Conference report:

Human Proteome World Congress Sydney 2010
Launch of the Human Proteome Project
19-23 September 2010 • Sydney Convention and Exhibition Centre, NSW, Australia

The HUPO 9th annual world congress 2010 was held in Sydney, Australia on September 19-23. The geographical remoteness of the congress venue had obviously prevented a number of scientists to make the trip but the more than a thousand delegates and exhibitors who actually gathered down under were rewarded in many ways – apart from the fact that the in-flight entertainment system of the Airbus A380 reduced the perceived overall travel time substantially even for scientists travelling from Europe.

The Congress & Exhibition was held at the Sydney Convention and Exhibition Centre which offered first class facilities to both delegates and presenters and is situated at the focal point of Darling Harbour, one of the world's most imaginative urban redevelopment projects, alive with shops, restaurants and visitor attractions. Its very nice location meant that accommodation and the central district of the city were all within walking distance and industry workshops could be held at bayside galleries with stunning views over Darling Harbour.

The Congress started with an Education and Training day covering the latest technologies and methods in the proteomics field, while the Clinical and HUPO Initiatives sessions had been incorporated into the main program, which had been expanded to four full days. Thereby, each day started with a plenary session before

the program was split into three themed parallel sessions covering the broad range of the latest proteomics developments and applications.

During the opening ceremony on Sunday evening, local aboriginal people welcomed all delegates on their continent with a lively and touching ceremonial didgeridoo and dance performance. The ceremony ended with the burning of aromatic herbs, which left behind a penetrating smell that jolted everyone from their jetlags but also unintentionally put things in perspective - as impressive as it was to watch the performance could not hide the fact that the indigenous people had other things to worry about than the problems associated with targeted proteomics.

Launching the scientific part of the conference, the HUPO2010 convenor Mark Baker woke up all delegates from their dreams and reminded everyone why they had come here in the first place: This year's annual conference promised to be an enthralling systems biology world congress featuring an exciting mix of invited speakers from clinical, biological, cellular and pure proteomic disciplines.

By the end of Mr. Bakers speech everyone had forgotten the stresses and strains of their travels and were assured several times to have arrived in the "birthplace of the word proteomics" and the "most beautiful harbor city of the world". Having spent a day or two in the city by then, most delegates had already learnt this on their own and even the biggest skeptics had to admit that Sydney is definitely a unique destination and a city of sophistication and fascinating variety.

Following Mr. Baker's words and on the same lines, a political representative of the local government stressed the need for interdisciplinary interactions in the science community and pointed out that having known the members of the organizing committee in person for years, she was sure that a terrific scientific program was in store for all delegates and that she was even more convinced that this program was to be complemented by a spectacular social program – and she was right as the conference featured a spectacular Sydney Harbour gala cruise amongst many other social amenities.

In the opening plenary session, Leroy Hood presented his ideas of a shift from reactive to proactive 'P4' medicine, which aims to be predictive, personalized, preventive and participatory. Thereby, the vision is that instead of waiting for clinical symptoms to appear, physicians will eventually be able to see early warning signs of malignancies from a pinprick of blood analyzed by genomic instruments and proteomics technologies. In this spirit, Mr. Hood's talk was a perfect introduction for many of the talks to follow.

Day two of the conference started with an exciting plenary session in the course of which Carl Borrebaeck nicely presented his vision of recombinant antibody microarray-based proteomics. Covering a lot of ground he described how his lab is generating data for cancer biomarker discovery to assess the risk for tumor relapse and monitoring disease progression and in doing so he nicely pointed out where in the clinical decision tree such assays could be implemented.

In the parallel sessions that followed, the well-attended session on clinical biomarkers attracted most delegates. Hanno Langen grabbed the opportunity to present the current status of Roche's colon rectal cancer protein panel, which impressively demonstrated that the discovery of candidate marker proteins can be done by high throughput proteomics methods but the major bottleneck was the

validation of those candidates including clinical endpoint validation – going beyond the sphere of action of any academic lab. Along the lines of Carl Borrebaeck he made a strong point that even after all those efforts, the intended use of Roche's marker panel in the clinical decision tree was not to diagnose colorectal cancer directly but only to screen risk groups and identify potential patients to undergo colonoscopy.

The morning of day three of the conference was stamped by the inspiring talk of Brian Chait and a very well-attended session on quantitation by mass spectrometry. In his plenary lecture, Mr. Chait nicely presented how his lab is developing new approaches for isolating macromolecular complexes in a form that allows for the determination of their state in the living cell and how the quantitative comparison of such complexes that have been isolated in defined temporal states can generate animated views of working macromolecular complexes.

In the following parallel session, Tine Thingholm presented an excellent quantitative study in which she combined an iTRAQ label-based discovery strategy and a targeted Selective Reaction Monitoring (SRM) label-free strategy to quantitate and validate changes between the total proteome from human diabetic myotubes and healthy control subjects. In general, the attractive strategy of combining a quantitative discovery-driven approach with targeted, MS-based validation experiments was omnipresent during the whole conference but rarely presented as convincingly and professionally as in her talk. In the following presentation, Alexey Nesvizhskii presented a detailed comparison of several label-free protein quantification approaches, including MS/MS spectral counting and MS1 (intensity) based methods coupled with various normalization steps demonstrating the very robust performance of the simple spectrum counting based approach – when conducted intelligently.

The afternoon of day three was partly dedicated to a newly launched HUPO event to recognize the outstanding quality of research undertaken by early career researchers: Six selected 'Young Guns' finalists were given the chance to present their work in a brief oral presentation and each received an award plaque recognizing their research achievement. In another session to highlight the research of young scientists, the 10 best student poster presenters had 5 minutes of fame on the big stage talking through their posters in the competition for the '2010 HUPO Proteomics Idol'. Back to the regular schedule, the rest of the afternoon was dominated by a parallel session on targeted mass spectrometry which rather felt like a plenary session as it was very well-attended, reflecting the community's huge interest in this fairly new and rapidly changing area of the proteomics field.

Leading the way in this movement, Ruedi Aebersold gave what was one of the key plenary lectures of the conference. Unaffected by the fact that the bottom third of his slides went unseen by the audience due to technical difficulties he calmly discussed the generation of near complete yeast and human proteome maps. Those maps were created with synthetic proteotypic peptides and the resulting assays are made publicly accessible supporting the detection and quantification of the respective peptides by SRM in diverse samples and in many laboratories. Thereby, such maps constitute an invaluable resource for the whole proteomics community and will hopefully transform proteomics towards a technology capable of generating highly reproducible and quantitatively accurate data sets in many laboratories around the globe.

In this spirit, the Human Proteome Project (HPP) was launched on the last day of the conference. As reported in news media, the HPP seeks to produce a reference map of the entire human proteome through the combined efforts of hundreds of labs and researchers from around the globe. Thereby, the mission is to produce not only a comprehensive map of human proteins, but to provide tools for the proteomics community for further research and to inspire researchers in human health to draw upon the proteomics map for the development of new knowledge and therapies. In 2011, the combined HUPO 10th Annual World Congress, 5th EuPA Annual Scientific Meeting and the 8th SPS scientific meeting in Geneva will focus on translational proteomics, providing the perfect setting to subsume the achievements during the first year of the HPP – the bar is set very high, see you next year.

Andreas Frei
ETH Zurich
Institute of Molecular Systems Biology
Wolfgang-Pauli Str. 16, HPT E 52.1
8093 Zurich, Switzerland