BSPR 2022 was set among the timeless spires of Oxford University, where the top proteomics scientists in the UK met in person for the first time in 3 years.

The pre-conference activities started with a workshop on protein-protein interactions lead by Sandra Orchard from EBI, and Ed Huttling from the Gygi lab, before kicking off the following day. The symposium was opened with a keynote from Anne Claude Ginras focussed on the spatiotemporal element of signal transduction focussing on her work with BioID, mentioned the strength and limitations and introducing her idea of pre-prey pearson correlation analysis as a more robust way to build networks. She also highlighted that all the data her lab generated on HEK293 cells was available in the resource humancellmap.org.

The enabling technologies session saw great talks from Perdi Barran and Alex von Kriegsheim one exploring protein structures using native mass spectrometry and the other talking the power of multi-omics to discover new insights in hepatocellular carcinoma. The first day ended with the chemical biology session, where Sabine Flitsch, Ed tate and Aini Vourinen discussed a wide array of topics ranging from biocatalysts for proteins and peptides, proteins S-acetylation networks to profiling cysteine fragment reactivity against deubiquitinases.

Day 2 began with an explanation of the ever-expanding collection of P’s in medicine, which had gone from P3 to P5. This session had talks from Manuel Mayr who discussed the complexities of clinical proteomics and revealed one of the big bottle necks in the cardiovascular proteomics field was the lack of datasets with a large number of patients enrolled. Edward Emmott followed and he spoke about the sputum proteomics and finding biomarkers correlated within the data and finally Melissa Grant looked at gingival crevicular fluid and also found biomarkers relating to the regulation of immune cell and in particular neutrophils.

The imaging and spatial proteomics session kicked off by Melanie Bailey with element imaging to look at the distribution of elements within a cell as well as subcellular compartments. Harry Whitwell talked about the challenges and methodologies they used to analyse low sample amounts and how the quantitation of some peptides doesn't follow the normal dilution pattern that most do, which can affect quantitation. The low sample amounts theme was also central to the talk from Covaris which closed the session.

The systems/networks session was kicked off with a tour de force by Mike Gillette where he presented the vast amount of deep proteogenomics data that was acquired within CPTAC and how this was already helping to further characterise cancer, stratify patients and refine the molecular taxonomy. Charlie Barker, also focussed on cancer, presented his work on melanoma looking at constitutively active BRAF mutations. The session was closed with a talk from Aymen Al-Rawi looking at the how different binding partners of the CDK1 kinase can affect the phosphorylation dynamics and motif preferences.

The last session in the day was the Bioinformatics session. Here after some struggle with zoom, Evangelia Petsalaki discussing probabilistics networks for kinases and their substrates. Anjan Venkatesh then talked about using proteomics to study paralogs looking at what happens to the abundance of one when the other is lost. The plenary session on Tuesday saw a fascinating talk from Matthew Collins, discussing the challenges and opportunities of studying ancient proteins, ranging from T-rex sequencing down to the boom of proteomics in archaeology which took off in 2021.

Tuesday night also hosted the BSPR dinner and the legendary pub quiz, which maintained the spirit Kathryn Lilley imbued into it, and became a challenging but fun evening for all attendees, with some of the organisers featured in the quiz itself.

Wednesday was the last day, and first session was the collaborative segment between the BSPR and the British Mass Spectrometry Society. The first talk in the session was from Claire Eyers, showing us that the world of phosphorylation was not only centred around serine, threonine and tyrosine, but that there were important roles for non-canonical phosphorylation and that the traditional phosphor-proteomics methods are not well suited to study many of these. The second talk was from Jack Penny who discussed using gas phase fractionation to generate DIA libraries and how these provided impressive results when paired with diaPASEF. The final talk of the session was from Alejandro Brenes and it looked at the neutrophil proteomes in COVID19 and how saw a phenotype of long covid and found value in "contaminants" as potential clinical biomarkers.

The mid morning session was One health research, and this had talks from Alfredo Costello, Jenny Ho from Thermo and Sarah Hart. Alfredo talked about the interplay between viruses and the hosts and talked about the importance of studying the interactomes of virion RNA and some of the issues to think about when understanding and interpreting the results from these interactomes. Sarah Hart then talk about Leishmaniasis Mexicana, showing the dire consequences the disease can cause and her approach of studying the surface proteome of the parasite after knocking down components of the BBSome complex.

The final session was started by the announcement of the Young Investigator awards, where the society recognised the contributions of young investigators. This was followed by the Next Gen Tech session. This was started by Hagan Bailey who discussed the process of development of Nanopores to study proteins but promised the Mass Spectometrists in the room that their jobs were not quite a risk just yet. Xiao Qin then talked about mass cytometry and the analysis of PTMs in organoids with the last talk being from Edward Emmott talking about his single cell proteomics work using SCoPE-2 to study post translational modifications in Norovirus infection and how the virus needed to use PTM's to replicate.

The final talk in the meeting was a Plenary by the Nobel prize winner Peter Radcliffe, who discussed his journey to discover the oxygen sensing and signalling with hydroxylation and offered career advice to the young investigators in the room. With that the meeting was over, great science, great talks, great posters and phenomenal organisation, BSPR 2022 was done.