Ultra-high sensitivity mass spectrometry workflows for basic biology and biomedicine

Matthias Mann [1,2]

[1] Max Planck Institute of Biochemistry, Martinsried, Germany

[2] Novo Nordisk Foundation Center for Protein Research, Faculty of Health and Medical Sciences, University of Copenhagen, Denmark

email: mmann@biochem.mpg.de

ABSTRACT

In the last decades, Mass spectrometry (MS)-based proteomics field has made tremendous technological improvements and is now used across many areas of biology, biomedicine and biotechnology [1]. This coupled to advances in machine learning and artificial intelligence (AI) applied to 'omics' field allow the analysis of multi-cellular phenotypes on a single-cell level, so far almost always by genomic and transcriptomic methods. In this lecture, I will describe the MS-proteomics and computational workflows that we have developed to characterize tissue heterogeneity in close relation to the actual phenotype - the proteome. I will first introduce our new software suite called AlphaPept, an open-source ultra-fast data analysis tool box for MS-based proteomics. Our MS workflow includes trapped ion mobility (tims) – Parallel accumulation serial fragmentation (PASEF) technology (tims-PASEF), which when coupled with low flow chromatography and a brighter ion source, enables analysis of single cells and accurately describe their heterogeneity [2]. We leveraged this technology for Deep Visual Proteomics (DVP), where we combine high resolution multiplexed microscopy, automated image classification by AI and ultrasensitive MS analysis to dissect heterogenous cellular as well as sub-cellular structures under normal and pathological-states [3]. These integrated workflows involving different disciplines have the potential to advance cell biology and biomedicine.

REFERENCES

If necessary, provide **up to 3** references in the format below: **font style Arial, font size "8".**

[1] Aebersold R and **Mann M**. 2016, *Nature*. 15th September 2016
[2] Brunner AD, Thielert M,..., Theis FJ, **Mann M.** 2022, *Mol Sys Biol.* 18th March 2022
[3] Mund A*, Coscia F,Kriston A, Hollandi R,…, **Horvath P., Mann M.** 2022, *Nature Biotech*. 19th May 2022