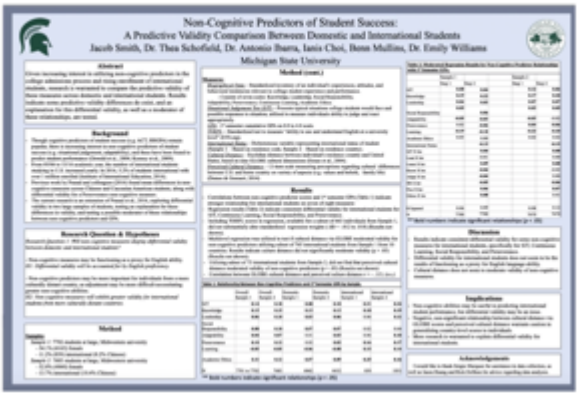
We've discussed this and, for example, agreed to limit all our posters to about 200 words (including title and affiliation) and they seem to be much better, as we concentrate on the visual elements. But, can we make them even more appealing and effective?

In spring 2019, our attention was drawn to this YouTube video (www.youtube.com/watch?v=1RwJbhkCA58) and we realised that there are other interesting solutions out there. The video itself is a little slow to develop, but espouses a bold and imaginative solution to poster designs. We wanted to know, however, if this would work for our subject areas as well. Since our initial discussions, numerous members of CPR have designed and taken their #BetterPosters to conferences including BMSS in Manchester and HUPO in Adelaide, and the feedback has been amazing! First of all, creating the #BetterPosters has been so much fun! The new format really forces you to focus on your science, your results and the most important take home message. Of course, not everyone is a fan of the new style of poster, usually arguing that there isn't enough 'science' on the poster. However, the use of QR codes linking to e-posters and publications allows people who are interested to gain more information about our work. More information than you could ever fit onto a traditional poster! Using this poster format, we have had so many more interactions and discussions, all of which have been surprisingly positive! For us, that is the most important thing; having more interactions with people to exchange opinions and ideas, whether it is about our research or our take on the #BetterPoster design. Using this new design and boiling your research down to the main findings makes your research understandable to **everyone** which in turn facilitates more interactions and discussions, and who doesn't want that! Why don't you have a look at the video, and think about how this might work for you– this is directed at poster presenters and their supervisors alike. You may experience pushback from those who only think about traditional posters, but stick with it, and you may be at the vanguard of a small but effective revolution! This is what 'poster 2.0' might look like after a reboot.

- A plain language summary of the key conclusion(s) in a huge part of the poster
- A QR code (linking to a web page, full preprint/poster or similar)
- An 'ammo' bar (the information/data/methods) e.g. on the left
- A 'silent presenter' bar e.g. on the right– a summary of the poster for quick reading

Look at the example in Figure 2, taken from the video.

From this:



To this:

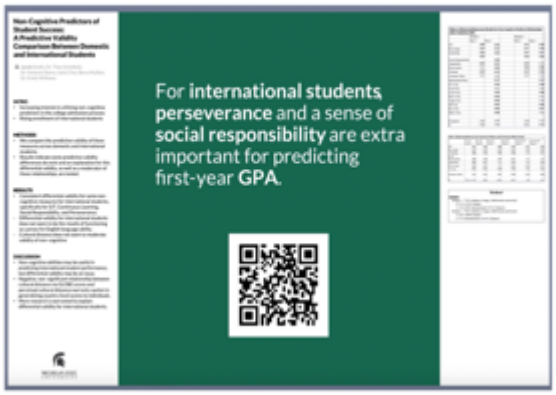


Figure 2. Reducing a poster to an eye catching, plain language, informative punchline, backed up by summaries and data, with a QR link for further information.

Would you be brave enough to do this? In CPR we have experimented with portrait #BetterPoster design which put on display at BMSS and HUPO in 2019 (Figure 3). However, wouldn't it be great if **most** of the posters were like this! We could really change the way in which we create impact in our posters. The big punchline really makes people stop, and even if they don't, they get the message.

And presenters, stop being so passive! You have put a lot of effort into the science, and the poster.You have every right to stop passers-by and say '*can I have a minute to show you my work*', or walk up to one of the 'big shots' – (they're not really big shots, they're just older, but they share all of your enthusiasm for science!) and say '*please may I explain my poster*'. In virtually every case, you'll be rewarded by an engaging, knowledgeable, enthusiastic response, and you'll feel fantastic. **Go for it.**

From this:

To this:

