Proteomics Services

METWARE BIO

Innovative Metabolomics Insights for Better Health

The Power of Our Proteomics Technology

Challenges in proteomics: limited sample volumes, large cohort sample, low instrument resolution.

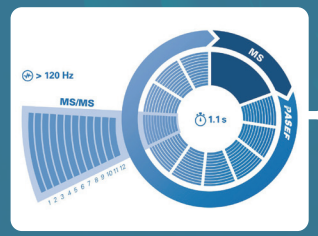
Limited sample size → Detection sensitivity

Quantification analysis for large-scale samples → Instrument stability, Detection dynamic range

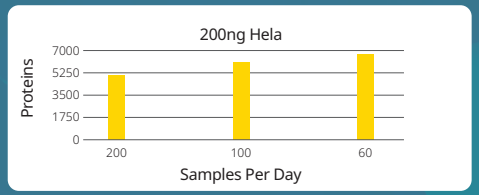
Mass spectrum specificity → Instrument resolution, Mass spectrum quality, PTM identification of position isomerism

PASEF Advantages

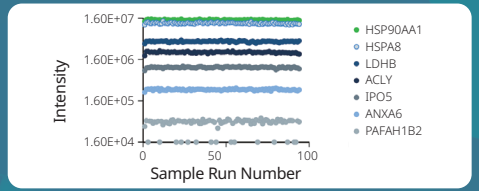
Achieving excellent detection throughput and stability with more proteins detected by less sample size using dual TIMS and PASEF technology.



High Throughput

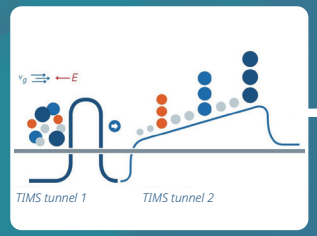


High Stability



Hardware Advantages

Our proteomics offer outstanding detection sensitivity and accuracy with an additional dimension of ion mobility.

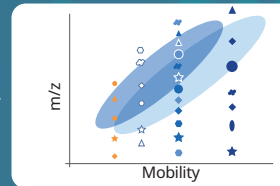


High Sensitivity

More detected proteins

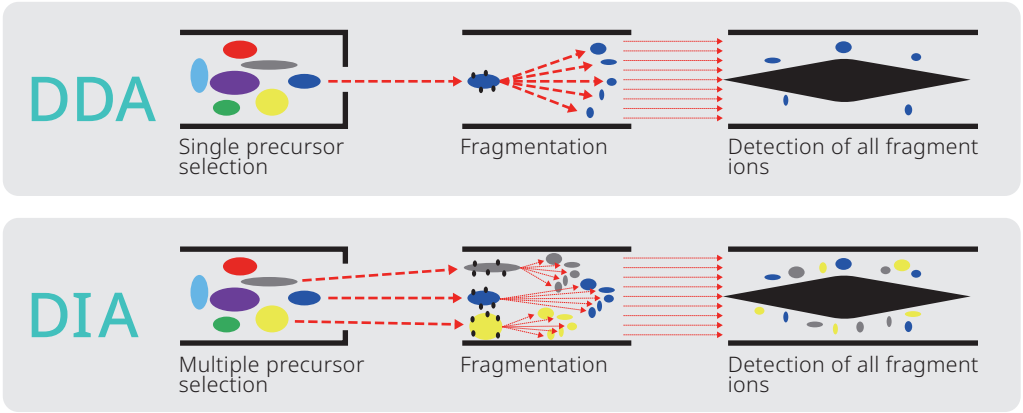
	Unique peptide sequence	Proteins
TIMS-PASEF	39,000	5,200
TIMS -PASEF OFF	20,000	3,200

