

DIA Quantitative Proteomics

DIA Quantitative Proteomics utilizes timsTOF HT mass spectrometer and diaPASEF (parallel accumulation-serial fragmentation) acquisition mode to achieve qualitative and quantitative protein analysis. This allowed faster scanning speed and enhanced ion utilization, which drastically improved identification accuracy, coverage, sensitivity, and throughput in protein detection with smaller sample input.



Sample specific protein extraction



Lower input requirements, larger detection scope



Almost 100% ion utilization, increased detection depth and sensitivity

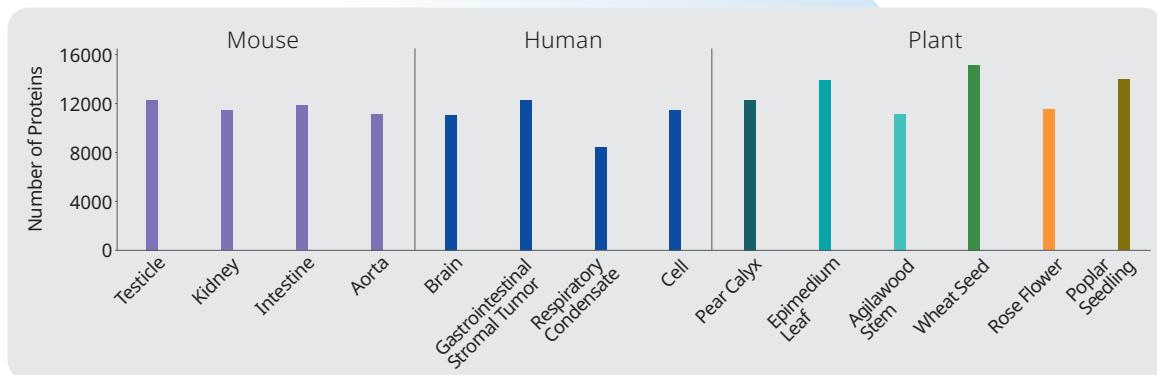


Fewer missing values, enhanced detection stability and accuracy



High throughput, suitable for cohort studies with large sample amounts

Project Experience



Average number of proteins identified

Case Study

Mouse tissue DIA quantitative proteomics results.

