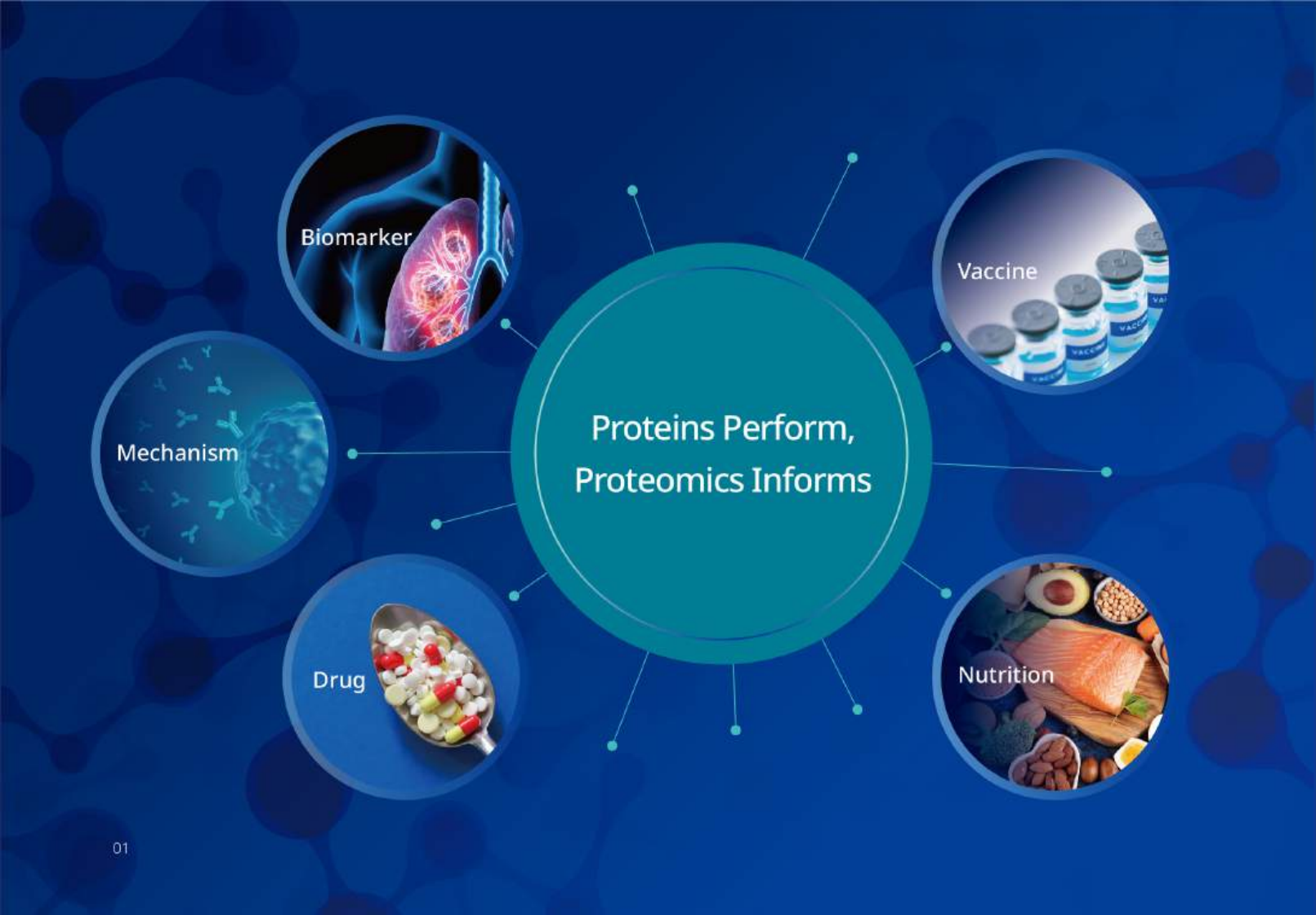
Proteomics Services

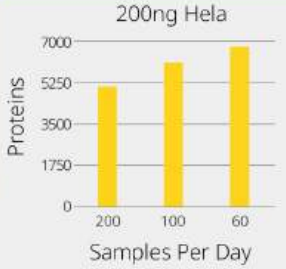
METWARE BIO

Innovative Multi-Omics Insights for Better Health

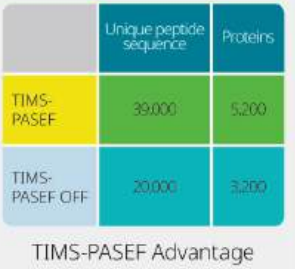

Biomarker
Vaccine
Proteins Perform,
Proteomics Informs
Mechanism
Drug
Nutrition

The Power of Our Proteomics Platform

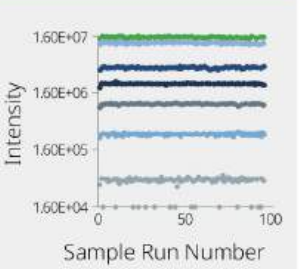
High Throughput



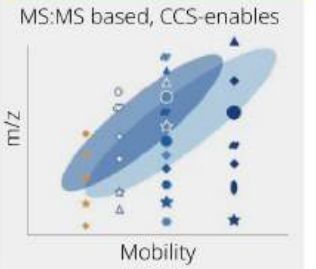
High Sensitivity



High Stability



Accurate Identification



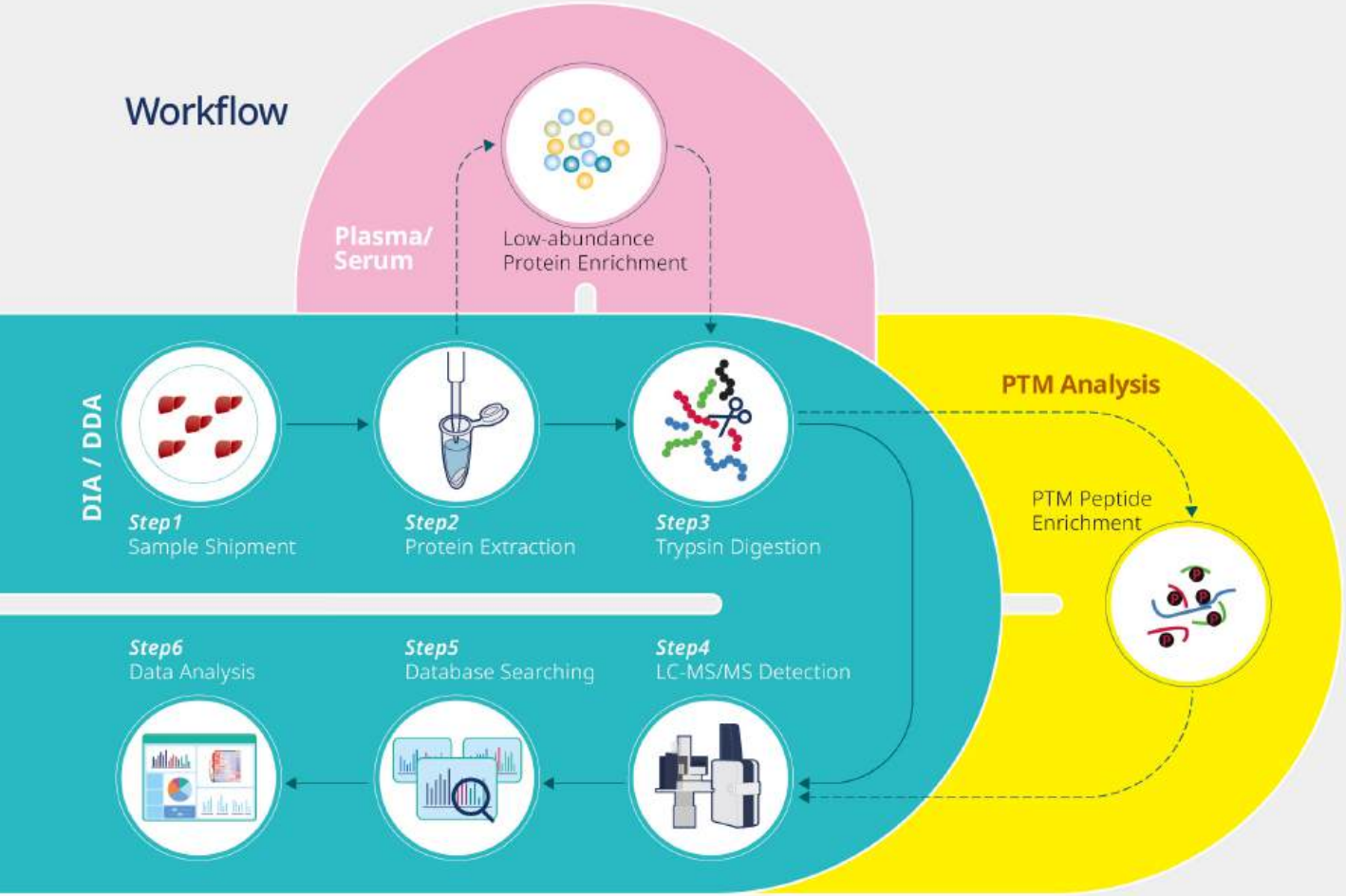
Comprehensive Analytical Portfolio

Global Proteome Profiling	Targeted Proteomics	PTM Analysis	Multi-Omics Joint Analysis
DIA Quantitative Proteomics	PRM Targeted Proteomics	Phosphorylation	Transcriptome + Proteome
