

## Wed, August 27

3:10 PM

## **Databases & Bioinformatics**

Session | Location: Lecture Hall D, VMP 6 / Philturm, Von-Melle-Park 6 20146 Hamburg

3:10 - 3:30 PM

Replacing "OR" Logic and Mass Accuracy with "AND/OR" Logic and Mass Resolving Power, as the Basis for Peak Assignment in Top-Down Mass Spectrometry Data.

Speaker

Jeffrey Agar

3:30 - 3:50 PM

Advancing Top- and Middle-Down Antibody Analysis Using Simulated FTMS Datasets

Speaker

Yury Tsybin

3:50 - 4:05 PM

Computational methods in top-down proteomics to address challenges in proteoform analysis

Speaker

Kyowon Jeong

4:05 - 4:20 PM

TDAuditor assesses deconvolution quality for the Blood Proteoform Atlas

Speaker

Prof. David Tabb

4:20 - 4:40 PM

The Implementation of Open Science Practices Can Enable A Faster Development Of Top-Down Proteomics

Speaker

Dr Juan Antonio Vizcaino

4:40 PM