Accurate Identification



MS:MS based, CCS-enabled

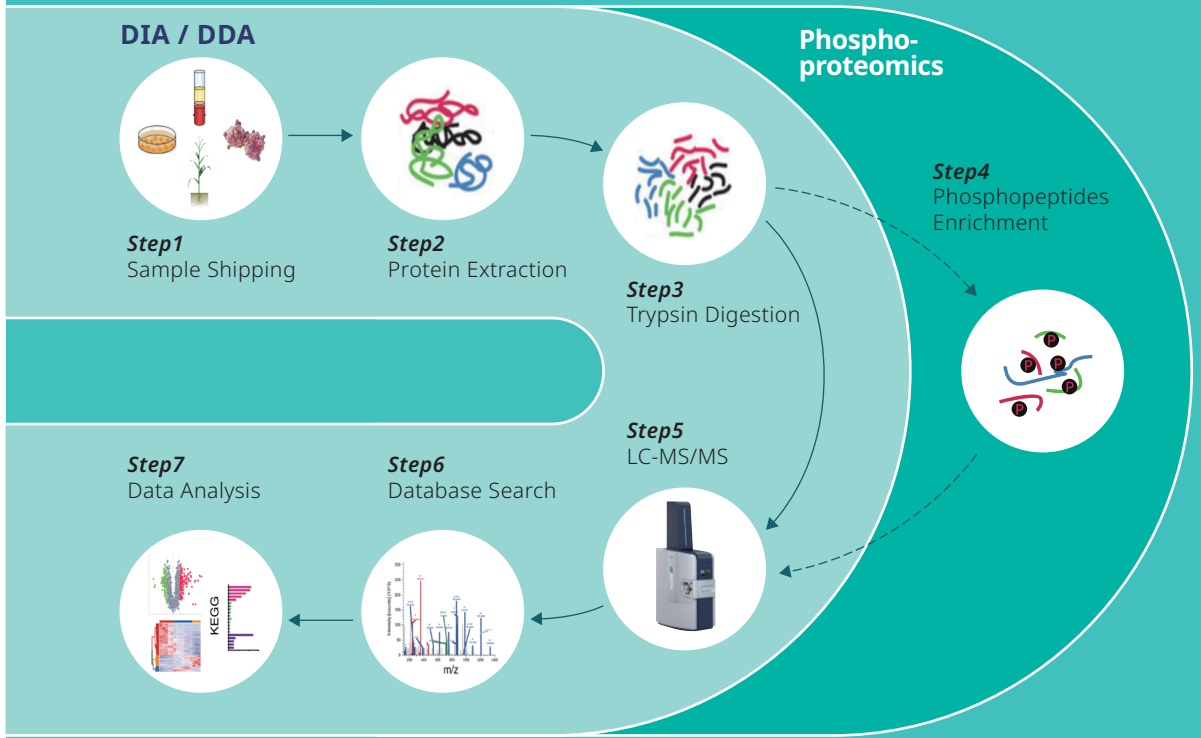
Comprehensive Proteomics Analysis



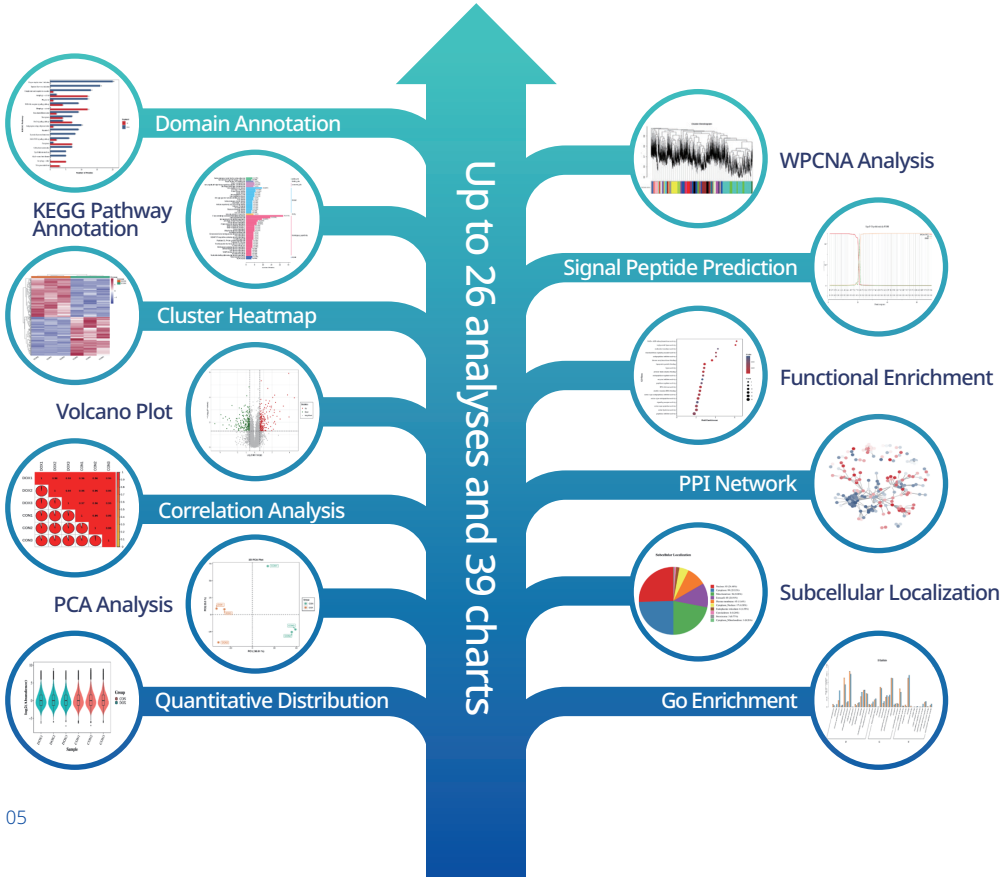
Which Proteomics Approach is for You?

Class / Services	DIA Quantitative Proteomics	DDA Quantitative Proteomics	Phospho-proteomics	TMT Labled Quantitative Proteomics
Acquisition Mode	DIA-PASEF	DDA-PASEF	DDA-PASEF	DDA
Lables	No	No	No	Yes
Qualitation	MS2	MS2	MS2	MS2
Quantitation	MS2	MS1	MS1	MS2
Application Scope	No sample limitations	No sample limitations	No sample limitations	Sample size limitations

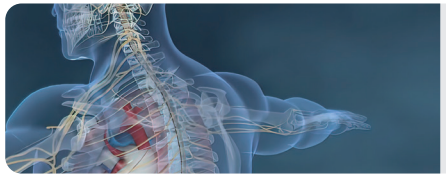
Workflow



Comprehensive Analytical Report



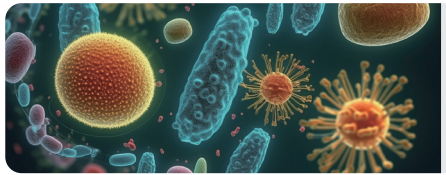
Insightful Solutions, Infinite Potential