Serum/Plasma Quantitative Proteomics	Olink®	Ubiquitination	Proteome + Metabolome
Low-Input Quantitative Proteomics	SomaScan®	Acetylation	Transcriptome + Proteome + Metabolome

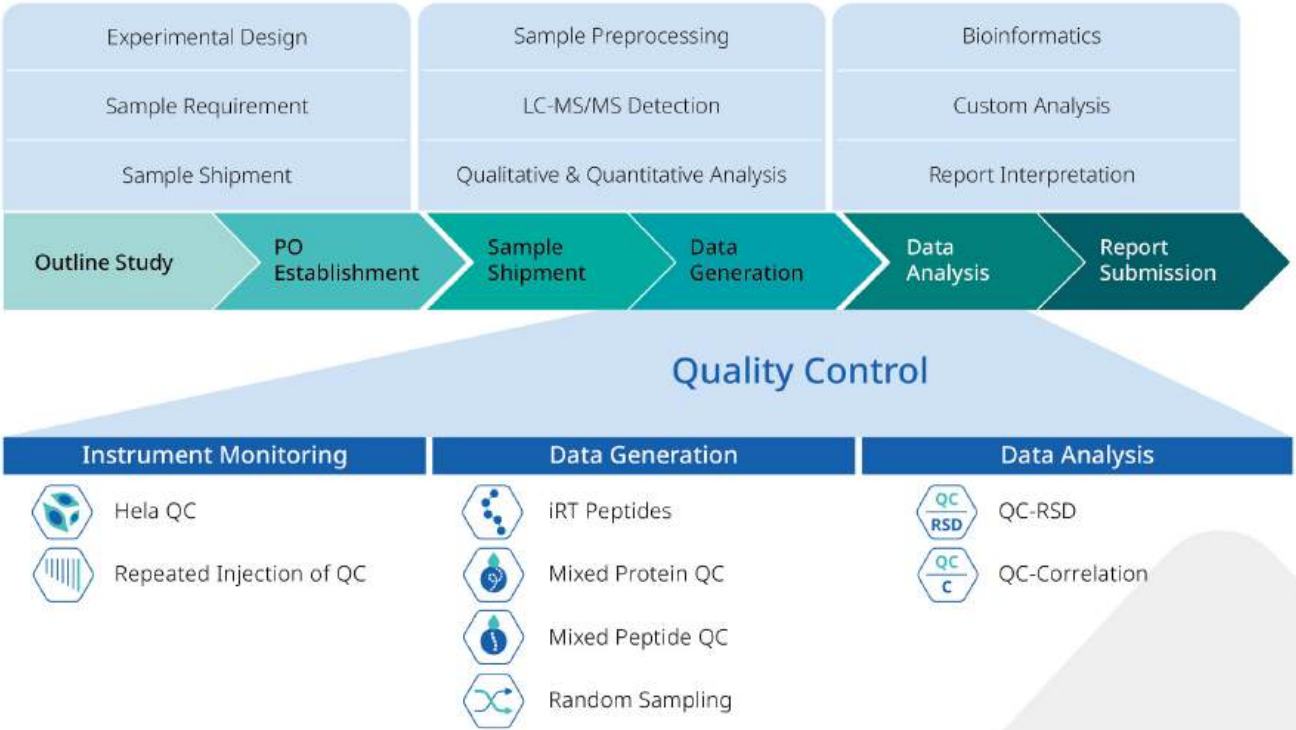
Olink® and SomaScan® services are provided through authorized third-party partners.

Looking for more proteomics, metabolomics, or multi-omics services? Email us at **support-global@metwarebio.com**.

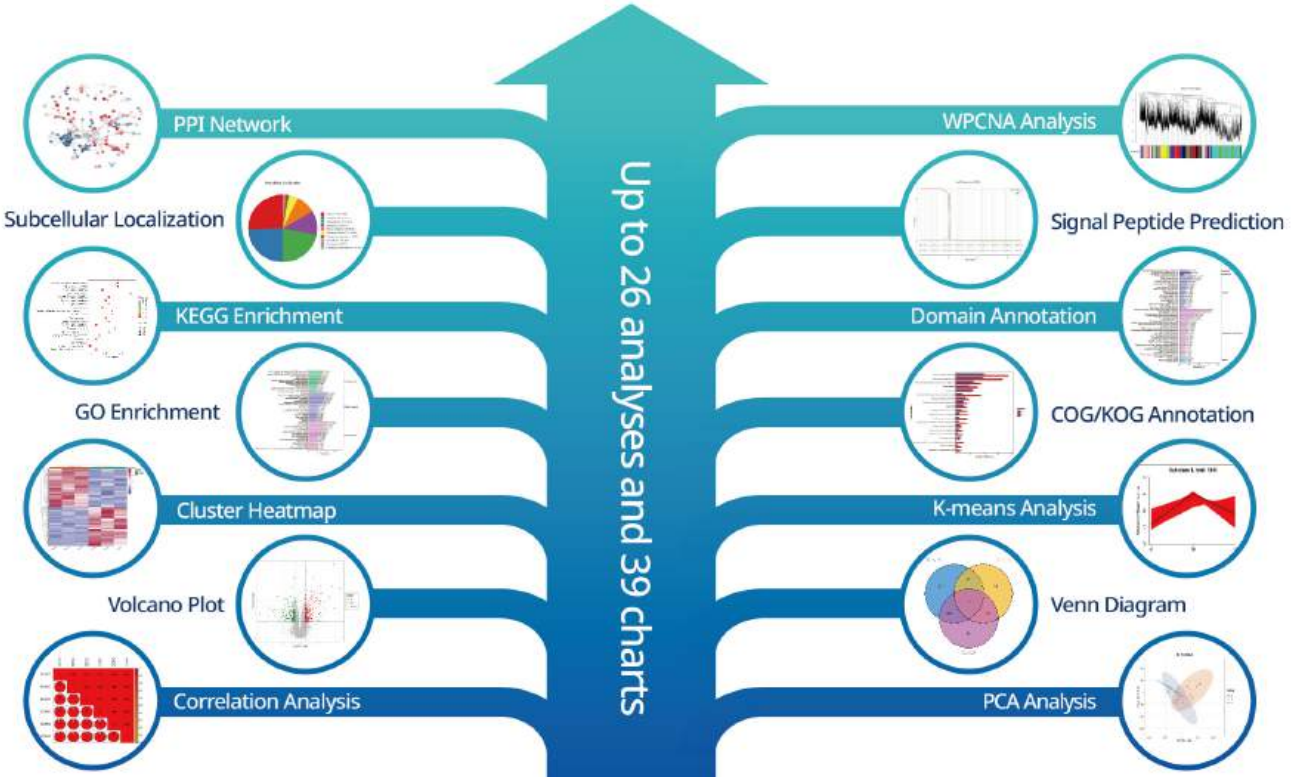
Workflow


Plasma/
Serum
Low-abundance
Protein Enrichment
DIA / DDA
PTM Analysis
PTM Peptide
Enrichment
Step1
Sample Shipment
Step2
Protein Extraction
Step3
Trypsin Digestion
Step4
LC-MS/MS Detection
Step5
Database Searching
Step6
Data Analysis