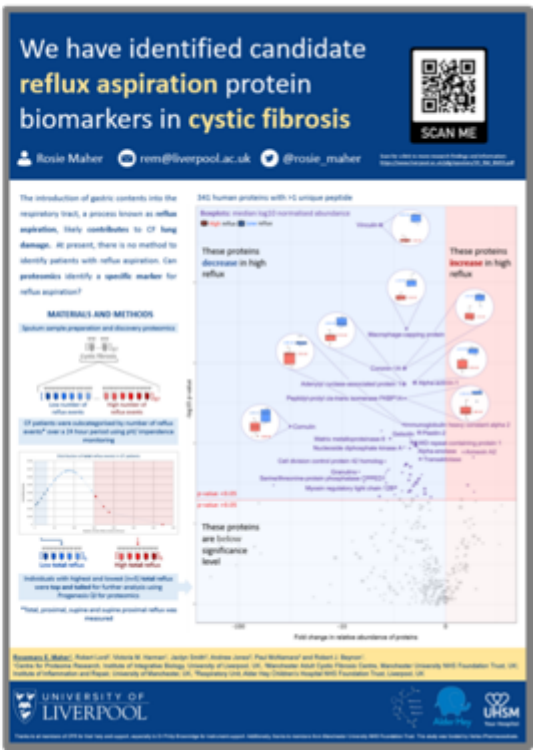


Figure 3. Rosie created a #BetterPoster, converting a traditional style poster into a more eye-catching, less cluttered poster. The QR code links to an e-poster that contains more information about their work and can be accessed by scanning the above QR code or by using the following link: https://www.liverpool.ac.uk/pfg/eposters/19_RM_BMSS.pdf

What is QR code?

A QR ('quick response') code is a 2-dimensional bar code that is often used to link to a web page. Thus, this QR code links to our web page. How can you access this though? The easiest way is to use the inbuilt QR code reader on your phone or other portable device (both iOS and Android). For example, in iOS 11 and later, simply open the camera app, point the camera at the QR code, and you'll be given an option to be taken directly to the web site. (You could also install QR code reading apps, but beware that some of these sneakily add a monthly subscription – this should not be needed.

You make a QR code by going to one of the free QR code generators that are on-line. The right QR code takes you to a code generator (if you compare them, you'll see that they look superficially similar, but are different).

Try it – the left hand QR code points to the CPR web site.

Some thoughts for meeting organisers. (We've made these mistakes in the past too).

Give posters time and space – schedule a poster session, don't jam them in with vendor booths and during lunches and coffees. The poster presenters, predominantly younger, early career scientists, deserve much better.

Use odd/even numbering to manage time for presentation and time for viewing. Schedule times for attendance and if you are a presenter, make sure you are there.

Put the posters in a large enough room that there is space for conversations, people flow, and a chance to step back and take a shot of the QR code.

Give the poster presenters a big lapel badge to say 'it's me!' and talk to them. Add poster numbers to name badges so poster presenters can be identified easily.

Supervisors – try to keep a distance from your students and let them go without stabilisers!

UK in particular, perhaps – STOP forcing portrait format posters – find a way to accommodate landscape posters even if you have to pay a bit more for a room/display boards. (If we have to be portrait, here's a template for the poster format discussed previously in portrait format (https://osf.io/g6xsm/)

Don't 'herringbone' (zig-zag) the posters – this creates little zones of deadness where nobody can do anything. Make the posters run linearly.

Here's an idea that has also been used. Try to cluster posters on related topics in groups of, say five. Then, ask a convener (perhaps, one of the supervisors) to gather all the five poster presenters together, and do a quick walk around (maybe glass in hand?), where each presenter tells the others briefly about their posters. The five neighbours will find it easy to talk to each other for the rest of the meeting. (One of us has done this as convener in meetings in the past, and it is a super ice breaker, especially for newcomers to an established meeting.)

Schedule posters early – they are a great way of breaking down shyness and creating a better buzz to the meeting

Accept electronic posters (ePosters) that complement traditional paper posters, allowing conference attendees to post comments, questions, or share them during and after the conference. It would also help if ePosters could be searched by 'buzz words'- 5 or so key words selected by the presenter so related topics can be found easily.

Universal agreement – why do we present posters? Is it to give a summary of a research paper (small figures with walls of text) or is it to engage with passers to entice them over to promote one to one discussion of your work (large colourful figures with little text). Maybe the organisers could be bold enough to set a word limit?

