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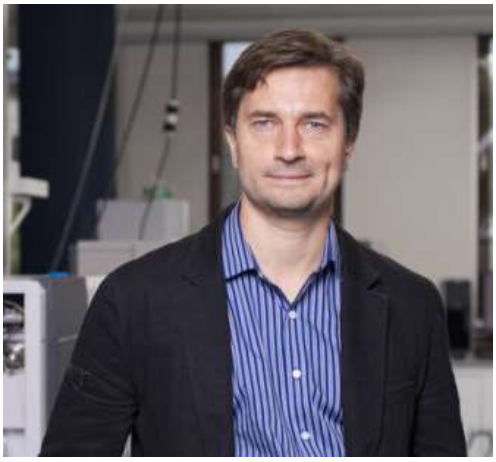

Improved analytical strategies for proteomic profiling of limited samples using ultra-low flow separations coupled to mass spectrometry.

Deep proteomic profiling of limited samples (e.g., rare cells, microneedle biopsies, extracellular vesicles (EVs) isolated from minute volumes of physiological fluids, i.e., liquid biopsies, or even single cells) and especially, characterization of post-translational modifications, e.g., glycosylation, of such specimens have been a major challenge because of very low abundance and high heterogeneity in biological matrices. With the advent of more powerful separation techniques coupled to more sensitive, higher duty cycle mass spectrometers, analysis of such limited samples is getting more feasible. However, each step of the analytical workflow, including sample preparation, separation, interfacing with MS, MS data acquisition, and data analysis, requires additional advancements and flawless integration to enable deep proteomic profiling of such scarce samples. In this presentation, I will overview our recent studies where we investigated alternative approaches to enhance the sensitivity and depth of glycomic and proteomic profiling of several types of limited biological specimens in comparison to conventional techniques.

April 24th, 2019

3:30 pm MC224

Coffee and cookies will be provided!