



### **Cross-platform evaluation of accuracy and precision for DIA methods on the timsTOF SCP and timsTOF Pro**

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The timsTOF Pro with diaPASEF acquisition strategy enables to acquire DIA at a high rate with the potential to deliver high proteome coverage at high sensitivity. The timsTOF SCP design of its novel ion source geometry promises up to five times higher ion transfer and ultra-high robustness. However, the added benefit of the ion mobility separation on the quantification accuracy and reproducibility remains to be thoroughly evaluated. Here, using a triple-proteome benchmark sample, we comparatively evaluated the performance of label-free DIA on the Bruker timsTOF Pro, timsTOF SCP, and Thermo Scientific Exploris 480 ( $\pm$  FAIMS). For this evaluation, the data were acquired using data-independent acquisition (DIA) methods and analyzed using Spectronaut (Biognosys). Preliminary results show that the timsTOF systems provide a higher number of peptide identification in DIA mode with high reproducibility. Performance comparisons for phosphoproteomic analysis, using an IMAC-enriched Jurkat digest, showed a larger number of phosphopeptide identification for the TimsTOF pro system. The timsTOF SCP matched the performance levels of the current state-of-the-art LC-MS system using ten times less input amount.