CCR – Impromptu

Thursday, September 4th 2025, 11:00 AM

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Applications of phosphoproteomics in cancer research

Phosphorylation is a central mechanism of cellular signalling, whereby kinases catalyse the transfer of phosphate groups from ATP to target proteins, modulating their activity. This process enables the transmission of signals through complex protein–protein interaction networks and ultimately governs cellular responses. When these networks are disrupted, e.g., through genetic mutations, epigenetic alterations, or pharmacological inhibition, pathway activity is altered, producing distinct phosphorylation signatures. Mass spectrometry–based phosphoproteomics enables phosphorylation to be measured on a proteome-wide scale, providing complementary information on signalling pathway activity that cannot be obtained from genetic or transcriptomic analyses. When combined with large-scale perturbation experiments, these data can be used to infer the structure of signalling networks and uncover context-specific rewiring. In addition, phosphorylated peptides can serve as predictive biomarkers of therapeutic response, as demonstrated in acute myeloid leukaemia, where phosphoproteomic profiling has shown promise in predicting sensitivity to the FLT3-targeted multi-kinase inhibitor midostaurin.

Venue: CCR Lecture Hall, Borschkegasse 8a
Time: September 4th 2025, 11:00 AM
Host: Thomas Vogl