Rigorous Quality Control



Comprehensive Analytical Report



Insightful Solutions for All Industries

Medical Research
Disease Mechanisms,
Molecular Diagnosis,
Biomarker Development,
Drug Targets

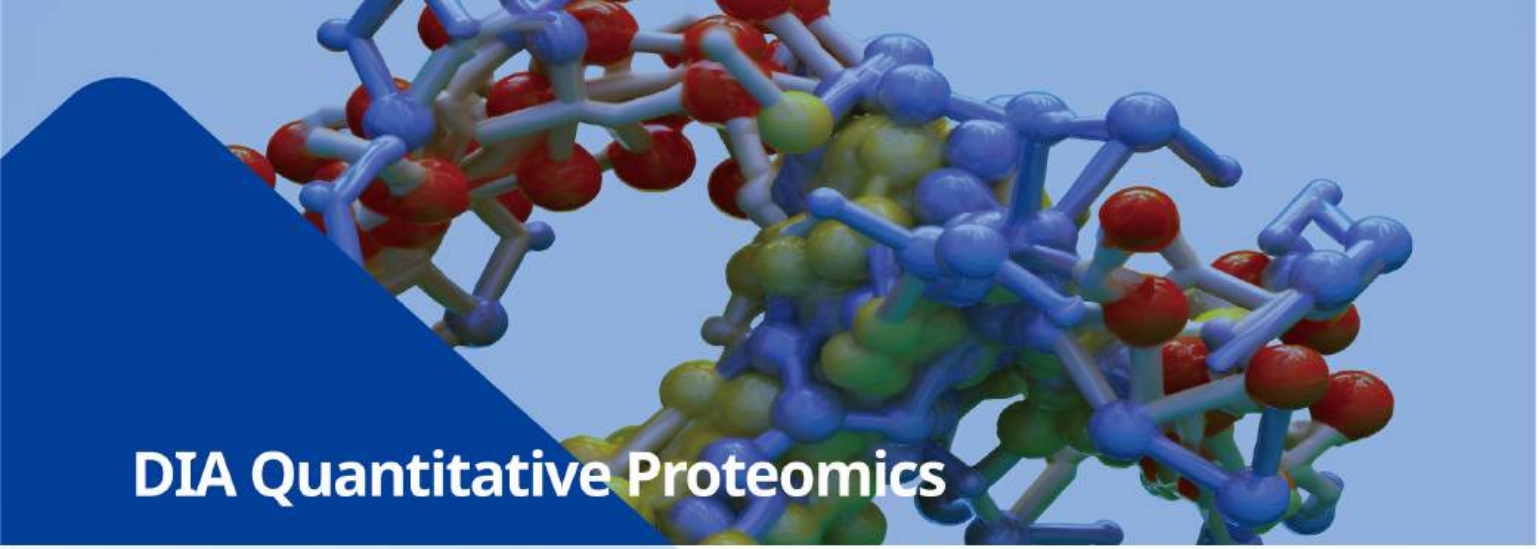
Animal Research
Reproductive Development,
Disease Mechanisms,
Nutrient Metabolism,
Animal Toxicology

Plant Research
Reproductive Development,
Abiotic Stress Response,
Disease Resistance,
Crop Improvement

Microbiology
Pathogenic Mechanisms,
Drug Resistance,
Stress-Related Proteins Screening,
Environmental Impact Mechanisms

Featured Publications

Year	Title	Journal	Species
2025	Multi-omics analysis reveals the pre-protective mechanism of Dendrobium flexicaule polysaccharide against alcohol-induced gastric mucosal injury	Int. J. Biol. Macromol.	rat
2024	Gut microbial co-metabolite 2-methylbutyrylcarnitine exacerbates thrombosis via binding to and activating integrin α2β1	Cell Metabolism	human
2024	First-line sintilimab with pegaspargase, gemcitabine, and oxaliplatin in advanced extranodal natural killer/T cell lymphoma (SPIRIT): a multicentre, single-arm, phase 2 trial	The Lancet Haematology	human
2024	FBXL4 protects against HFpEF through Drp1-Mediated regulation of mitochondrial dynamics and the downstream SERCA2a	Redox Biology	mouse
2024	Multi-omics analyses reveal mechanism for high resistant starch formation in an indica rice SSIIIa mutant	Carbohydrate Polymers	rice
2024	A Phytophthora infestans RXLR effector targets a potato ubiquitin-like domaincontaining protein to inhibit the proteasome activity and hamper plant immunity	New Phytologist	potato
2024	Transcriptomics and proteomics analyses reveal the molecular mechanisms of yeast cells regulated by Phe-Cys against ethanol-oxidation cross-stress	Food Chemistry	yeast
2024	Empagliflozin protects against heart failure with preserved ejection fraction partly by inhibiting the senescence-associated STAT1–STING axis	Cardiovascular Diabetology	mouse
2023	Gp78 deficiency in hepatocytes alleviates hepatic ischemia-reperfusion injury via suppressing ACSL4-mediated ferroptosis	Cell Death & Disease	mouse
2023	Metabolic flexibility during a trophic transition reveals the phenotypic plasticity of greater duckweed (Spirodela polyrhiza 7498)	New Phytologist	duckweed



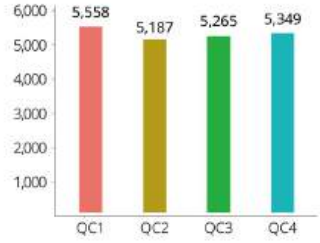
DIA Quantitative Proteomics

MetwareBio's DIA-Based Global Quantitative Proteomics Service leverages advanced 4D label-free LC-MS/MS platform and data-independent acquisition (DIA) scanning to achieve near-complete ion utilization and deep proteome coverage. This approach offers highly sensitive, accurate, and reproducible protein identification and quantification across large-scale studies. It is particularly suitable for high-throughput and clinically oriented research requiring comprehensive and consistent protein profiling across complex samples.

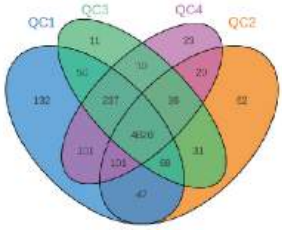
- 11,000 — Deep proteome coverage with 11,000+ proteins detected
- 100% — Ultra-high sensitivity with ~100% ion utilization
- <10% — High data completeness with <10% missing values
- CV <15% — Excellent quantification stability with median CV <15%

Data Stability

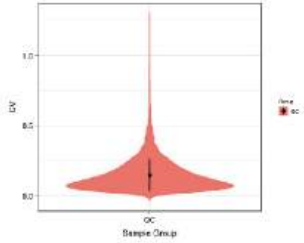
Protein indentifications CV across four low-input tissue QC samples was 3% with >80% overlap; median quantification CV was 11.6%, with 76% of proteins below 20%.



