

Program SCP - APMRS Vienna 2022

Day1, Tue 13.09.22				
time	ID	name	affiliation	title
09:00 - 09:15	intro	Klaus Kratochwill	President of APMA, Head of Core Facility Proteomics at Medical University of Vienna	Welcome words
09:15 - 09:55	D1_invite d1	Roman A. Zubarev	Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Stockholm, Sweden	From plasma desorption to blood plasma analysis - a historical mass spectrometry journey
09:55 - 10:10	D1_short talk1	Anna-Sophia Egger	Universität Innsbruck, Institut für Biochemie	Multi-omics investigation of amino acid dynamics in autophagy
10:10 - 10:25	D1_short talk2	Lucas Keuter	Institute of Food Chemistry, WWU Münster	Combination of proteomic methods enables in-depth analysis of metabolic effects and cellular toxicity of natural products in different cell lines
10:25 - 10:40	D1_short talk3	Isabella Burger	TU Wien Institute of Chemical Technologies and Analytics	Proteomics, metabolomics and molecular networking as interplaying tools for identification and characterization of fungal RiPPs
10:40 - 11:20	coffee break			
11:20 - 11:35	D2_short talk4	Manuel Matzinger	IMP, Vienna, Austria	Establishment of reproducible, sensitive and automated one-pot workflows for high throughput single cell proteomics.
11:35 - 11:50	D2_short talk5	Rupert Mayer	IMP, Vienna, Austria	Wide Window Acquisition, AI-based data analysis and micropillar array chromatography enable deep proteome coverage and high throughput for a wide sample range, including single cell proteomic inputs.
11:50 - 12:05	D1_short talk4	Micha Birklbauer	University of Applied Sciences Upper Austria, Bioinformatics Research Group, Hagenberg, Austria	Identifying Crosslinks in MS2-MS3-based Workflows with MS Annika
12:05 - 12:45	D1_invite d3	Robert Ahrends	Institute of Analytical Chemistry, University of Vienna, Austria	Probing the Membrane Landscape and Identifying Key Lipids Critical for Platelet Activation by Lipidomics
12:45 - 13:00	D1_short talk5	Yasmin Borutzki	Inorganic Chemistry, University of Vienna	Programmed cell death: Investigations of molecular signatures of apoptosis and ferroptosis in ovarian cancer cells
13:00 - 14:00	lunch break			
14:00 - 14:40	D1_invite d4	Roman A. Zubarev	Department of Medical Biochemistry and Biophysics, Karolinska Institutet, Stockholm, Sweden	Chemical Proteomics – Lessons for SCP
14:40 - 15:20	D1_invite d5	Ruth Birner Grünberger	Institute of Chemical Technologies and Analytics, TU Vienna, Austria	Lipid hydrolysis in cancer
15:20 - 15:25	D1_short talk6	Juan Manuel Sacnun	Medical University of Vienna	Secretomics Analysis of the Cross-Talk between Endothelial and Mesothelial Cells in a Co-Culture System
15:25 - 16:00	coffee break			
16:00 - 16:15	D1_short talk7	Maximilian Schinagl	TU Wien, Meduni Graz	A closer look at proteomic changes in liver fibrosis
16:15 - 17:15	D1_invite d6	Josef Penninger	Institute, University of British Columbia, Vancouver, Canada	ACE2

