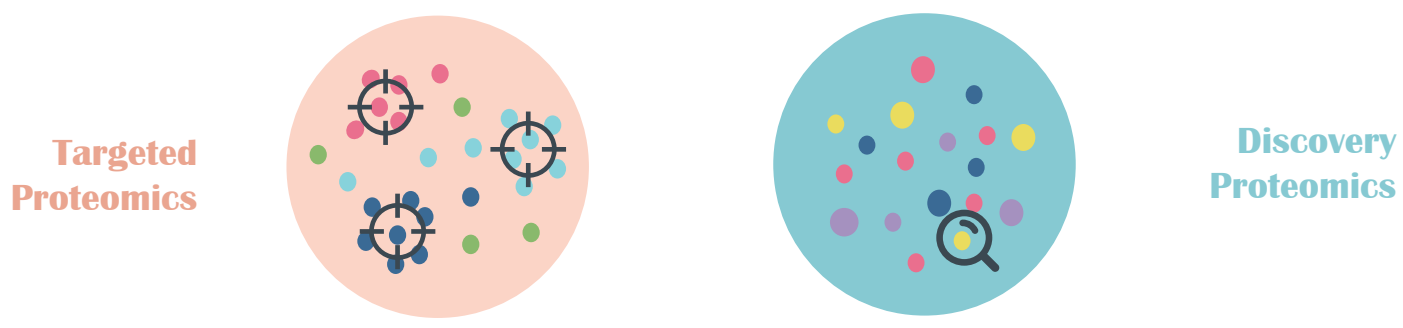
Creative Proteomics

PROTEOMICS

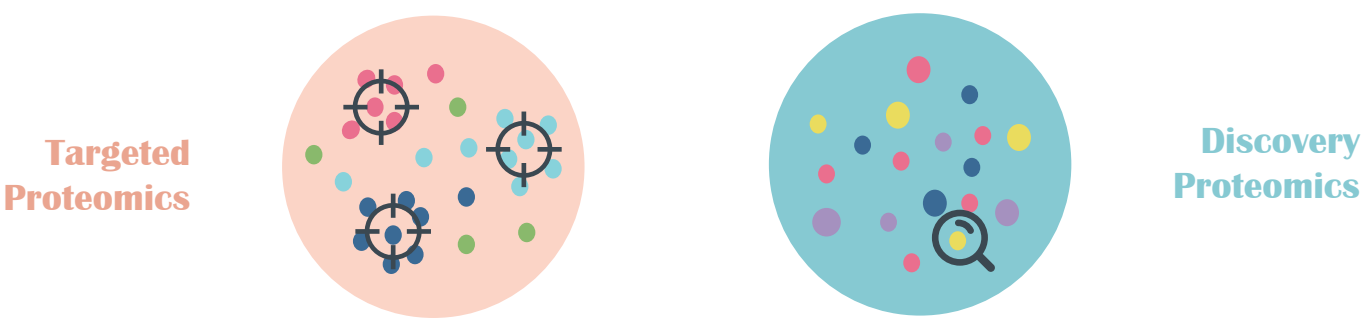
TARGETED VS DISCOVERY

TARGETED AND DISCOVERY PROTEOMICS

At present, strategies for proteomics research can be divided into discovery proteomics and targeted proteomics. Discovery proteomics is more concerned with protein screening and dynamics, while targeted proteomics focuses more on detecting target proteins/peptides to achieve the absolute quantification.



CHARACTERISTICS



SRM / MRM eliminates a large number of interfering ions through two-stage ion selection. The chemical background of the mass spectrum is reduced, and the signal-to-noise ratio of the target detector is significantly improved, thereby achieving high detection sensitivity.

PRM can quantify 50 proteins simultaneously in an hour without the use of antibodies. Comprehensive scanning of product ions can be easily done without selecting ion pairs and optimizing the fragment energy.

Compared with the traditional SRM/MRM technology, the PRM can detect all target ions from the target ion pair fragment detection conversion, reducing workload and with higher resolution.

SWATH-DIA is suitable for high-throughput large-scale protein quantitative analysis. The peak information of the MS1 precursor ion and MS2 fragment ion is very complete, so retrospective analysis after some time is necessary. It can be easily operated without grouping. The number of SWATH-DIA quantitative peptides has greatly increased, enhancing the number of the corresponding quantifiable protein and the sequence coverage of the detected protein.

In MSX-DIA, the mass range is divided into much narrower precursor isolation windows, each of which is usually about 4 m / z wide. All ion and fragment spectra can be collected without losing any information. The data is easy to trace. Even if certain proteins or compounds cannot be found at current levels, they can be traced back in the future.

EXAMPLES OF APPLICATIONS

Targeted proteomics is used for in-depth analysis and quantitative measurement of selected proteins in biological samples. Information on the protein of interest is required before analysis. Our **TPro™ Platform** is designed to quantify up to 150 proteins with high precision and throughput in a dynamic range of 6 orders of magnitude.

Supplementary tool for ligand binding assay (LBA) in the area of monoclonal antibody (mAb) dose pharmacokinetics (PK).

Systems biology and clinical proteomics research.

Predict transporter-mediated drug clearance and promote drug discovery / development research.

The goal of discovery proteomics is to gather information about all proteins and protein structures in biological samples. With little knowledge on the sample, discovery proteomics can identify thousands of proteins and protein structures in one experiment. Our **DPro™ Platform** can analyze up to 9,000 proteins per sample under different conditions and identify significantly regulated proteins.

Host cell protein analysis.

Identification of chemical modifications.

The workhorse of biomarker discovery.

Drug target discovery.

Contact Us

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