Number of proteins identified

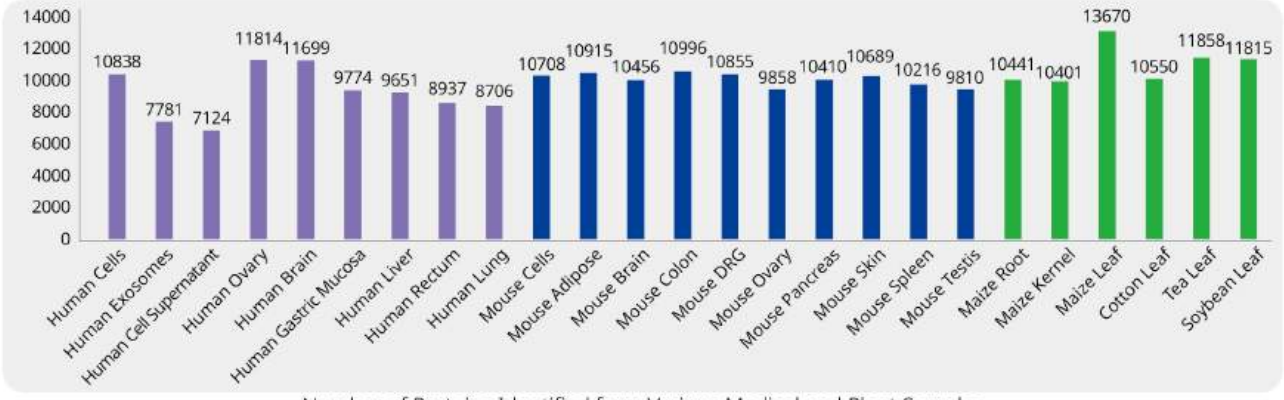


Venn Diagram of common proteins



CV distribution of protein quantitative value

Project Experience



Number of Proteins Identified from Various Medical and Plant Samples

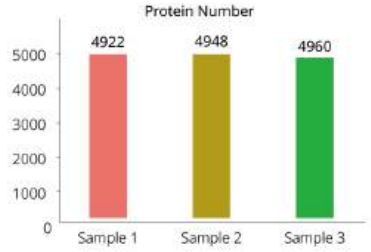
Serum/Plasma Quantitative Proteomics

MetwareBio's Blood Quantitative Proteomics Service utilizes magnetic bead-based enrichment of low-abundance proteins combined with advanced 4D label-free LC-MS/MS analysis to achieve deeper coverage, higher sensitivity, and better reproducibility in plasma and serum protein profiling. This strategy effectively overcomes the limitations of conventional blood proteomics caused by the dominance of high-abundance proteins, enabling more comprehensive detection of disease-relevant proteins and unlocking new opportunities for biomarker discovery, disease mechanism exploration, and clinical translation.

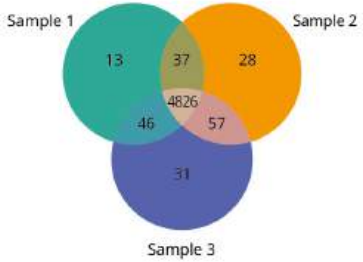
- Efficient Enrichment of Low-Abundance Proteins Using Magnetic Beads
- Advanced 4D Label-Free LC-MS/MS Platform with Superior Sensitivity
- Deep Proteome Coverage for Comprehensive Biomarker Profiling
- High-Throughput Workflow for Robust and Reproducible Data Acquisition

Data Stability

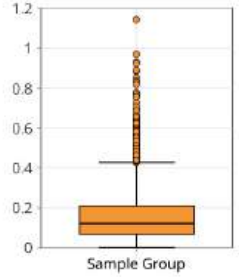
Protein indentifications CV across three technical replicates was 0.39%, with >95% overlap; quantification CV had a median of 16.3%, and 73% of proteins were below 20%.



Number of proteins identified

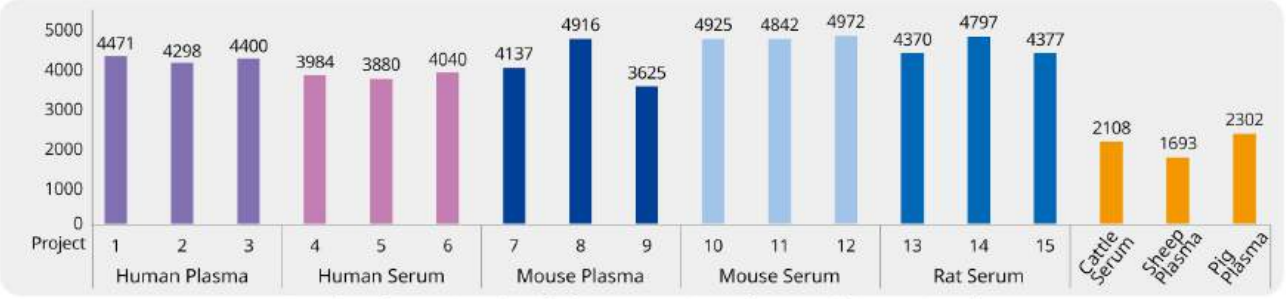


Venn Diagram of common proteins



CV distribution of protein quantitative value

Project Experience



Number of Proteins Identified Across Various Plasma and Serum Samples

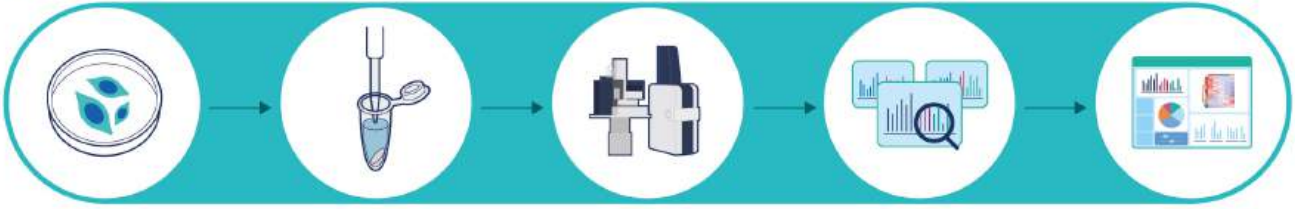
Sample Requirements: A minimum of 50 µL, preferably 100 µL, of serum or plasma is required for blood proteomics analysis.

Low-Input Quantitative Proteomics

MetwareBio's Low-Input Quantitative Proteomics Service combines the powerful SISPROT one-pot sample preparation technology with the diaPASEF acquisition strategy on an advanced 4D LC-MS/MS platform. The SISPROT method significantly reduces sample loss and enhances protein yield, enabling efficient protein extraction, digestion, and quantification from ultra-low-input samples such as biopsy tissues, pollen, oocytes, and subcellular organelles. This optimized workflow delivers broad proteome coverage with high reproducibility, making it especially suitable for discovery-driven studies involving limited or precious sample types.

- SISPROT One-Pot Workflow for Minimal Sample Loss
- Advanced 4D LC-MS/MS Platform with High Sensitivity
- Deep Proteome Coverage from Ultra-Low Inputs
- High Throughput and Reproducibility in Large Sample Sets

