

5TH EUROPEAN SYMPOSIUM ON SINGLE CELL PROTEOMICS

VIENNA, AUGUST 27 - 28TH 2024

Day	Time	Topic	Speaker	Time	Topic	Speaker
Day 1	8:00	Registration		13:00 – 14:00	Lunch	
	9:00 – 9:10	Opening Remarks <i>Karl Mechtler & Manuel Matzinger</i>		14:00 – 14:35	Molecular Pixelation: Spatial proteomics of single cells by next generation sequencing <i>Michele Simonetti</i>	
	9:10 – 9:45	Elucidation of tumor cellular interactions using high-throughput proteomics <i>Tami Geiger</i>		14:35 – 15:10	The views and some data of newcomers to the field of single-cell proteomics <i>Kris Gevaert</i>	
	9:45 – 10:20	Quantitative accuracy of DIA proteomics with low amounts. <i>Vadim Demichev</i>		15:10 – 15:25	Global analysis of protein turnover dynamics in single cells <i>Pierre Sabatier</i>	
	10:20- 10:55	Linear models to interpret and explain single-cell proteomics data <i>Christophe Vanderaa</i>		15:25 – 16:30	Poster session (with refreshments)	
	10:55 – 11:20	Coffee		16:30 – 17:05	Feeding the 5000 (IDs) via Mass Analyzer Development, for Miraculous Results from Tiny Inputs. <i>Hamish Stewart</i>	
	11:20 – 11:55	Lipidomics: on track toward a readily accessible discipline <i>Jürgen Hartler</i>		17:05 – 17:40	Alternative separation- and mass-spectrometry-based approaches to analyze various modalities of biomolecular species in single-cells and limited samples <i>Alexander Ivanov</i>	
	11:55 – 12:30	Single cell metallomics <i>Gunda Köllensperger</i>		17:40 – 17:55	Strategies to analyse single-cardiomyocyte proteomics data. <i>Consuelo Marín-Vicente</i>	
	12:30 – 12:45	Integrating spatial transcriptomics and deep visual proteomics for precision oncology <i>Fabian Coscia</i>		From 18:00	Symposium dinner	
	12:45 – 13:00	Spatial proteomics of the human atherosclerotic microenvironment <i>Luke Gamon</i>				
Day 2	9:00 – 9:35	Deep spatial proteomics toward subcellular resolution with nanoPOTS and laser ablation <i>Ying Zhu</i>		13:40 – 14:15	Co-profiling of proteomes and transcriptomes across single human pancreatic islet cells <i>James Fulcher</i>	
	9:35 – 10:10	Label-free proteome profiling of single cells with high throughput <i>Ryan Kelly</i>		14:15 – 14:50	From bulk to single cell proteomics to characterize the effects of CeLMOD drugs on Multiple Myeloma <i>Charline Keller</i>	
	10:10 – 10:45	Microfluidics assisted sample preparation for scpMS <i>Susan Ibi Preus</i>		14:50 – 15:05	Single Cell Analysis of Proteoforms Using single-cell proteoform imaging mass spectrometry (scPiMS) <i>Pei Su</i>	
	10:45 – 11:15	Coffee		15:05 – 15:30	Coffee	
	11:15 – 11:50	A Single-Cell Proteomics by Mass Spectrometry based map of the human CD34+ hematopoietic stem and progenitor cell compartment <i>Erwin Schoof</i>		15:30 – 16:05	SCP analysis of human brain neutrophils elucidates functional states <i>Alejandro Brenes</i>	
	11:50 – 12:25	Challenging sample preparation and mass analyzers: A comprehensive exploration of cellular heterogeneity in cultured cells with unprecedented quantitative accuracy. <i>Manuel Matzinger</i>		16:05 – 16:40	Discovery of Survodotide – a novel Glucagon/GLP-1 Receptor Dual Agonist <i>Wolfgang Rist</i>	
	12:25 – 12:40	Mass spectrometry-based proteomics of clinically relevant murine cancer models derived single cell samples <i>Joachim Smollich</i>		16:40 – 17:00	Award ceremony & closing remarks <i>Karl Mechtler & Evelyn Rampler</i>	
	12:40 – 13:40	Lunch				