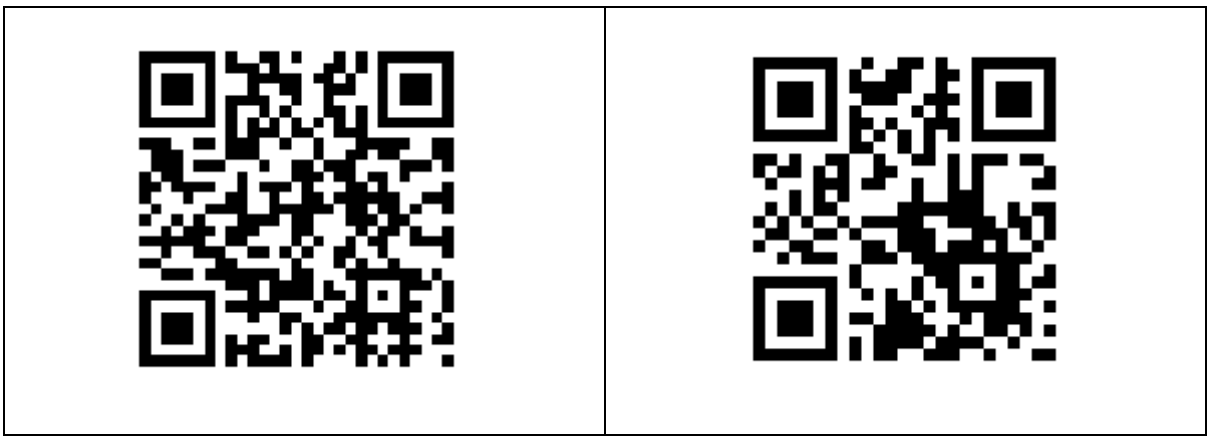
These are not particularly radical thoughts and we're sure some of them have been tried and tested before, but it would be a brave meeting that considered some of these principles and planned for radically new, lively, poster sessions. We can only say 'why not try?'.

Acknowledgments

This article has been edited from an article previously published in BMSS 'Mass Matters' newsletter. These thoughts initially came from three PhD students (Iris Wagner, Natalie Koch and Rosie Maher), and reflect our opinions only -our goal is to try to create some discussion about the whole poster experience. Your opinions may differ.

