

IC HDX

AstraZeneca R&D, Gothenburg, Sweden, 16th-17th May 2017

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The inaugural International Conference in Hydrogen Deuterium Exchange Mass Spectrometry (IC HDX) was held in May in Gothenburg, Sweden. It consisted of a workshop day followed by the main two-day conference, and was very well attended with over 150 delegates from academia, industry and instrument vendors. The conference was hosted at the AstraZeneca Conference Centre, just a few miles from the city.

The workshop was very interactive, with discussions focussed on how the community can improve their data collection and analysis approaches. Morning sessions were themed Sample Preparation, Instrumentation, Fluidics and Data Collection, and Data Analysis. In the afternoon, various different software solutions were presented, and workshops were given by the sponsor companies. There was a lot of discussion as to the best way to handle and process data, in particular statistical testing and the analysis of exchange kinetics.

The first day of the conference proper started with a fantastic historical perspective of hydrogen exchange from Walter Englander (University of Pennsylvania), in which he also shared, in no uncertain terms, his opinions of the way data are often presented, analysed and described 'these days'. This was followed by another invited lecture from Perdita Barran (University of Manchester), who described the interplay of different mass spec techniques for solving biological problems: native MS, IM-MS and HDX-MS. Talks that followed included subjects such as how to visualise our data, HDX-MS analysis of kinase regulation, of protein folding, and of virus-antibody complexes, top-down analysis of MAbs, and a fascinating talk from Jeppe Buur Madsen (University of Southern Denmark) describing how he performed in-cell HDX-MS on

alpha-synuclein to address whether it forms a stable tertiary structure in a cellular environment. Kasper Rand (University of Copenhagen) spoke about how we can improve the "HDX toolbox", including the use of microchip technology for pepsin digestion and post-deuterium-labelling deglycosylation. Yoshimoto Hamuro (SGS Life) gave a talk entitled "The Devil in the Detail for HDX-MS Practice" with lots of helpful tips and tricks. Five poster presenters then gave five-minute long 'flash' presentations, before the poster session began. This was a very busy, discussion-filled 90 minutes, with plenty of sharing of ideas and networking among the community.

After the poster session, we all headed to the Universeum, Gothenburg's Science Museum, where we were welcomed by the city's deputy major... and a glass of bubbly. We were then free to explore the museum at our leisure, with its large rainforest area with free-flying birds, plus sloths and lizards, a section about Space, and an outlet for the competitive amongst us with the physical challenges in the Health exhibition. The conference dinner was then held in the museum's aquarium, alongside the sharks and stingrays and other swimming sorts. A Swedish buffet plus a generous wine allowance made for a networking experience enjoyed by all.



Rainforest at Gothenburg's Universeum science centre, where the conference dinner was held.

The second day included invited lectures from John Engen (Northeastern University), Thomas Jørgensen (University of Southern Denmark) and Pat Griffin (The Scripps Research Institute). John Engen's talk centred around how we can exploit developments in peak capacity to improve our HDX-MS workflow and data, to include higher pressure UPLC, the use of ion mobility and substituting UPLC with CE. These useful practical insights were liberally sprinkled with example applications, particularly addressing very large protein complexes, such as the 1.3 MDa 26S proteasome. Jørgensen highlighted how HDX-MS can be used to analyse protein oligomers, with reference to some very nice work with alpha-synuclein oligomers and antithrombin dimers. Pat Griffin demonstrated how using a robust HDX-MS workflow

to analyse an impressive number of protein-ligand interactions can guide and drive medicinal chemistry and drug discovery efforts. There were a number of other fantastic talks throughout the day covering protein folding, biosimilar analysis, millisecond HDX, gas-phase HDX, and investigation into membrane protein drug transporters. The meeting concluded with the announcement of the second IC HDX conference, planned to be held in Calgary in 2019.

In my opinion, this was a fabulous conference, with talks from many of the top names in HDX-MS from around the world. In this expanding scientific area, there was a great feeling of community, friendship, and willingness to share knowledge and help and support others.



The conference offered a schedule packed full of engaging talks from HDX experts from around the globe.

