

Symposium: „Bridging Genotypes with Phenotypes via Proteoforms”

21.2. Monday	Speaker	Title of the talk
CET		
8:30	Petra Arck, Vice-Dean	
8:35	Hartmut Schlüter	Proteoforms – What are they and why are they important?
8:50	Neil Kelleher	Building a Community of Top-Down Proteomics to Advance Proteoform Measurement & Biology
9:10	Alois Jungbauer	Impact of proteoforms for manufacturing of biopharmaceuticals
9:25	Elena Dominguez-Vega	Expanding functional characterization to proteoforms
9:40	Ole Jensen	Studying proteoform diversity in cells, tissues and tumors by mass spectrometry
9:55	Julia Chamot-Rooke	Unlocking the potential of proteoforms in the field of infectious disease
10:10	Charlotte Uetrecht	Flying viruses – understanding corona- and norovirus lifecycles
10:20	<i>Coffee Break</i>	
11:00	Maria Martin	Capturing proteoform and function in the UniProt Protein Knowledgebase
11:15	Oliver Kohlbacher	The FLASH* Suite for the Analysis of Top-Down Proteomics Data
11:30	Juan A. Vizcaino	Bioinformatics challenges related to proteoform-centric data in the Human Proteoform Atlas project: what do we need to move forward?
11:45	Peter Horvatovich	Protein sequence variability in humans
12:00	Maša Babovic	Multimodal Top-Down Mass Spectrometry of therapeutic proteins
12:15	Irene Fernandez-Cuesta	Micro and nanofluidic devices for single molecule analysis.
12:30	<i>Lunch break</i>	
14:00	Jihyung Kim	FLASHDeconvQ: A fast and accurate open-source quantification algorithm for top-down proteomics
14:15	Christoph Gstöttner	Unravelling the structural and functional heterogeneity of recombinant SARS-CoV-2 RBD domains
14:30	Manasi Gaikwad	Quantification of proteoforms in commercial protein sample using intact protein mass spectrometry
14:45	Marcel Kwiatkowski	CoMetChem – A strategy to reveal site-specific histone reaction rates of acetylation and deacetylation
15:00	Aymelt Itzen	A biochemical approach to the understanding of post-translational modifications during bacterial infections
15:15	Andreas Tholey	Improved identification of proteoforms in top-down proteomics using FAIMS with internal CV stepping
15:30	<i>Coffee Break</i>	
16:00	Lloyd Smith	New Frontiers in Proteomics – Proteoforms, Proteoform Families, and the Human Proteoform Project
16:30	Yuri Tsybin	Mass spectrometry data types in top-down analysis of proteoforms
16:45	Bernd Thiede	High resolution quantitative proteomics using SILAC-2-DE-LC/MS
17:00	Hartmut Schlüter	Tissue sampling for proteoform analysis
17:15	Sandra Blois	Impact of galectin-glycan networks in reproductive diseases
17:30	Veit Schwämmle	PTM crosstalk and histone proteoforms
17:45	Discussion	
22.2. Tuesday		
CET		
8:45	Neil Kelleher	The Human Proteoform Atlas
9:00	David Tabb	Combining search engines is key to maximizing proteoform identification.
9:15	Sandra Orchard	Proteoforms in UniProt – the need for stable identifiers and data standards.
9:30	Anastasia Walter	How to write a COST proposal
10:00	<i>Coffee Break</i>	
10:30	COST-planning & Proteoform Atlas	
11:00	Sophia Hober	The Human Protein Atlas
11:15	Hartmut Schlüter	Farewell speech