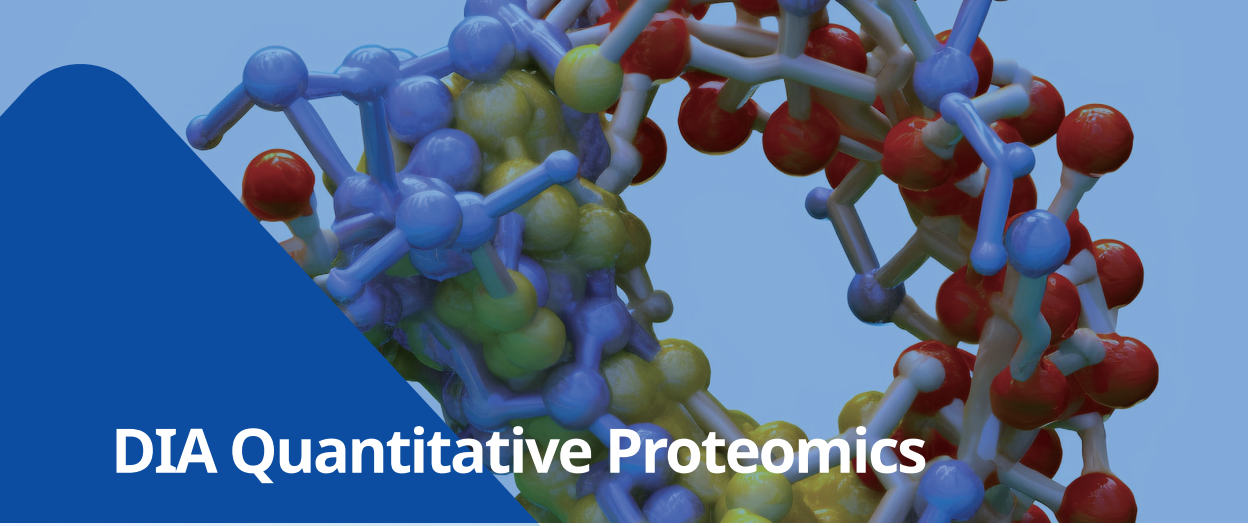
Medical Research
Disease Mechanisms, Molecular Diagnosis, Biomarker Development, Drug Targets

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

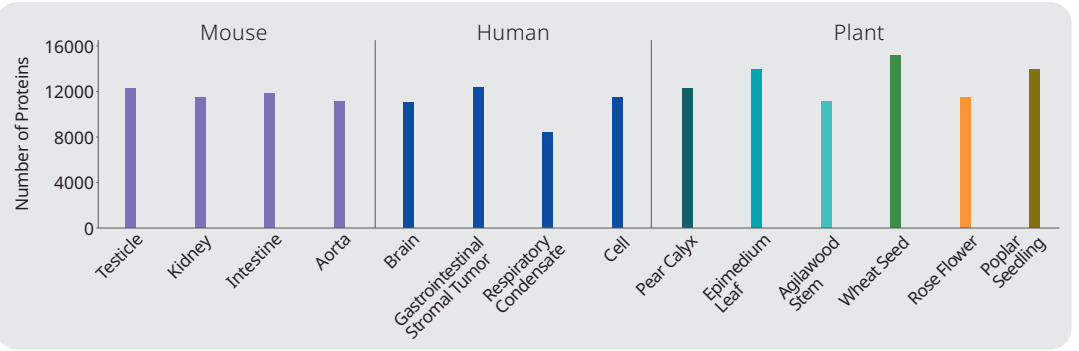


DIA Quantitative Proteomics

DIA Quantitative Proteomics utilizes timsTOF HT mass spectrometer and diaPASEF (parallel accumulation-serial fragmentation) acquisition mode to achieve qualitative and quantitative protein analysis. This allowed faster scanning speed and enhanced ion utilization, which drastically improved identification accuracy, coverage, sensitivity, and throughput in protein detection with smaller sample input.

- Sample specific protein extraction
- Lower input requirements, larger detection scope
- Almost 100% ion utilization, increased detection depth and sensitivity
- Fewer missing values, enhanced detection stability and accuracy
- High throughput, suitable for cohort studies with large sample amounts

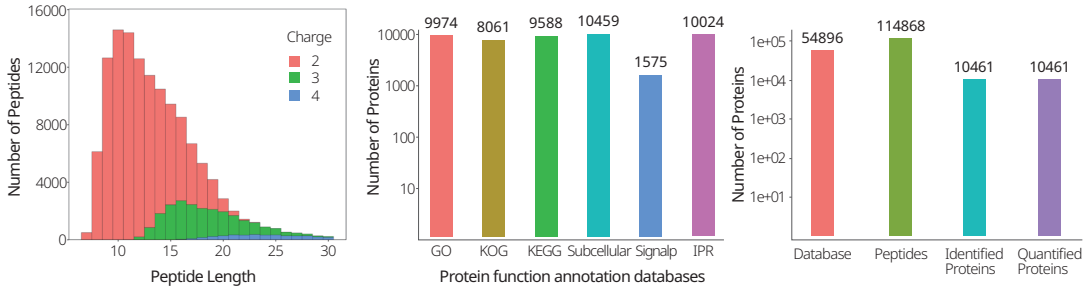
Project Experience



Average number of proteins identified

Case Study

Mouse tissue DIA quantitative proteomics results.



