



4D Proteomic Profiling of 200 Individuals: A High Throughput Workflow from Sample Preparation, dia-PASEF and PASER-MS to Profiling

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There is a need in establishing a defined plasma proteomic baseline of a healthy population to establish normal reference ranges for all quantifiable peptides. High throughput MS data acquisition coupled to a fast bioinformatics tool for real-time analysis and QC reporting is essential. We investigate 4D proteomic plasma profiles of 200 individuals by employing the followings: 1) automated sample preparation; 2) timsTOF Pro dia-PASEF (Parallel Accumulation Serial Fragmentation) and PASER platform; 3) dia-PASEF MS acquisition and implementation of automated LCMSMS quality controls; 4) novel library building algorithm to calibrate and normalize CCS (collisional cross-sectional) values; 5) CCS-enabled DIA-NN for neural networks search algorithm (Tims DIANN) for analyzing data. Development of a robust, precise, quantitative and automated 4D proteomic profiling workflow with dia-PASEF MS methodology and novel bioinformatics tools will be discussed.

Biography:

Qin Fu earned her Ph.D. degree in Genetics from the University of Minnesota and received post-doctoral training in Immunology at the University of California, San Francisco. She has research experience in human genetics, autoimmunity, drug resistance, cardiovascular diseases, and biomarker discovery and validation. Her current research interests include automated MS sample preparation, multiplexed targeted MS assays, and biomarker discovery and validation. Dr. Fu is the Director of the High-Throughput Laboratory in the Advanced Clinical Biosystems Research Institute at Cedars Sinai Medical Center.