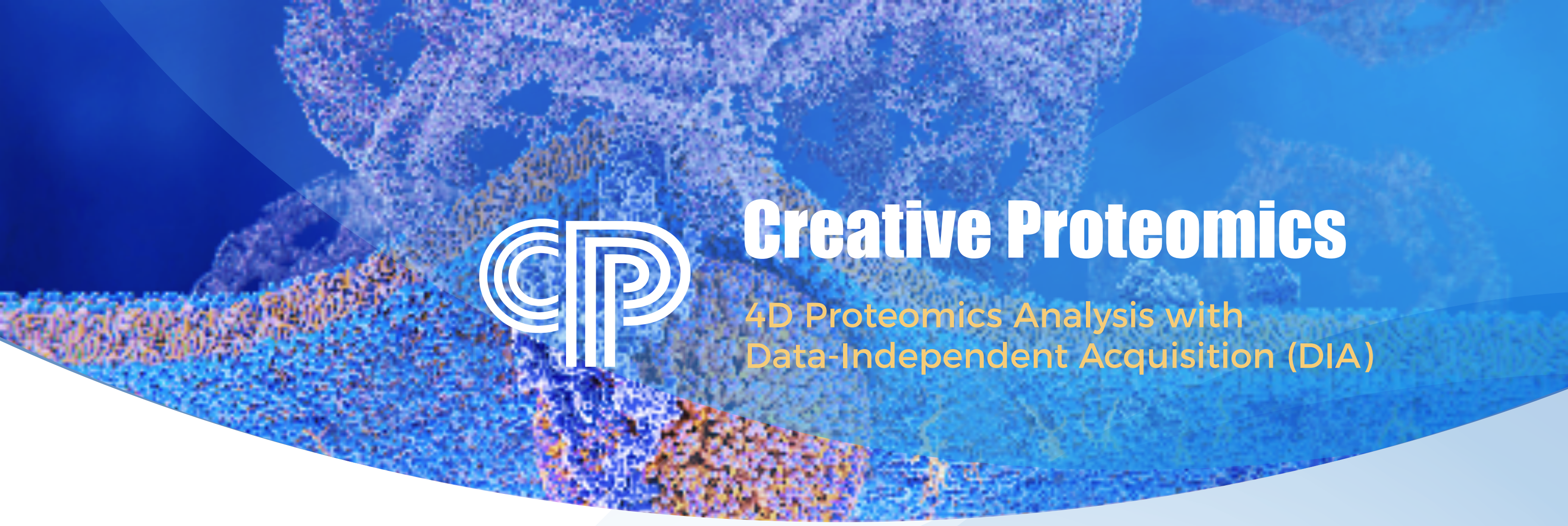


Creative Proteomics

4D Proteomics Analysis with Data-Independent Acquisition (DIA)

- Unlocking deeper insights, maximizing coverage, and accelerating your research.

Data-independent acquisition (DIA) is a holographic mode of mass spectrometry data acquisition based on electrostatic field orbitrap. The entire scan range of the mass spectrum can be divided into several windows based on the mass-to-charge ratio (m/z). Then, all the parent ions in each window are fragmented and detected. Fragmentation ion information of all parent ions is collected for protein identification and quantification. Compared to data-dependent acquisition (DDAzzmode, DIA has the advantages of panoramic scanning, deep data coverage, high reproducibility, and accurate quantification.

Conventional proteomic studies conduct protein identification/quantification based on three dimensions after proteolytic digestion: retention time, the mass-to-charge ratio (m/z), and ion intensity of peptides. With the development of Trapped Ion Mobility Spectrometry (TIMS) and Parallel Accumulation Serial Fragmentation (PASEF) techniques, additional ion mobility dimension has been introduced, making 4D proteomics technology the latest quantitative approach.

4D-DIA proteomics combines the advantages of 4D proteomics and DIA technology, while overcoming some of their inherent limitations. Based on Bruker timsTOF Pro platform, 4D-DIA proteomics improves ion utilization and identification accuracy, allowing for comprehensive improvements in proteome coverage depth, sensitivity, and throughput with less sample input and faster scanning speeds. At Creative Proteomics, we are committed to delivering the highest quality 4D proteomics services with data independent acquisition (DIA), we have the expertise, technology, and experience to meet your research needs.

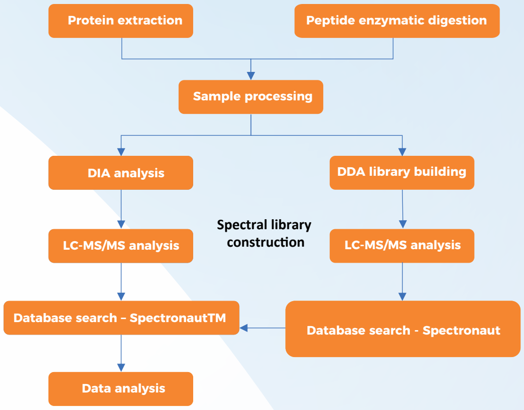
Why Choose 4D Proteomics with Data-Independent Acquisition (DIA)?

- 50% detection rate of low-peak intensity proteins
- Higher integrity and reproducibility of protein data
- Nearly 100% ion utilization, greatly improving detection sensitivity
- Fewer injections, shorter gradients, and deeper coverage
- Stronger support for PTM identification

Scope of Application

- Large-scale samples, such as clinical samples, crop population traits, etc.
- Protein detection in complex systems
- Low-abundance protein determination
- High-throughput PTM analysis

Workflow of 4D-DIA Proteomics



Protein extraction

Peptide enzymatic digestion

Sample processing

DIA analysis

DDA library building

Spectral library construction

LC-MS/MS analysis

LC-MS/MS analysis

Database search - SpectronautTM

Database search - Spectronaut

Data analysis

Instrument Platform at Creative Proteomics

4D-DIA Proteomics services are performed using nano-flow liquid chromatography and cutting-edge mass spectrometers (Bruker tims TOF Pro or Orbitrap Exploris™ 480).

Sample Preparation and Services

- The QC analysis of enzymatic digestion and peptide desalting is strictly controlled
- DDA-Spectral Library generated using HPLC technology and sample fractionation

Quality Standard

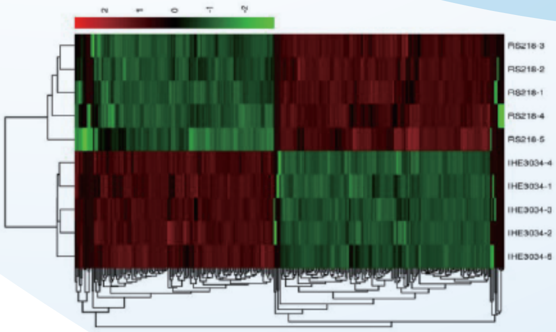
- The summary includes all methods and data analysis
- Reports are provided in Excel and PDF format, with RAW files available upon request

Turnaround Time

- Typical 4-5 weeks from sample QC acceptance to data report delivery

Data Analysis

- GO (Gene) category analysis
- KEGG Pathway analysis
- DEPs (differentially expressed proteins) cluster analysis
- GO enrichment analysis
- KEGG pathway enrichment analysis
- Volcano plot, Venn diagram, etc.



Hierarchical clustering