MEDICAL UNIVERSITY OF VIENNA

CoreFacilities Guest Lecture

Resolving and understanding cellular heterogeneity by single-cell proteomics

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Lead:
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Wednesday, May 20th
11:00 CET
Anna Spiegel Seminar Room (3rd Floor)
Host:
Boryana Petrova Dr

Abstract:

Advances in proteomic technologies have now achieved the sensitivity to enable proteome analysis at the single-cell level, opening exciting opportunities to study cellular processes at a resolution that remains inaccessible in bulk measurements. In this presentation, I will describe how we have established a mass spectrometry–based pipeline that enables deep proteome profiling quantifying thousands of proteins across thousands of individual cells, and how we leverage this to investigate cellular heterogeneity in cell lines, organoids, and primary tissue.

Specifically, I will present: (i) a time resolved analysis of how cells in a pancreatic cancer cell line model adapt to KRAS inhibitor treatment, providing insights into the mechanisms underlying the acquisition of drug resistance; (ii) a characterization of the proteomic consequences of polyploidy in an organoid model of early onset pancreatic cancer; and (iii) the application of single cell proteomics to annotate immune cell identities in the mouse spleen and to resolve their transitional activation states.

Collectively, these examples highlight the power of single cell proteomics to resolve distinct cell states within heterogeneous populations and to advance our understanding of cellular regulatory processes.