

User Meeting

Vienna, IMP, Monday, 26th August 2024

From new products & solutions to learning how to increase MS performance and productivity in your lab and expert insights on how to set up Single Cell Proteomics

Time	Title	Speaker
15:00 - 15:30	Arrival & coffee	
15:30 - 15:45 (15')	Welcome Post ASMS update - introduction Stellar MS	André Müller <i>Thermo Fisher Scientific</i>
15:45 -16:05 (20')	Principles, tips & tricks for setting up DIA on Orbitrap MS platforms	Dominic Hoch <i>Thermo Fisher Scientific</i>
16:05 -16:25 (20')	Developing and implementing „Single Cell Proteomics“ workflows on Orbitrap MS systems – Roadmap to success using „OnePot solution“	Manuel Matzinger <i>IMP</i>
16:25 -16:45 (20')	The past, present and future of low-flow LCMS-based proteomics	Runsheng Zheng <i>Thermo Fisher Scientific</i>
30 min	Coffee Break	
17:15 -17:35 (20')	Digital transformation powered by ARDIA - concept, vision and benefits for Proteomic Core facilities	Eike Logé <i>Thermo Fisher Scientific</i>
17:35 -17:55 (20')	Ultra-high throughput workflow for robust and sensitive quantitative single cell analysis	Bernard Delanghe <i>Thermo Fisher Scientific</i>
17:55 -18:15 (20')	Reanalysis of immunopeptidomics data reveals novel bacterial epitopes	Rupert Mayer <i>IMP</i>
18:15 - 20:00 (open)	Closing words, fingerfood & drinks	