Day2, Wed 14.09.22				
time	ID	name	affiliation	title
09:00 - 09:40	D2_invite_d1	Bogdan Budnik	Wyss Institute at Harvard University, Boston, MA, US	Single-cell Multi-omics and PTM-omics are the next two challenges that need to be resolved in our march towards a comprehensive digital Pathomics
09:40 - 10:20	D2_invite_d2	Anjali Seth	Head of Single Cell Proteomics at Cellenion, Lyon, France	cellenONE and single cell proteomics sample preparation, a happy match
10:20 - 10:35	D2_short_talk_1	Andrea Gerdemann	Institute of Food Chemistry, University of Muenster	Determination of metabolic alterations caused by polyphenols in hepatocellular carcinoma cells using HILIC-MS/MS
10:35 - 11:05	coffee break			
11:05 - 11:45	D2_invite_d3	Erwin Schoof	Technical University of Denmark	Leveraging latest-generation data acquisition and MS instrument architecture for improving single cell proteomics experiments
11:45 - 12:00	D2_short_talk2	Adela-Eugenie Vrsanova	German Cancer Research Center (DKFZ), Heidelberg, Germany	Label-free single-cell proteome analysis through captured droplet sample preparation
12:00 - 12:15	D2_short_talk3	Lisa Panzenboeck	Department of Analytical Chemistry, Faculty of Chemistry, University of Vienna, Vienna, AUSTRIA	Metabolomics and Lipidomics Analysis of Human Meningioma Tissue and Cerebrospinal Fluid Within a Single Analytical Run
12:15 - 12:55	D2_invite_d4	Benjamin Furtwängler	Faculty of Health Sciences, University of Copenhagen, Copenhagen, Denmark	Real-time search assisted single-cell proteomics applied on human hematopoiesis
12:55 - 13:55	lunch break			
13:55 - 14:35	D2_invite_d5	Alexander Ivanov	Barnett Institute for Chemical & Biological Analysis, Northeastern University, Boston, MA, US	Probing bottom-up, top-down, and native proteomic profiling and glycomic characterization of ng- and sub-ng-level samples, including small cell populations and single cells.
14:35 - 15:15	D1_invite_d2	Fan Liu	FMP Leibniz, Berlin, Germany	Developing proteome-wide cross-linking mass spectrometry and its application in biology
15:15 - 15:35	coffee break			
15:35 - 16:15	D2_invite_d6	Chris Rose	Genentech	Intelligent data acquisition strategies for single cell proteomics
16:15 - 16:55	D2_invite_d7	Ying Zhu	Pacific Northwest National Laboratory, Richland, WA	Advancing sample preparation and MS data acquisition for single-cell and spatial multiomics
16:55 - 17:10	D2_short_talk6	Karl Kristian Krull	German Cancer Research Center (DKFZ), Heidelberg, Germany	Increasing proteomic depth of low-input samples by feature matching in diaPASEF data
from 17:10	Conference Dinner			

Day 3, Thu 15.09.22				
time	ID	name	affiliation	title
09:00 - 09:40	D3_invite d1	Alexander Makarov	ThermoFisher Scientific, Bremen, Germany	Orbitrap mass spectrometry for single-cell proteomics
09:40 - 10:20	D3_invite d2	Gurmil Gendeh	HP Inc, Corvallis, OR	Enabling single cell proteomics sample preparation using Inkjet-based digital dispensing
10:20 - 10:35	D3_short_talk1	Bernhard Seidl	Institute for Bioanalytics and Agro-Metabolomics, Department of Agrobiotechnology (IFA-Tulln), University of Natural Resources and Life Sciences (BOKU), Vienna	CPExtract, a novel software tool for the comprehensive detection of tracer-derived metabolites in high resolution mass spectrometry data
10:35 - 11:05	coffee break			
11:05 - 11:45	D3_invite d3	Ákos Végvári	Karolinska Institutet, Stockholm, Sweden	Experimental design for improved proteome profiling in single cell proteomics
11:45 - 12:25	D3_invite d4	Harmjan Vos	UMC Utrecht, Netherlands	Single cell proteomics identifies distinct cell types in 3D culture
12:25 - 12:40	D3_short_talk2	Tobias Rainer	University of Innsbruck	Immobilized enzyme reactors: a promising tool for online sample processing in single cell proteomics
12:40 - 12:55	D3_short_talk3	Marlene Pühringer	Department of Analytical Chemistry, Faculty of Chemistry, University of Vienna	Exploring the lipidome of microalgae by novel mass-spectrometry-based lipidomics workflows
12:55 - 13:55	lunch break			
13:55 - 14:35	D3_invite d5	Fabian Coscia	MDC Berlin	Spatially resolved tissue proteomics with single-cell sensitivity
14:35 - 14:50	D3_short_talk4	Gerhard Hagn	Department of Analytical Chemistry, University of Vienna	Long COVID Syndrome, multi-omics plasma analyses, anti-inflammatory signature
14:50 - 15:20	coffee break			
15:20 - 16:00	D3_invite d6	Ryan T. Kelly	Brigham Young University, Provo, UT, US	Comparison of data acquisition strategies for label-free single-cell proteomics
16:00 - 16:15	D3_short_talk6	Katharina Hohenwallner	Department of Analytical Chemistry, Faculty of Chemistry, University of Vienna, Vienna, Austria	Comprehensive LC-MSn based ganglioside profiling in native and differentiated human mesenchymal stem cells
16:15 - 16:30	closing	Karl Mechtler	IMP, Vienna	closing remarks