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PCT-SWATH: pressure cycling technology coupled with SWATH mass spectrometry for fast, deep and reproducible proteomic analysis

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Fast, quantitatively accurate, deep and reproducible proteomic analysis of complex biological samples remains a major hurdle in systems biology and systems medicine. Here, we propose a method to convert the proteome contained in small (biopsy) cell or tissue sample into a digital data set that contains signature fragment ion patterns for all peptides derived from the sample. These datasets can be then perpetually mined in silico. In essence the method converts the physical proteome in a (clinical) sample into a permanent digital representation. The method is built on pressure-cycling technology and SWATH-MS. The entire workflow can be completed within 12 hours. Subsequent targeted data analysis offers unprecedented performance in identifying and quantifying low-abundance signaling protein networks in human tissues in an extendable manner. We have applied this method to a kidney cancer cohort, and uncovered dis-regulated signaling protein networks.

Keywords: cancer biopsy tissue, SWATH-MS, pressure-cycling technology

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