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Creative Proteomics

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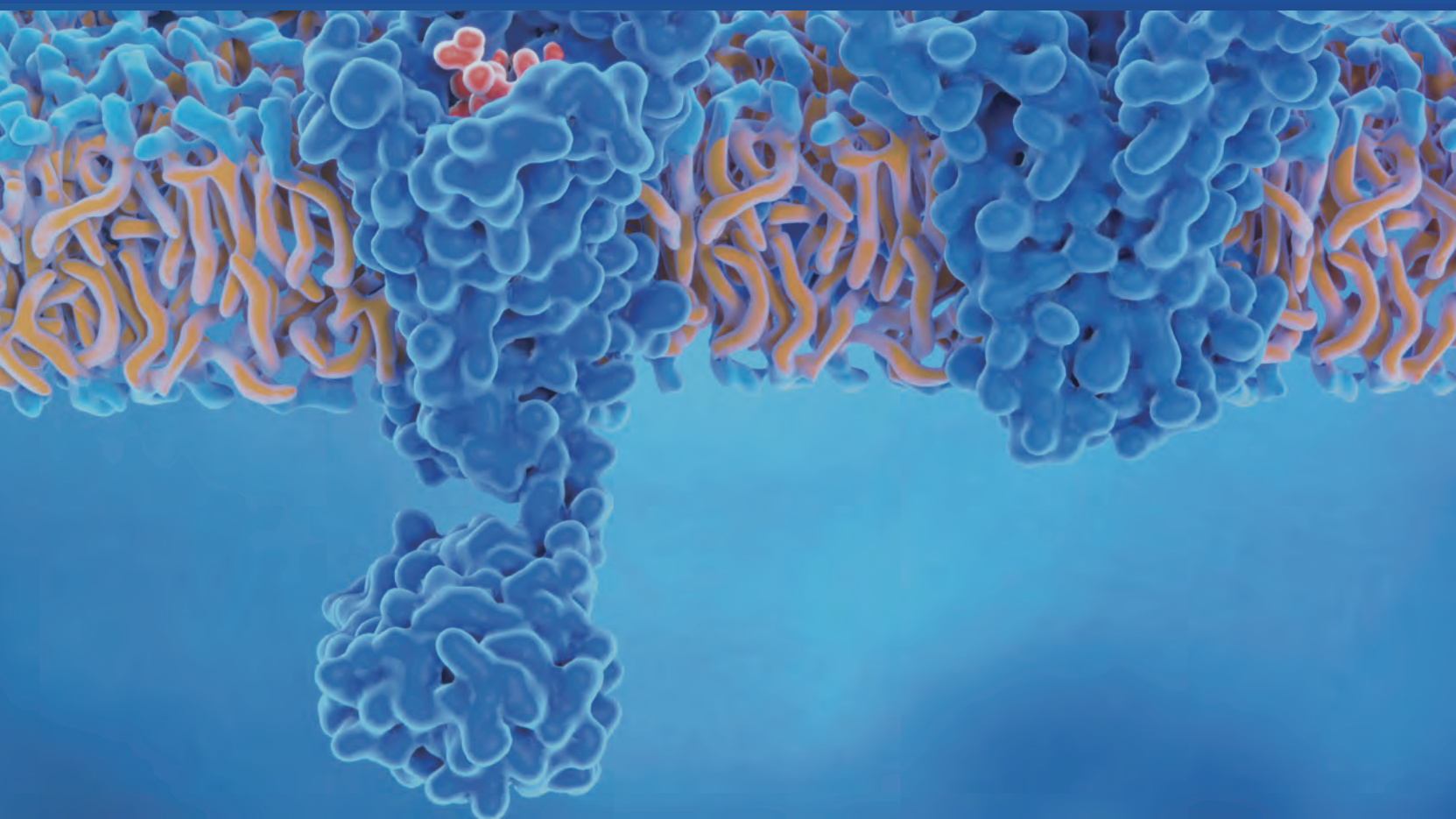
Proteomics Services



Proteomics Services

Creative Proteomics is a leading proteomics service provider, specializing in high-quality protein analysis solutions for researchers, scientists and institutions worldwide. Our company is dedicated to advancing scientific discovery and improving human health throug h the study of proteins and their functions. With years of experience in the field of proteomics, we have developed state-of-the-art technologies and methods to provide comprehensive proteomics se rvices, including protein identifi - cation, quantification, characterization, post-translational mod ification and interaction analysis.

