Sample processing

Protein Quantitation

DIA-MS sample runs



plate triplicates









LIBRARY BUILD

Pooled samples

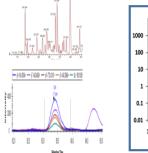
Data Independent Acquisition (DIA or SWATH)

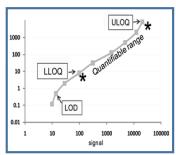


Triple TOF (Sciex)



Protein Quantitation





... for 10,000's of peptides 1,000's of proteins

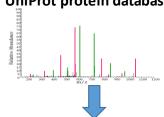
Data Dependent Acquisition (library build)

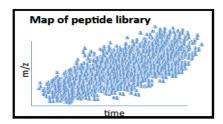


Triple TOF (Sciex)

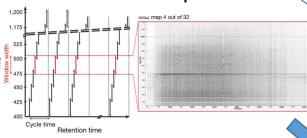


Search spectra against human UniProt protein database





DIA ion Map



OpenSWATH
by ETH zürich

