

Report: Top Down Proteomics Workshop Date/Time: June 6, 2018, 5:45-7:00 PM

Location: Room 31ABC, San Diego Convention Center

Presiding: Nick Young, Baylor College of Medicine and Paul Thomas, Northwestern University

Estimated Attendance: 150-200

The theme of this year's Top Down Proteomics workshop was "Robustness and Reproducibility". As a nascent technology, it is essential that we work as a community to focus on common challenges and to foster the growth of the field across many labs through collaboration and education. Eight talks were scheduled each of 5 minutes and were all selected to spark discussion and be as community focused as possible. This left approximately half of the time for discussion and debate. The first talk came from Paul Danis, CEO of the Consortium for Top Down Proteomics, who introduced that organization, invited responses to a survey that he created and requested that anyone who desires would join the consortium (for free). Following Paul Danis was Neil Kelleher from Northwestern University. He spoke on a cell-based proteome project focused on proteoforms and how we as a community can work toward this goal. After Neil came Yury Tsybin from Spectroswiss Sarl, who spoke about Pilot Project #2 of the Consortium for Top Down Proteomics, a community-based project focused on the interlaboratory comparison of top down analysis of monoclonal antibodies. After Yury, Luis Schachner, a graduate student from Northwestern University spoke. His talk was about native top down proteomics. This sparked considerable discussion about the nature and challenges inherent to Native Top Down Proteomics. Next spoke Leah Schaffer, a graduate student from the University of Wisconsin. Her talk highlighted the challenges of achieving robust and reproducible quantitative results with top down proteomics. This also sparked considerable discussion especially the challenges of bringing top down proteomics into non-expert laboratories. Everyone agreed that the goal of our interest group and the consortium for top down proteomics is to make top down proteomics more accessible. Next Benjamin Cutak from Sigma Aldrich spoke about standards for top down proteomics. There were many useful suggestions about how to make the current top down standards represent a broader class of protein characteristics. Next, Richard LeDuc of Northwestern University addressed the workshop on the use and need to address ambiguity in proteoforms with clearly and rigorously defined specifications. Following Richard, Matthew Holt, a graduate student from Baylor College of Medicine spoke about a proposed way to concisely, yet clearly, write about proteoforms and the sets of proteoforms that share unifying characteristics within the prose of results and discussion. This resulted in some discussion about whether a concise and descriptive nomenclature is needed. This evolved into a discussion including material the previous talk from Richard LeDuc. Most agreed that there is a need for both verbose and concise descriptive nomenclature for different purposes. One to list as a complete description of each proteoform and another to descriptively discuss proteoforms and the distinct characteristics thereof. In closing the session we announce the need for a new co-president for the ASMS 2019 conference in beautiful Atlanta, GA next year!