DDA Quantitative Proteomics

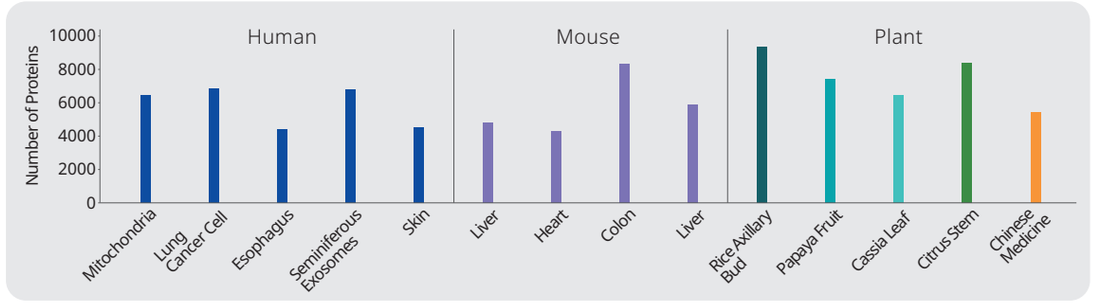
DDA Quantitative Proteomics utilizes timsTOF HT spectrometer and the ddaPASEF (parallel accumulation-serial fragmentation) acquisition mode to achieve qualitative and quantitative analysis. DDA Quantitative Proteomics offers simplicity in operation, free from expensive labeling reagents, reduced data complexity, and improved detection sensitivity.

- Sample specific protein extraction
- Minimize sample manipulation for intact biological characteristics
- Accurate qualitative and quantitative analysis with excellent data stability
- High sensitivity with more low-abundance proteins detection

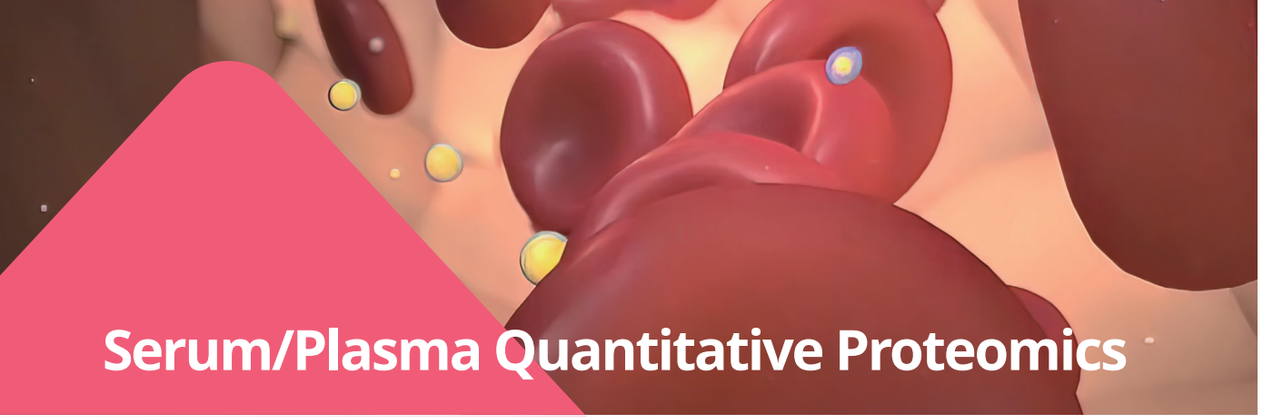
Data-Dependent Acquisition Mode

In the ddaPASEF acquisition mode, precursor ions with high ion intensity are selected from the MS1 spectra to set the mass spectrum scan range to specific narrow mass windows. The selected target precursor ions are sequentially fragmented in the MS2 spectra, with their retention time, mass-to-charge ratio, ion intensity, and ion mobility recorded for subsequent protein qualitative and quantitative analysis.

