

I would first like to give a huge thank you to the British Society for Proteome Research for selecting me for the MJ Dunn Fellowship to attend the 2023 joint BSPR-EuPA meeting held in the beautiful and vibrant city of Newcastle upon Tyne. The organising committee put together an incredibly diverse and exciting programme of talks and posters, amplified by the bringing together of researchers not only from the UK and EU but also worldwide. A big thank you and congratulations must also be extended to Professor Matthias Trost and his lab for organising this wonderful meeting. It was an absolute pleasure to have the opportunity to discuss my own research over my poster focussing on the use of cross-linking mass spectrometry to determine lipoprotein-based interactors of the SARS-CoV-2 spike protein.

Professor Mike MacCoss kicked off the meeting with his plenary lecture exploring the use of next generation translational proteomics to determine protein drivers of Alzheimer's Disease. Here Prof. MacCoss exemplified the power in using a cohort of very well-matched patients rather than attempting to obtain larger and larger cohorts that can introduce varying comorbidities. A big take home here was the need to dig a little deeper into proteomic datasets and rather than just quantifying at a protein level, attention must be placed at a peptide level as peptides from differing regions of the same protein may be differentially changing, as beautifully shown in the case of amyloid and tau proteins. Prof. MacCoss ended by introducing the Mag-Net protocol which involves the use of hyper-porous strong-anion exchange magnetic microparticles, acting to enrich for membrane bound particles while also largely reducing the dynamic range of the plasma proteome, enabling greater depth of quantitation. The end of the opening plenary lecture gave way for the first night social event held in the Discovery Museum.

There were certainly too many illuminating and inspiring talks to list however I want to introduce a few that I particularly enjoyed. The first full day was opened by Professor Markus Ralser highlighting their work using high-throughput DIA-based methodologies to determine metabolic and proteomic landscapes after genetic perturbation at genome-scale. Professor

Alexey Nesvizhskii discussed the ever-expanding toolbox of MSFragger with a particular focus on glycopeptide identification, a tool I have found incredibly useful in my own research of late. Professor Justin Benesch highlighted the complementarity of mass photometry alongside native mass spectrometry. Professor Tamar Geiger explored the power of single cell proteomics to probe tumour complexity. What was particularly evident at this meeting was the large strides being made in the single cell community, with a particular focus here on new instrumentation. Dr Nicola Ternette gave a fascinating and exciting talk exploring TCR-like antibody cancer therapeutics. Finally, the meeting was drawn to a close by Professor Sara Zanivan investigating the role of cancer-associated fibroblasts.

It was also incredible to see a large focus of the meeting given to support Early Career Researchers, not only through the selection of many to give talks but also through organised workshops and seminars, as well as with the wonderful presence of the Young Proteomics Investigators Club. A fantastic talk was given by Dr Alejandro Brenes, ultimately to be awarded best early career presentation, where he discussed the importance of data normalisation while also introducing the wonderful Immunological Proteome Resource. I must end by also mentioning what a fantastic choice for the conference dinner to be held at the Wylam Brewery, serving wonderful beer alongside delicious food, followed by a band giving the opportunity for everyone to let loose.

Once again thank you to the British Society for Proteome Research as well as everyone involved in organising this wonderful meeting. I met some incredible scientists who I very much look forward to seeing again at the next meeting.