Workflow



Step1
Sample Shipment

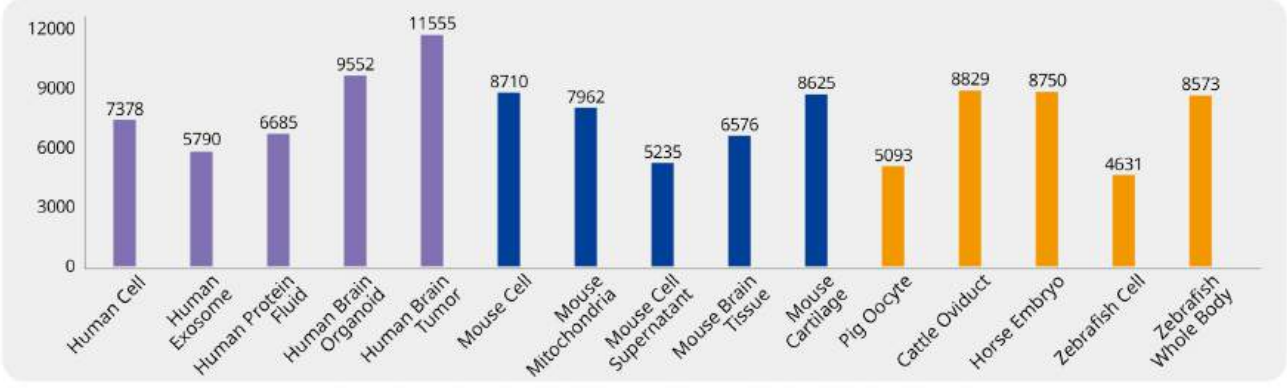
Step2
One-Step Sample Preprocessing

Step3
LC-MS/MS Detection

Step4
Database Searching

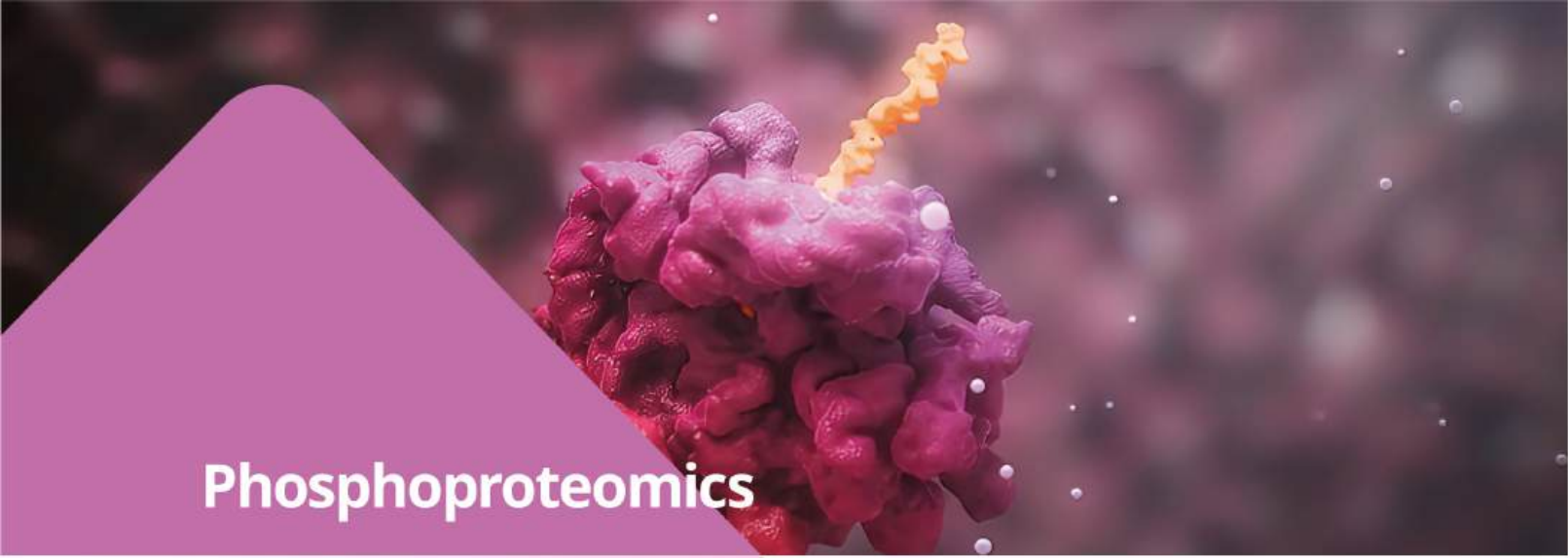
Step5
Data Analysis

Project Experience



Number of Proteins Identified from Various Medical and Animal Samples

Sample Requirements: Low-input analysis requires only 1 μL blood, 1 mg tissue, 10 oocytes, or 10,000 mammalian cells.



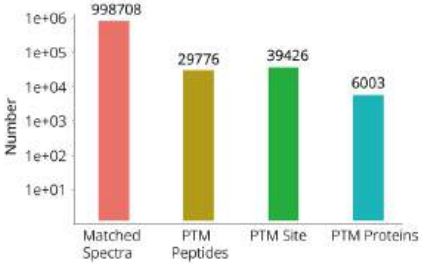
Phosphoproteomics

MetwareBio's Phosphorylation Proteomics Service offers sensitive and comprehensive profiling of phosphorylation events using optimized phosphopeptide enrichment strategies combined with advanced 4D label-free LC-MS/MS analysis. This platform enables accurate site localization, high-confidence identification, precise quantification, and robust reproducibility. The service supports research in signal transduction, cell cycle regulation, oncology, and disease mechanism exploration.

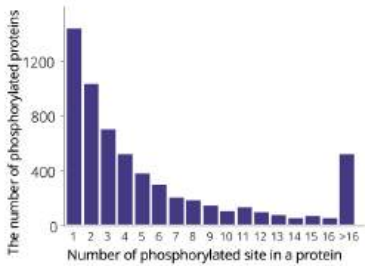
- High-Efficiency Phosphopeptide Enrichment Using Ti-IMAC Materials
- Advanced 4D Label-Free LC-MS/MS for High Sensitivity and Coverage
- Comprehensive Site-Level Data Interpretation and Functional Insights
- Flexible Data Analysis Solutions Customized to Research Needs

Case Study

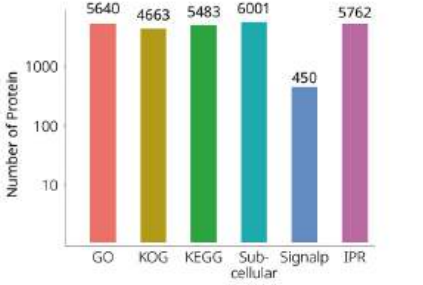
Mouse tissue phosphorylation proteomics analysis results.



Phosphorylation Identification Results

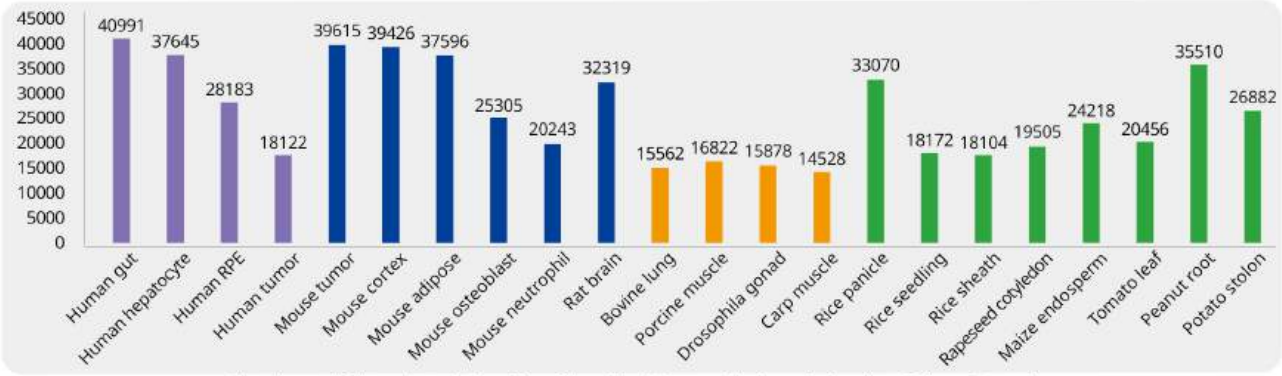


Phosphorylated Site Distribution



Phosphorylated Protein Function Annotation

Project Experience



Number of Phosphorylation Sites Identified Across Various Animal and Plant Samples

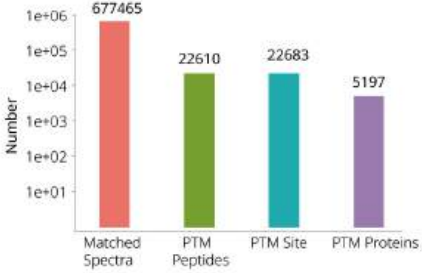
Ubiquitin Proteomics

MetwareBio's Ubiquitination Proteomics Service delivers sensitive and comprehensive profiling of ubiquitinated peptides through an optimized enrichment workflow and cutting-edge 4D label-free LC-MS/MS analysis. The service offers accurate site localization, broad ubiquitination landscape mapping, reliable quantification, and strong data reproducibility, advancing studies in protein degradation, signaling networks, cancer biology, and therapeutic target discovery.

