Report: Top Down Proteomics Workshop **Date/Time:** June 4, 2019, 5:45-7:00 PM

Location: Room A402-403, Georgia World Congress Center
Presiding: Frederik Lermyte, University of Warwick and Nick Young, Baylor College of Medicine
Estimated Attendance: 150-200

The theme of this year's Top Down Proteomics workshop was "Advancing Widespread Adoption and Expanding Applications". Six short talks of 3-5 minutes were scheduled in blocks of two, each followed by 15 minutes for open discussion. The aim of this setup was to engage the audience as much as possible. For the same reason, speakers were asked to design their presentations to raise questions and provoke debate. The first talk came from Neil Kelleher (Northwestern University), who reported back on the First European Top-Down Proteomics Symposium, held at the Institut Pasteur in Paris in February. This was followed by a talk by Caroline DeHart (Northwestern University) on ways to democratize top-down proteomics, *i.e.* how to run the experiments in practice and make the techniques more accessible to non-expert laboratories and core facilities, which was one of the main issues raised during last year's workshop. This first session prompted considerable audience discussion, with the importance of confidence measures for top-down proteomics drawing particular attention. The third talk was given by Paul Thomas (Northwestern University), who introduced the FAIR repository for experimentally verified proteoforms. This was followed immediately by a talk by Yuri van der Burgt (Leiden University Medical Center) who discussed applications of top-down proteomics in clinical chemistry, with emphasis on both quantification and glycoform analysis by top-down MALDI-ISD FTICR-MS. This was again followed by a round of discussion. The third session was kicked off by Joe Loo (UCLA) who focused on top-down protein analysis in the context of native MS, addressing a point that was raised last year. This highlighted the (potential) ability of top-down MS to provide information on higher-order structure whilst simultaneously allowing proteoform identification. Also discussed in this talk was a proposal for a uniform nomenclature to distinguish different top-down proteomics workflows. Finally, Lindsay Morrison (Waters) delivered a talk on top-down proteomics from the perspective of an instrument manufacturer. In particular, this focused on the hardware and software evolutions that would be required to truly make top-down proteomics a routine approach, linking back to the talk on democratization of the technique. During the discussion following these two talks, a comment was made about internal fragments in top-down proteomics and whether it is feasible to routinely include these in data analysis. A point was also raised about the complementarity of different fragmentation techniques and the potential utility of using several of these to fully characterize native and denatured intact proteins. Before closing the session, the need for a new co-presider for the ASMS 2020 conference in Houston, TX was announced.