Project Experience



Average number of proteins identified

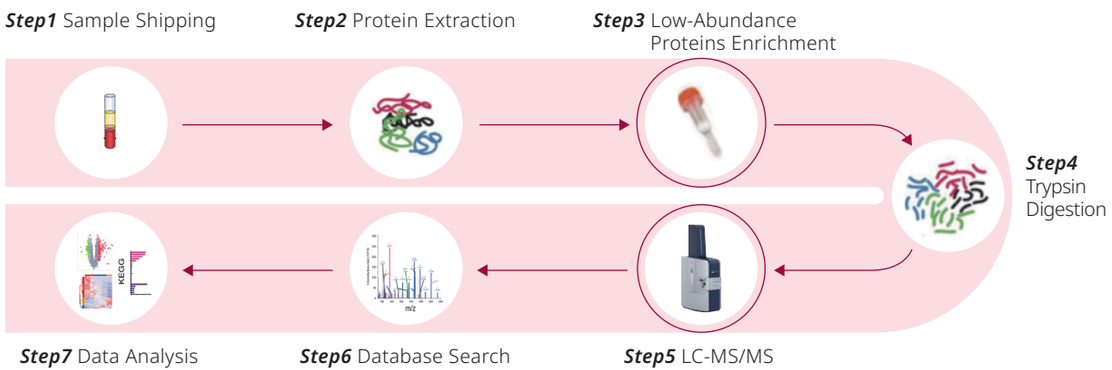


Serum/Plasma Quantitative Proteomics

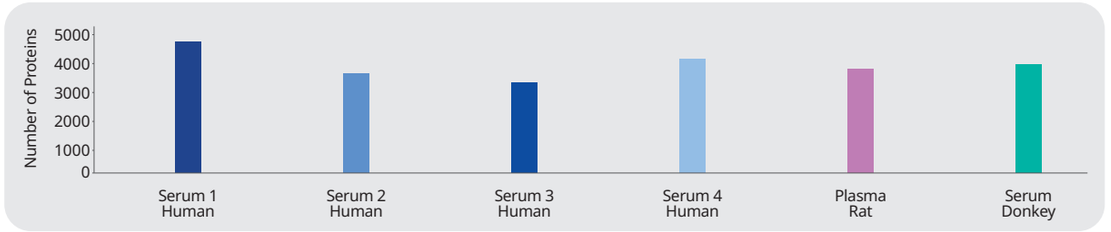
Blood Quantitative Proteomics is a specialized method developed specifically for blood samples. Blood contains a diverse range of proteins with significant differences in abundance, with high-abundance proteins dominating. In conventional proteomics, signals from low-abundance proteins relevant to many disease indicators in the blood are often overshadowed by signals from high-abundance proteins, resulting in fewer detected proteins. Our quantitative blood proteomics approach first enriches the middle-to-low abundance proteins in the blood using methods such as high-abundance protein depletion or low-abundance protein enrichment. Subsequently, the samples are analyzed using the diaPASEF scanning mode, which offers high throughput, increased protein detection, and improved depth of analysis.

- Efficient low-abundance proteins enrichment using magnetic beads
- High-throughput 4D protein profiling detection technology
- Profound detection depth with more low-abundance proteins detected
- High sensitivity and resolution mass spectrometry platform