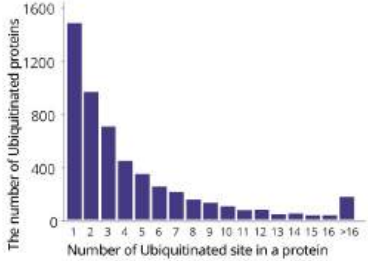
- Ultra-Specific Enrichment with High-Affinity K-ε-GG Antibodies
- Advanced 4D Label-Free LC-MS/MS Platform for High Accuracy and Sensitivity
- Comprehensive Site-Level Data Processing and Interpretation
- Tailored Bioinformatics Solutions for Specialized Research Needs

Case Study

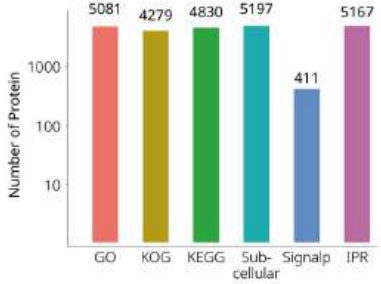
Mouse tissue phosphorylation proteomics analysis results.



Ubiquitination Identification Results

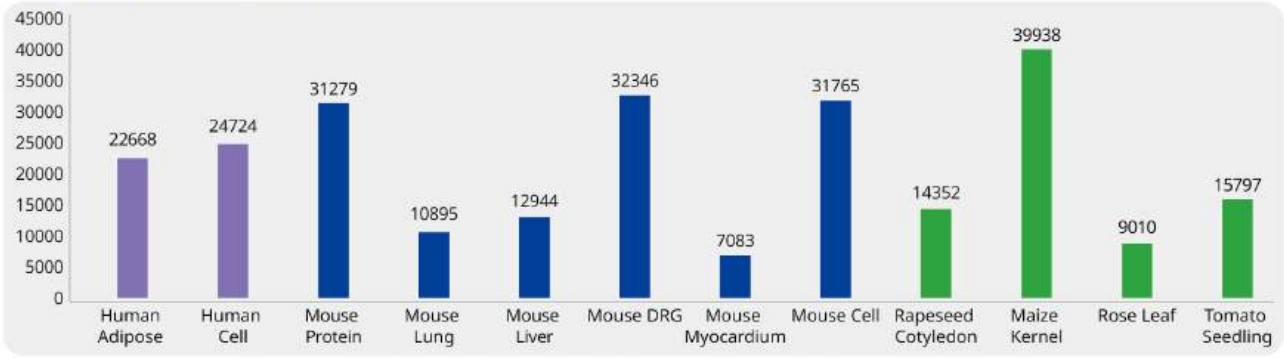


Ubiquitinated Site Distribution



Ubiquitinated Protein Function Annotation

Project Experience



Number of Ubiquitination Sites Identified Across Various Medical and Plant Samples

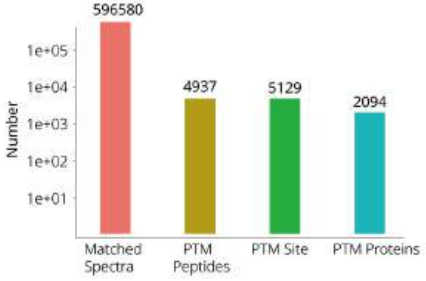
Acetylation Proteomics

MetwareBio's Acetylation Proteomics Service provides high-sensitivity, site-specific profiling of protein acetylation, powered by a highly specific enrichment strategy and advanced 4D label-free LC-MS/MS technology. This platform ensures high-confidence site identification, extensive acetylation coverage, precise quantification, and robust analytical reproducibility. It empowers research across epigenetics, transcriptional regulation, oncology, and biomarker discovery.

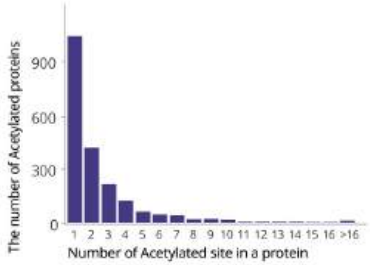
- High-Specificity Enrichment for Comprehensive Acetylation Site Profiling
- Advanced 4D Label-Free LC-MS/MS for Accurate Quantification
- Comprehensive Site-Level Data Analysis and Biological Interpretation
- Flexible Bioinformatics Solutions Tailored to Research Objectives

Case Study

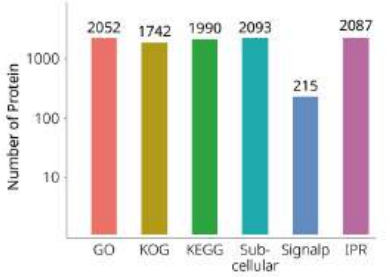
Mouse tissue phosphorylation proteomics analysis results.