Our Advanced Analytics Platform

Thermo Q Exactive™ series

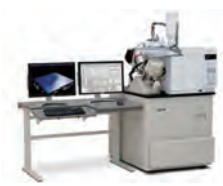
AB Sciex 6500+

Thermo Orbitrap Fusion Lumos

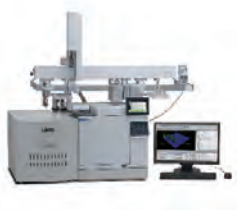
Thermo Orbitrap Exploris 480

Bruker timsTOF Pro

Thermo TRACE 1310-ISQ LT



LECO Pegasus BT 4D GCxGC-TOFMS



LECO PEGASUS BT

Protein Identification Services

Identification of individual proteins is a common problem in the field of biochemistry. Creative Proteomics utilizes LC-MS/MS technology to provide protein identification from gel bands/mixture solutions. LC-MS/MS offers higher sensitivity and almost 100% possibility, as well as an unparalleled ability to accurately identify multiple protein components from a single protein gel band compared to MALDI-TOF. Besides, Creative Proteomics is able to provide protein N- and C-terminal sequencing services by MALDI-ISD or Edman degradation techniques.

Protein Gel Band/Mixed Solution Identification

Technical Features

- High throughput: Identifying dozens to thousands of proteins within each experiment.
- Accurate and reliable: Achieving high mass accuracy (less than 1 ppm) and resolution (over 4×10^4) and providing high-quality data.
- Wide range of applications: No species requirements or restrictions and it is applicable to all species.

Scope of Application: Species with available protein databases or known target protein sequences

De novo protein sequence analysis can be used to figure out what a sample is if it can't be found in a database.

Protein N/C-Termini Identification by MALDI-ISD or Edman Degradation

Technical Features

- Edman degradation enables the sequencing of proteins with an unblocked N-terminus.
- MALDI-ISD enables the sequencing of both N and C-termini (including blocked N-terminus)
- Low sample volume
- High precision and accurate results

Scope of Application: Suitable for all types of N/C-terminal sequence detection

Protein Quantification Services (relative quantification)

	LABEL-FREE QUANTIFICATION ANALYSIS	TMT/ITRAQ QUANTIFICATION ANALYSIS	SILAC QUANTITATIVE ANALYSIS
TECHNICAL FEATURES	• No need to use a stable isotope containing compound to label the protein. • Cost-effective experiment: no need for expensive isotope labeling reagents • Minimal sample manipulation: reducing sample loss and preventing biological characteristic alterations • Efficient: Overcomes shortcomings of labeled quantification in quantifying multiple samples, regardless of sample conditions. • Less sample amount requirement	• Wide range of applications: In vitro labeling technique for protein analysis of most biological samples, including cells, tissues, plasma, serum, CSF, plant samples, etc. • High sensitivity: Low detection limit for low abundance proteins • High throughput: Qualitative and quantitative analysis of multiple samples simultaneously, suitable for differential protein analysis of samples with multiple treatments or from multiple processing times • Reliable results: Simultaneous quantification and characterization, direct quantification according to the signal intensity of reporter groups • High degree of automation: Liquid-phase and mass spectrometry are used in conjunction, supporting good separation performance and fast analytical efficiency • High repeatability: Samples are mixed for analysis, eliminating systematic errors	• In vivo labeling technology, high labeling efficiency • In vivo labeling, closer to the real state of the sample • High efficiency and stability of isotope labeling, not affected by lysate, good reproducibility and high reliability of results • Less sample volume requirement than chemical labeling • Can be used to label a variety of cells in a variety of media
SCOPE OF APPLICATION	• Suitable for quantitative comparison of large number of samples • Suitable for experimental designs that require no label attachment • Require protein reference database	• Suitable for any sample types • Label up to 18 samples simultaneously • Require protein reference database	• Drug action target studies • Disease marker screening • Applicable only to cells in living cultures, not analyzable for tissue samples, body fluid samples, etc. commonly used in biomedical research, and too costly to implement for labeling of animal models. • Require protein reference database