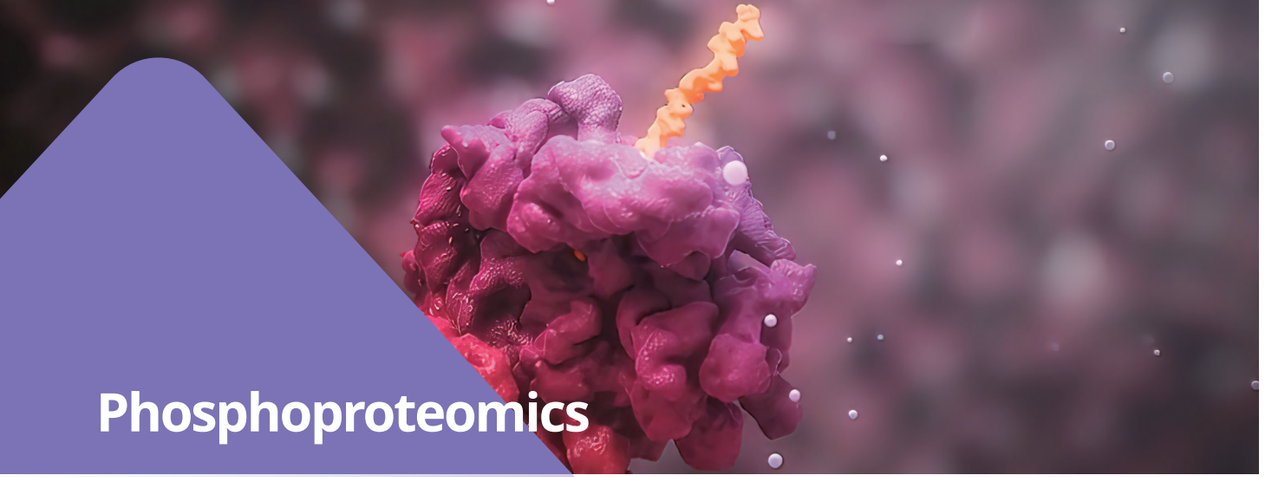
Workflow



Project Experience



Average number of proteins identified



Phosphoproteomics

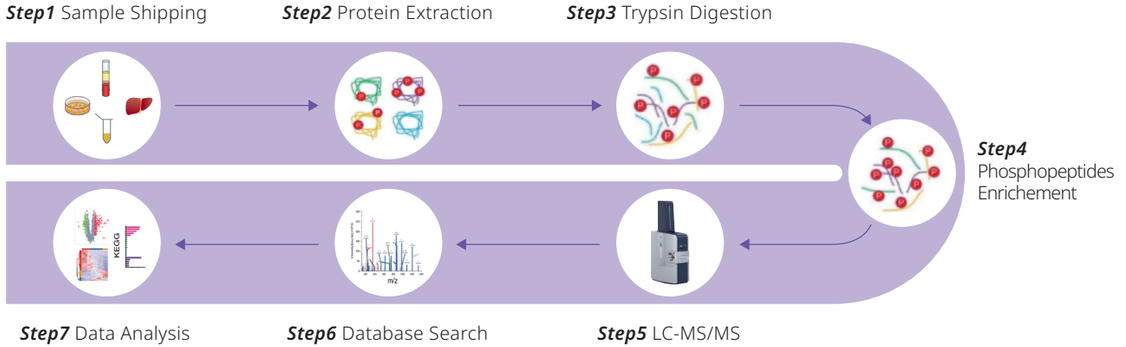
Phosphoproteomics aims to identifying phosphorylated proteins and peptides in diverse samples, accurately localizing and quantifying phosphorylation sites, and ultimately elucidating their biological functions.

Highly specific antibodies for comprehensive coverage of modified proteins

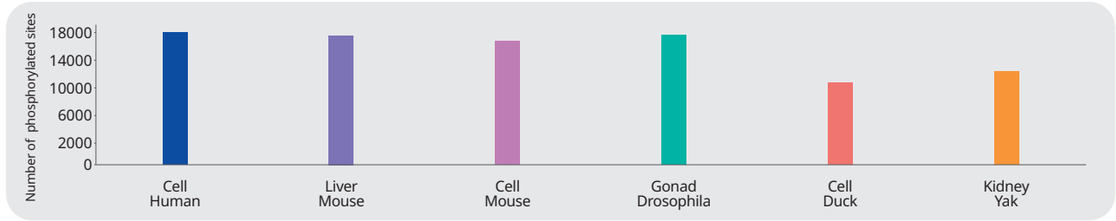
High sensitivity and resolution mass spectrometry platform