Acetylation Identification Results

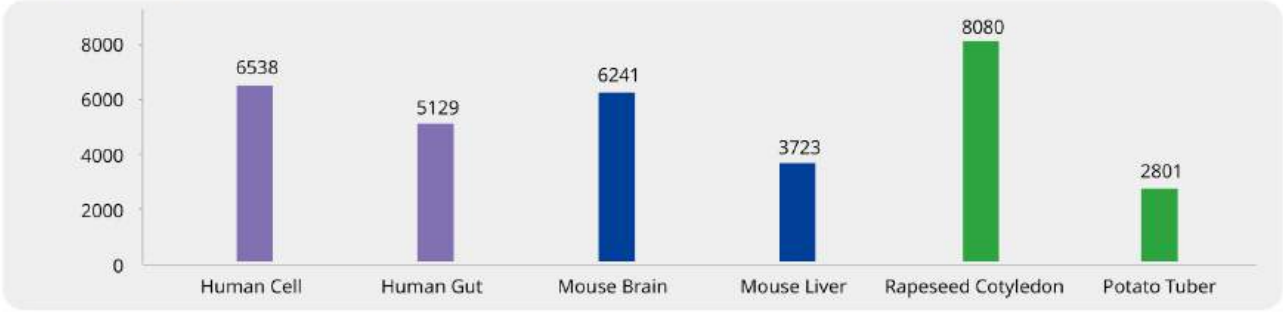


Acetylated Site Distribution

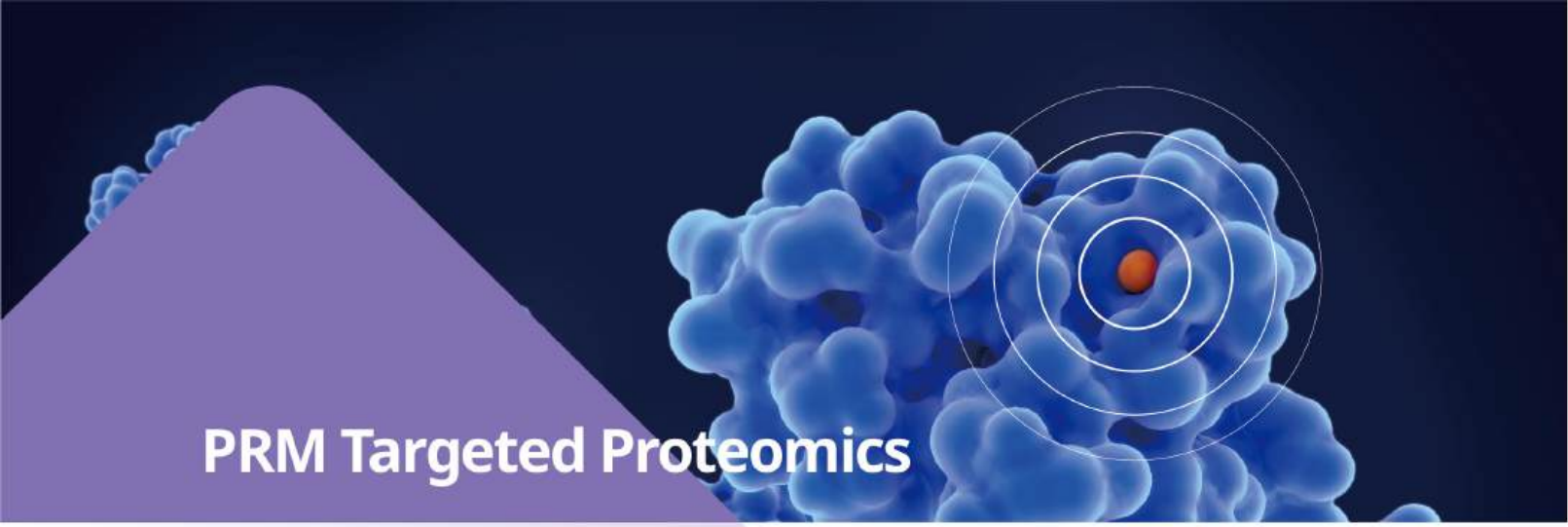


Acetylated Protein Function Annotation

Project Experience



Number of Acetylation Sites Identified Across Various Medical and Plant Samples



PRM Targeted Proteomics

MetwareBio's PRM-Based Targeted Proteomics Service delivers high-sensitivity, high-precision quantification of specific proteins using the parallel reaction monitoring (PRM) strategy on an advanced 4D LC-MS/MS platform. Compared to discovery-based methods such as DDA or DIA, PRM offers superior reproducibility and lower variability, particularly in complex biological matrices. This makes it an ideal choice for biomarker validation, drug target analysis, and pathway-specific studies, especially for verifying key protein candidates across large sample cohorts.

- Advanced 4D LC-MS/MS Platform for High Sensitivity and Selectivity
- Targeted Quantification with Excellent Reproducibility
- Broad Compatibility with Diverse Sample Types
- Scalable Workflow for Multi-Sample and Multi-Batch Analysis

Workflow

Step1
Sample Shipment

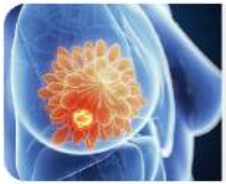
Step2
Sample Preprocessing

Step3
DIA/DDA Library Construction

Step4
PRM Targeted Detection

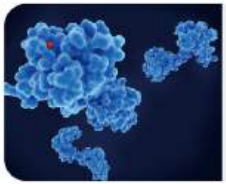
Step5
Data Analysis

Application



Biomarker Verification

Validating candidate disease biomarkers across samples with high specificity and reproducibility.



Pathway Protein Quantification

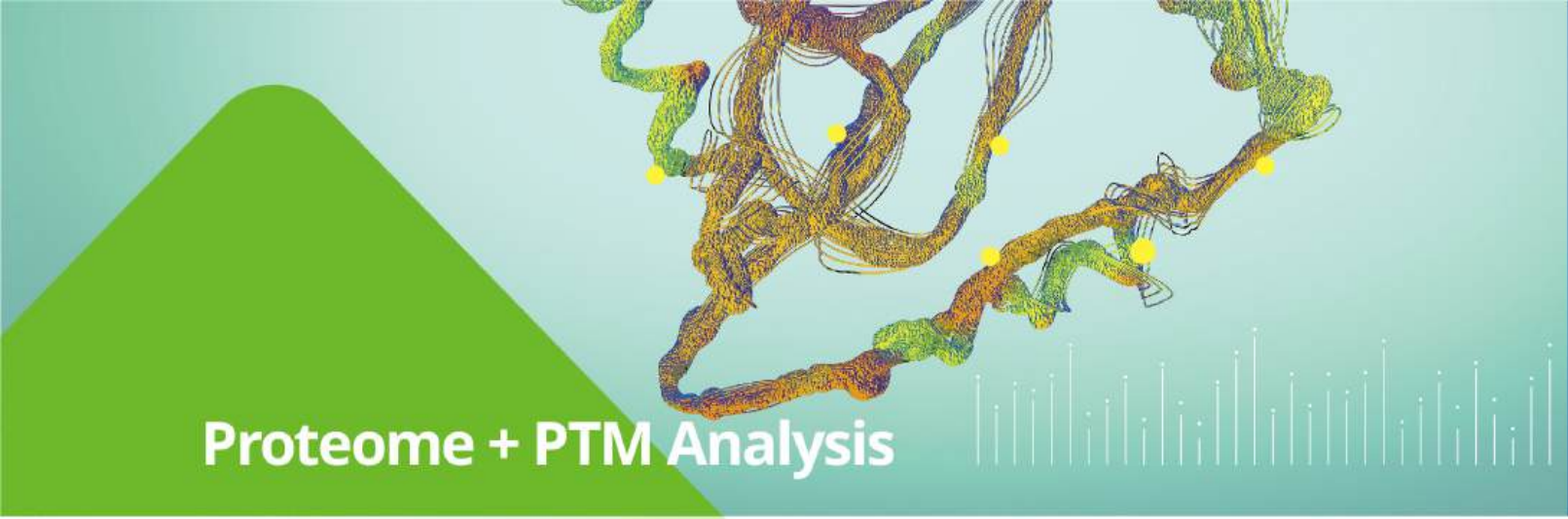
Targeted measurement of key signaling proteins to study pathway dynamics and regulation.

Drug Mechanism Validation

Assessing drug targets and downstream effects through precise protein-level quantification.

Clinical Sample Profiling

High-throughput quantification of proteins across patient samples for classification or diagnosis.

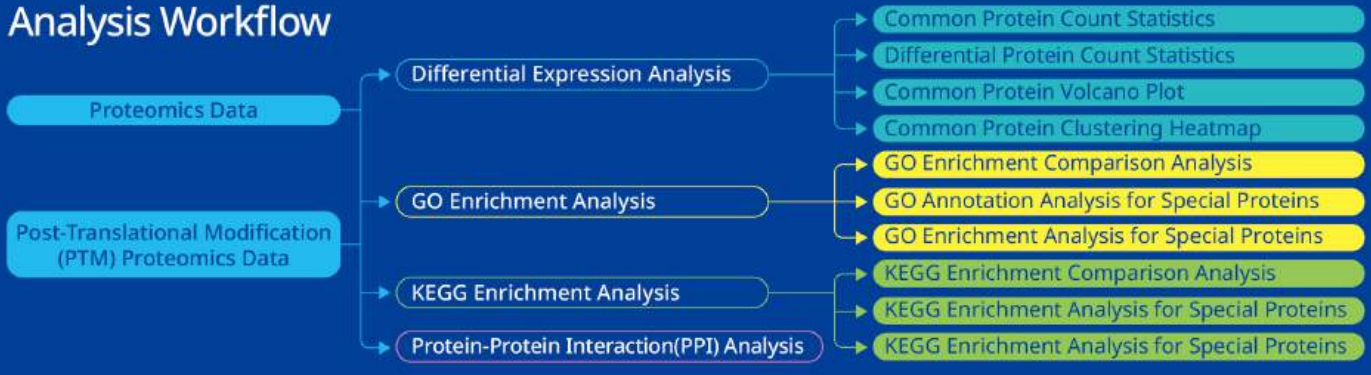


Proteome + PTM Analysis

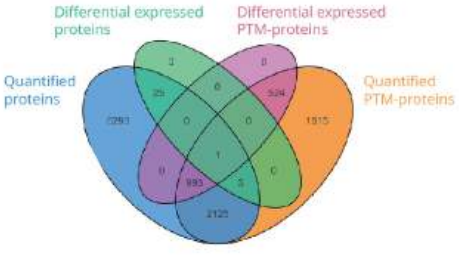
MetwareBio's Proteome + PTM Combined Analysis Service integrates comprehensive proteomic profiling with targeted post-translational modification (PTM) analysis to provide a holistic view of protein expression and regulation. Utilizing advanced 4D LC-MS/MS platform and validated enrichment workflows, this integrated approach enables high-precision quantification of total proteins alongside key PTMs such as phosphorylation, acetylation, ubiquitination, and more. By correlating protein abundance with modification states, the service offers valuable insights into functional protein dynamics under various biological conditions, supporting research in cell signaling, disease mechanisms, and therapeutic target discovery.