Target Protein MRM Quantitative Analysis

Technical Features

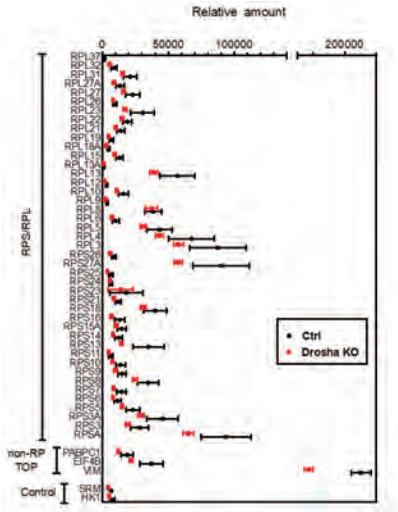
- With high sensitivity, by using triple quadrupole MS, one (or more) of these fragment daughter ions of the target ion can be selected for quantitation purposes. Only compounds that meet both these criteria, i.e., specific parent ions and specific daughter ions corresponding to the mass of the molecule of interest, are isolated within the mass spectrometer. By ignoring all other ions that flow into the mass spectrometer, the experiment gains sensitivity, while maintaining exquisite accuracy.
- Absolute quantitative analysis without antibody dependence
- Highly accurate identification of low-abundance proteins, with quantification across 4 orders of magnitude

Scope of Application

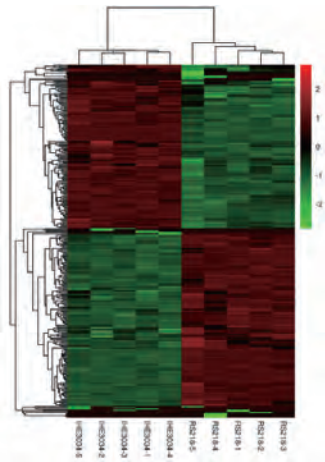
- Suitable for validation of protein expression differences in known protein sequences
- Can detect lower-abundance proteins
- Only one target protein can be detected in one MRM experiment
- Relative or absolute quantification of target proteins/peptides,

Protein Labeled vs. Label-Free Quantification

TECHNOLOGY	PROTEIN LABELED QUANTITATIVE			LABEL-FREE QUANTITATIVE	
	In vivo labeling techniques	*In vitro* labeling techniques			
	SILAC	iTRAQ	TMT	Label-free (DDA)	Label-free (DIA)
SAMPLE TYPE	Culturable cells	All samples	All samples	All samples	All samples
THROUGHPUT	2-3	2-8	2-18	No limit	No limit
PROTEIN IDENTIFICATION NUMBER	+++	+++	+++	++	++++
DYNAMIC RANGE	++	++	++	+++	+++
QUANTIFICATION ACCURACY	+++++	+++	+++	++	+++



iTRAQ-TMT mass spectrometry was performed using Q Exactive mass spectrometer



Hierarchical clustering of the protein samples in label-free proteomics

Protein Modification Analysis

Protein post-translational modifications (PTMs) are chemical modification processes that occur during or after protein translation. Protein post-translational modifications (PTMs) increase the functional diversity of the proteome by adding functional groups such as phosphate, acetate, amide, or methyl groups to proteins and affect almost all aspects of normal cell biology and pathogenesis. Protein post-translational modifications play a key role in many cellular processes, such as cell differentiation, protein degradation, signaling and regulatory processes, regulation of gene expression, and protein interactions.

At Creative Proteomics, we offer comprehensive services for analyzing post-translational modifications (PTMs) in proteins to find and measure the different types of PTMs. Our advanced mass spectrometry-based methods can accurately detect and characterize low-abundance PTMs, providing valuable insights into the biological functions of proteins.

