



Clinical Proteomics in interesting times

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Recent advances in ultra-sensitive sample preparation in concert with laser capture microscopy now allow accessing individual cells for proteome analysis. Together with high-throughput approaches and robust novel MS instrumentation, we can now attempt to develop approaches to systematically map the 3D proteome in biological superstructures such as organs and tumours. In my presentation I showcase the combination of these advances in order to systematically map proteins across a tumour section. In coordination with unbiased data analysis tools we can now extract spatial protein abundance profiles without the requirement for tissue feature annotation and can systematically analyse pathways involved in the pathology of the particular cancer in the spatial context of the tissue (“Pheno-Proteomics”). The future integration with MALDI imaging techniques for spatial lipid and small molecule detection will facilitate a more comprehensive understanding of the 3-dimensional space of a biological structure at molecular level.