- Comprehensive Profiling of Protein Expression and Modifications
- Advanced 4D LC-MS/MS Platform for High Sensitivity and Accuracy
- Extensive Expertise in PTM-Specific Enrichment and Analysis
- Integrated Insights into Protein Function, Regulation, and Dynamics

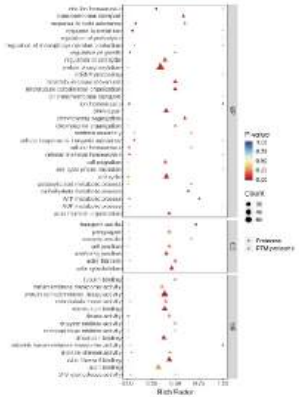
Analysis Workflow



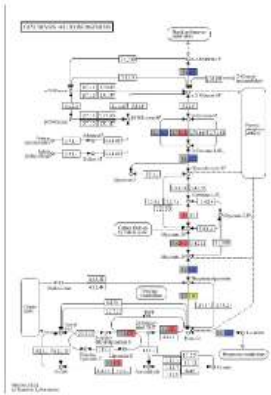
Analysis Results



Common Protein Count Statistics



GO Enrichment Comparison



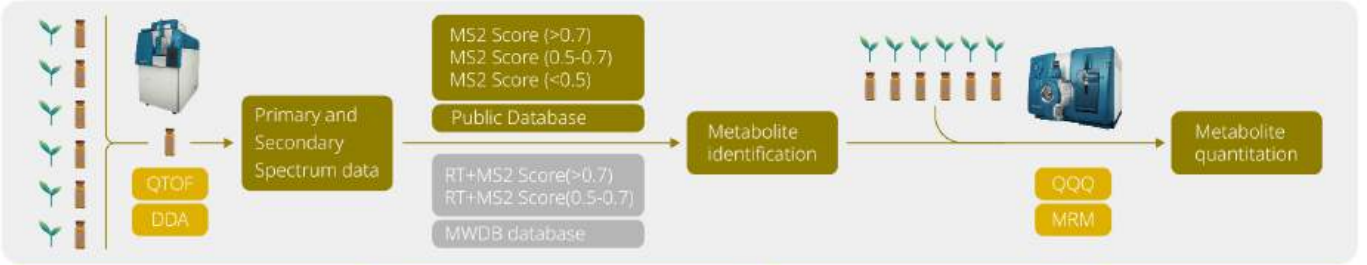
KEGG Pathway Map

Transcriptome + Proteome + Metabolome

In systems biology research, biological processes and gene regulatory networks are complex and dynamic. It is often insufficient to use a single dataset to study systems biology. Correlating transcriptomic data that has a large number of differentially expressed genes together with differential proteins detected by proteomics, and metabolites detected by metabolomics, can pinpoint key genes, proteins, metabolites, and metabolic pathways that are closely associated with internal changes in the system, and thereby explain biological problems in a more holistic approach.

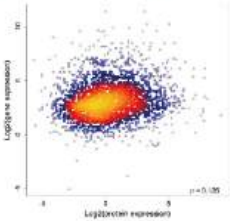
- Coexpressed transcriptome, proteome and metabolome
- Major regulation networks construction
- Converged metabolic pathway
- Holistic view of biological systems

The Power of Our Metabolomics Technology

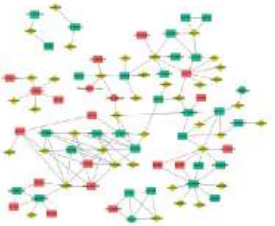


Global Metabolite Profiling	Targeted Metabolomics	Lipidomics	Our Expertise
61,000+ plant metabolites	1,000+ metabolites	4,000+ lipids	100+ patents
3,000+ animal metabolites			1,000+ publications
			20,000+ projects

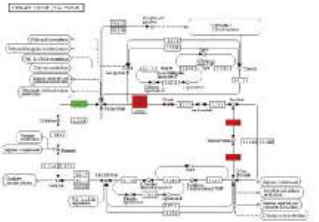
Joint Analysis



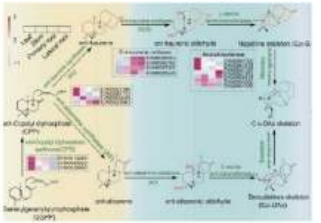
Gene Enrichment Circle Map



Correlation Network



KEGG Map



Converging Metabolic Pathway

Analyze Omics Data With Ease

Cloud Tools

- Data Processing
- Differential Analysis
- Functional Enrichment Analysis

50+ Cloud tools

- Multi-omics Association Analysis
- Gene Sequence Analysis
- File Format Conversion

Cloud Process

Customize analysis parameters

Get started for FREE!

https://cloud.metwarebio.com/

Sample Requirement

Categories	Sample	DIA / DDA / PRM		Phosphorylation		Ubiquitination/ Acetylation	
		Recommended	Minimum	Recommended	Minimum	Recommended	Minimum
Animal Tissues	Normal tissues (heart, liver, spleen, lungs, intestines, kidneys, red bone marrow etc.)	20 mg	5 mg	30 mg	15 mg	100 mg	50 mg
	Yellow bone marrow	50 mg	20 mg	50 mg	30 mg	200 mg	100 mg
	Bone, Shells, Eggshell	1 g	500 mg	/	/	/	/
	Hair	500 mg	200 mg	/	/	/	/
	Fatty tissue, Skin, Synovial membrane	200 mg	100 mg	/	/	/	/
Liquid Samples	Serum/Plasma	10 µL	1 µL	/	/	/	/
	Serum/Plasma (low-abundant proteins enrichment)	100 µL	50 µL	/	/	/	/
	Cerebrospinal fluid, Joint fluid, Lymph fluid, Ascites	200 µL	100 µL	/	/	/	/
	Amniotic fluid	200 µL	100 µL	200 µL	100 µL	600 µL	300 µL
	Milk	50 µL	10 µL	200 µL	100 µL	600 µL	300 µL
	Aqueous humor, Vitreous body	200 µL	100 µL	/	/	/	/
	Tear fluid	200 µL	100 µL	/	/	/	/
	Urine, Alveolar lavage fluid (BALF)	5 mL	2 mL	/	/	/	/
	Cellular supernatant	25 mL	10 ml	/	/	/	/
	Fermentation broth	10 ml	5 ml	/	/	/	/
	Lipid droplet	300 µL	200 µL	/	/	/	/
	Saliva (mammals)	200 µL	100 µL	/	/	/	/
Cells	Primary Cells	3×10^6	1×10^6	2×10^7	1×10^7	4×10^7	2×10^7
	Transmissible cells	1×10^6	5×10^5	1×10^7	5×10^6	4×10^7	2×10^7
	Sperms, Platelets	1×10^7	5×10^6	1×10^8	5×10^7	4×10^8	2×10^8
Plant Tissues	Young tissues (young leaf, seedling, petal, etc.)	50 mg	20 mg	200 mg	100 mg	1 g	500 mg
	Mature tissues (root, stem, fruit, pericarp, etc.)	500 mg	200 mg	500 mg	300 mg	2 g	1 g
	Pollen	40 mg	15 mg	/	/	/	/
Micro-organisms	Bacteria	100 mg	100 mg	300 mg	150 mg	500 mg	200 mg
	Fungi	200 mg	200 mg	300 mg	150 mg	1 g	500 mg
Special Samples	Exosome (sediment)	25 µl	15 µl	/	/	/	/
	Protein	100 µg	50 µg	1 mg	500 µg	5 mg	3 mg

Replicates: A minimum of 3 replicates is required; 3-6 replicates for animal samples; 6-10 for clinical samples.

Bridging Proteomics and Metabolomics for Better Health

Metware Biotechnology Inc. (MetwareBio) is focused on developing and applying innovative multi-omics technologies to life science and health research. By leveraging state-of-the-art mass spectrometry technologies, unique detection workflow, and large curated in-house database, MetwareBio offers one-stop multi-omics solutions to academic research, clinical studies, and biotech/pharmaceutical developments.

MetwareBio technical achievements have been presented and published in over 1,000 publications, including Cell, Nature Genetics, PNAS, Nature Communications, National Science Review, and many other international peer-reviewed journals. Working with MetwareBio means you have all the metabolomics and multi-omics expertise supporting your research and development.

METWAREBIO

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