- Disulfide bond proteomics
- Glycosylation proteomics
- Phospho-proteomics
- Ubiquitinated-proteomics
- S-Nitrosylation
- Methyl-proteomics
- Acetyl-proteomics
- SUMOylated-proteomics

PTM Qualitative analysis

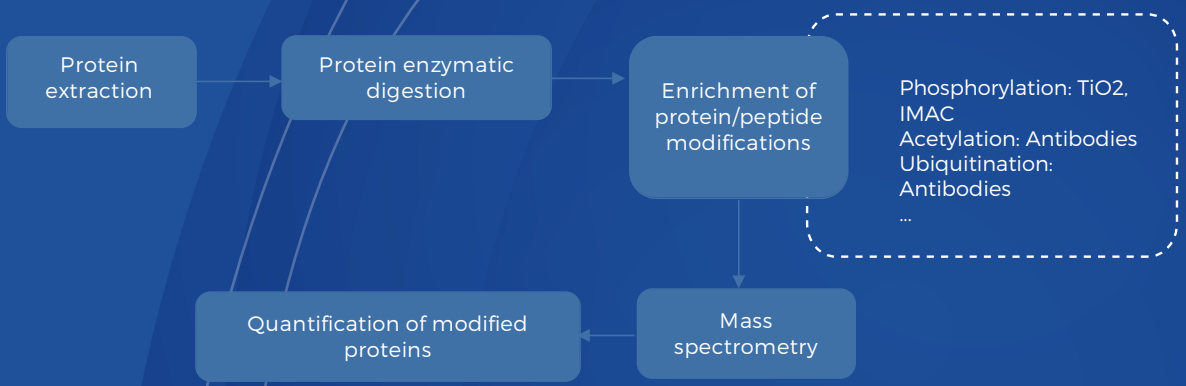
- Modification site analysis
- Large-scale modification site analysis

PTM Quantitative analysis

- Large-scale quantitative modification proteomics analysis
- Phosphorylation, ubiquitination, acetylation, etc.

Technology Features

- Processing standard procedures with high enrichment efficiency and specificity for certain types of modified peptides will improve the efficiency of modified peptide detection
- Accurate identification of modification sites based on high precision, high sensitivity, and high resolution mass spectrometry
- Single-protein modification site identification and large-scale proteomic modification site identification and analysis
- Can be combined with iTRAQ/TMT or label-free methods for quantitative studies



Protein Interaction Analysis

TECHNOLOGIES	CO-IMMUNOPRECIPITATION (CO-IP)	CROSSLINKING PROTEIN INTERACTION ANALYSIS	GST PULL-DOWN ASSAY	LABEL TRANSFER PROTEIN INTERACTION ANALYSIS
IN VIVO / IN VITRO	*In vivo*	*In vivo* and *in vitro*	*In vitro*	*In vitro*
ANALYTICAL RANGE	• Determine whether two target proteins bind *in vivo* • Identify a new interaction partner for a specific protein • Isolation to obtain interacting protein complexes in their natural state	• Analysis of transient protein interactions *in vivo* is performed • Analysis of low affinity *in vitro* protein interactions	• Demonstrate possible interactions between two known proteins • Finding unknown molecules that interact with known proteins	• Discovery of new interactions • Confirmation of putative interactions proposed by other methods • Detection of weak or transient protein interactions
ADVANTAGES	• Interacting proteins are post-translationally modified and in their natural state • It is performed in the natural state and can avoid artificial influence • Interacting protein complexes in their natural state can be isolated.	• High throughput analysis Analysis of easily dissociated and loosely structured protein complexes • High sensitivity, low requirement for protein traits, small absolute sample size required • Analysis is not affected by protein length • Different cross-linking agents can obtain more information on spatial structure and interactions	• Easy to operate, direct detection of interactions	• High sensitivity, multi-protein complex detection
DISADVANTAGES	• Low affinity and instantaneous protein interactions may not be detected • Binding of two proteins may not be direct, but may have a third party acting as a bridge in between • Must predict what the target protein is before the experiment to select the final antibody	• Low abundance of cross-linked peptides and complex cross-linked forms • Difficult to identify by mass spectrometry	• Require spreparation of sufficient amounts of soluble recombinant protein • Only stable or strong interactions can be detected • Protein interactions can be interfered with by endogenous proteins	• Difficult to identify by mass spectrometry

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