Footnote

Two more QR codes. LH: the YouTube video, RH: the link to the portrait format



Save the Date

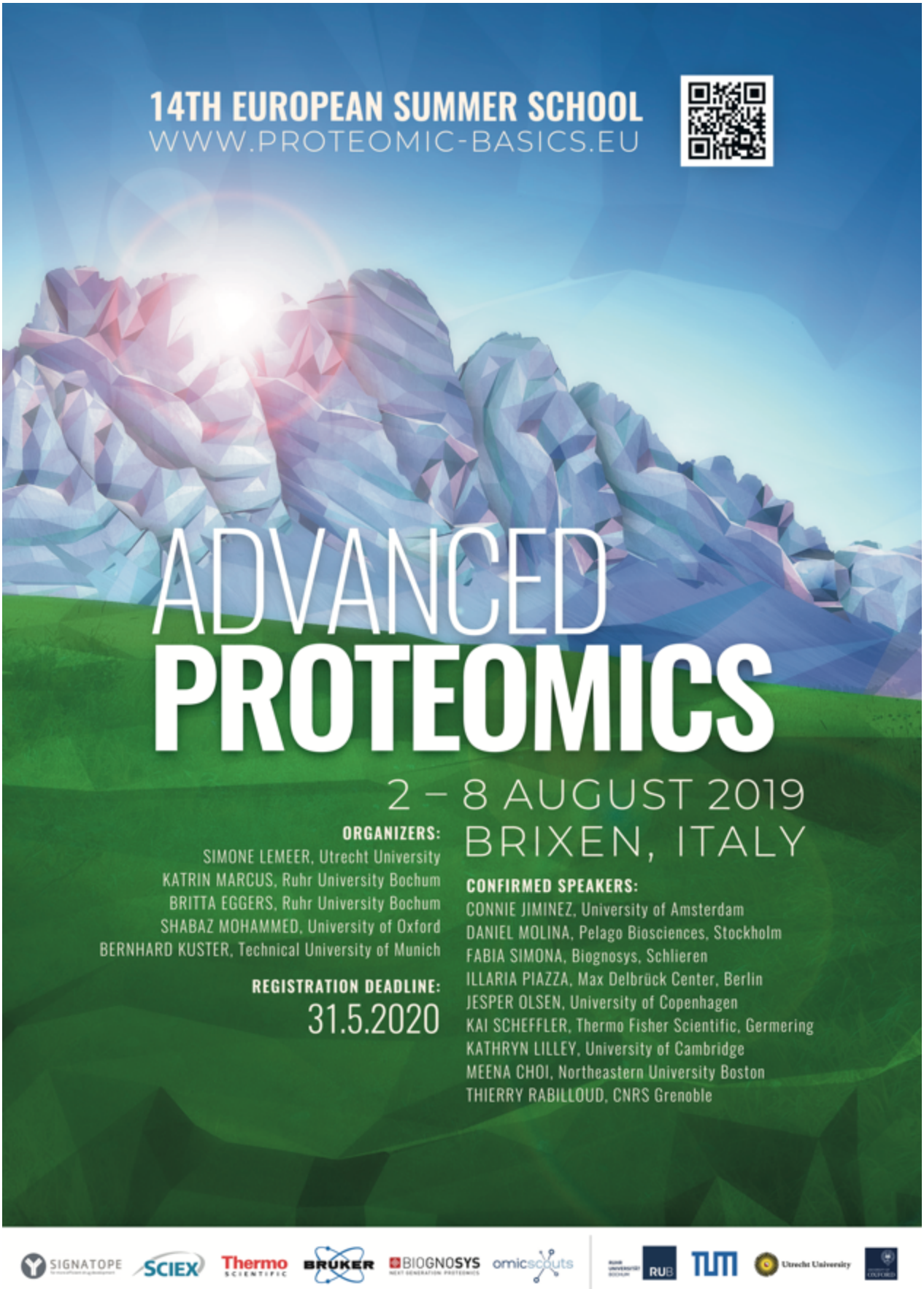
Satellite Conference

MS and Proteomic Analysis in Animal Sciences and Agriculture

Sunday 5 July 2019, 10:30 – 17:30
St. Anne's College, University of Oxford, Oxford OX2 6HS

Mass spectrometry and proteomics are important tools for animal welfare, produce quality analysis and food safety. For instance, early diagnosis of mastitis in livestock and rapid detection of the pathogens responsible for this disease are essential first steps towards the fight of antibiotic resistance. Mass spectrometry (MS) as a diagnostic tool provides the basis for several applications to the animal sciences and agricultural industry, exploiting its ability of rapidly and accurately targeting metabolites, lipids, proteins and bacterial consortia. Currently, MS and MS-based 'omics' are used for the detection of antibiotics, mycotoxins and other (bio)chemical compounds of relevance for product safety. However, it could also be applicable to the fields of livestock and crop production, and further optimized for high-throughput analysis (e.g. of milk), assessing animal welfare and produce quality through profiling and multiplexing. The overall aim of this meeting is to build a network between experts from the UK in the (farm) animal and crop sciences and experts in the field of mass spectrometry and proteomics applied to the analysis of biological matrices. This satellite meeting is aligned with the aims of 'One Health' initiatives in terms of animal and human welfare.

Save the Date



Open Positions

Senior Scientific Officer, Metabolomics, Beatson

Competitive Salary (range £28,000 – £38,000 depending on experience)

The Cancer Research UK Beatson Institute supports cutting edge research into the molecular mechanisms of cancer development and is one of the leading research institutes in Europe. The Institute provides an outstanding research environment, underpinned by state-of-the-art core services and advanced technologies, with special emphasis on imaging, metabolomics, proteomics and *in vivo* models.

We currently have an exciting and rare opening to join the Institute's Metabolomics facility which uses mass spectrometry to support cancer metabolism research projects, where the aim is to increase our understanding of alterations in metabolic pathways in cancer and to use this knowledge to aid in the development of novel therapies.

We are looking for a Senior Scientific Officer to assist in the operation of our state-of-the-art instrumentation (Thermo Q-Exactive, Altis triple quadrupole (QQQ) LC-MS and Agilent GC-QQQ). The successful candidate will liaise with researchers, acquire high quality LC-MS data and carry out regular instrument maintenance. As part of a newly restructured team, the role provides a fantastic opportunity to significantly contribute to the future shaping and success of the Metabolomics Facility.

You should possess a PhD in a Biochemistry related discipline and strong laboratory skills. It is essential to have experience in LC-MS and/or GC-MS in metabolomics or a related field. Previous experience working with GC and QQQ instruments would be an advantage. Knowledge of data analysis software packages for metabolomics and/or lipidomics is also desirable. Excellent communication skills, enthusiasm and the ability to work well in a team are essential as the role involves active interactions with the facility users.

For informal enquiries please email David Sumpton at d.sumpton@beatson.gla.ac.uk

All applications must be made via our website at

http://www.beatson.gla.ac.uk/Careers/Scientific-Officers/

Closing date for applications is 14 February 2020

Research Associate in Cancer Proteomics, UCL Institute for Women's Health

The post-holder will be required to contribute to a CRUK-funded research project aimed at identifying biomarkers for the early detection of ovarian, pancreatic and colorectal cancers. They will be responsible for sample handling and processing for proteomic-based biomarker discovery and validation, including running commercial assays, developing and implementing new mass spectrometry-based assays, data analysis and write-up of results. They will also contribute to the smooth running of laboratory facilities, including maintenance and running of mass spectrometry instrumentation and sample preparation and analysis for different collaborative projects.

For more information and to apply please click on the header. It is hyperlinked to the website.

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).

If you wish to contribute an article, advertise jobs, meetings or courses in the next newsletter, please email Karin Barnouin (kbarnouin@bioapicem.com). Please submit by 1 May 2020.