



IMaSS
Italian Mass Spectrometry
Society

IMaSS Single Cell Day 2022 -Hybrid event

Parma, 12-10-2022

A scientific meeting dedicated to the world of single cell analysis

- 9:30-10:10 **Registration and Welcome breakfast**
- 10:10-10:30 **Prof. Barbara Montanini, Dr. Andrea Armirotti** *Welcome and introduction to the meeting*

Session Chair: Andrea Armirotti

- 10:30-11:00 **Erwin Schoof**, Technical University of Denmark; **Leveraging single cell proteomics to better understand human hematopoiesis_virtual**
- 11:00-11:20 **Francesca Ruscitti**, Chiesi Farmaceutici; **Multi-omics approach in support to target identification_in presence**
- 11:20-11:50 **Paul Humphrey and Christof Mitterer**; Thermo Fisher Scientific; **Single cell proteomics – Going beyond one cell at a time_in presence**
- 11:50-12:20 **David Hartlmayr**, Cellenion Proteomics Application Specialist; **An automated workflow for label-free and multiplexed Single Cell Proteomics using the cellenONE_in presence**
- 12:20-12:50 **Ronald Cutler**, Albert Einstein College of Medicine; **Exploring cell-to-cell variation during aging_virtual**
- 12:50-14:00 Lunch & Poster Session *Towards Single Cells Proteomics*

Young Session Chair: Lolita Piersimoni & Barbara Montanini

- 14:00-14:15 – Selected *Flash* oral communication from Poster session (3 young investigators, 5 mins)

Session Chair: Simone Sidoli

- 14:15-14:45 - **Pierre-Olivier Schmit**, Bruker; **Enabling routine single cell proteomics analysis: presenting the timsTOF SCP based solution_in presence**

- 14:45-15:15 – **Mario Armelao** – SCIEX; **Improved data-independent acquisition (DIA) and data-dependent acquisition (DDA) performance on low-level proteomic samples using a novel Zeno trap_in presence**
- 15:15-15:45 **Prof. Nikolai Slavov**, Director Single Cell Proteomics Center, Northeastern University, USA_ **Driving biology with single-cell proteomics: New data acquisition and interpretation methodology for sensitive protein analysis_virtual**
- 15:45-16:00 **coffee break**
- 16:00-16:30 **Claudia Ctortecka**, Broad Institute of MIT and Harvard; **Under the looking glass: revealing proteome heterogeneity at single-cell and low input using the timsTOF SCP technology_virtual**
- 16:30 – 17:00 **Karl Mechtler**, Research Institute of Molecular Pathology (IMP); **An automated workflow for multiplexed single-cell proteomics sample preparation_in presence**
- All speakers: Wrap-up/discussion/round table

This event is made possible thanks to the support of:

Thermo, Bruker, Euroclone/Cellenion, Sciex, Chiesi

Scientific & organizing committee:

Barbara Pioselli, Lolita Piersimoni, Silvia Catinella, Barbara Montanini, Andrea Armirotti , Simone Sidoli, Claudio Iacobucci

To register, please follow: <https://forms.gle/CX5nSswUt4SBbaUK7>