High-throughput 4D protein profiling detection technology

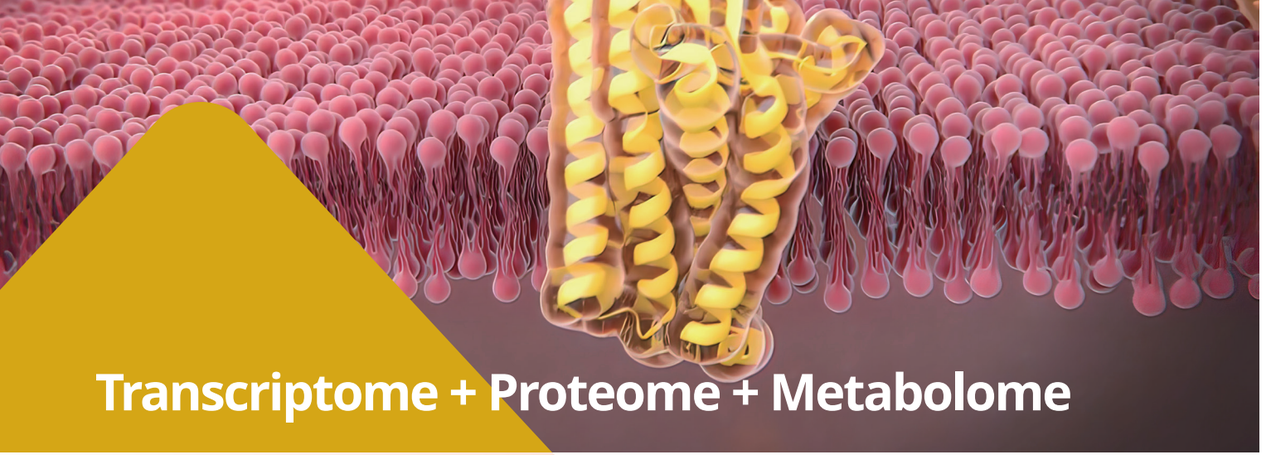
Workflow



Project Experience



Average number of phosphorylated sites identified

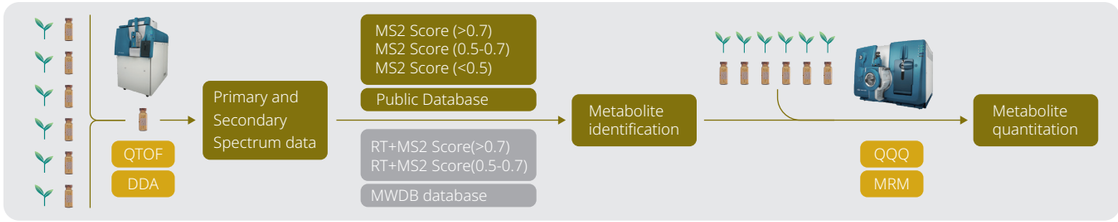


Transcriptome + Proteome + Metabolome

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.

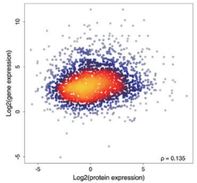
- Coexpressed transcriptome, proteome and metabolome
- Converged metabolic pathway
- Major regulation networks construction
- Holistic view of biological systems

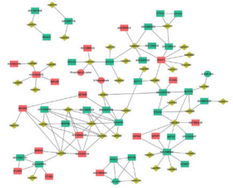
The Power of Our Metabolomics Technology

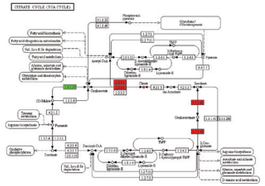


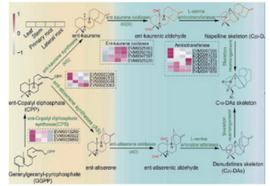
Global Metabolite Profiling	Targeted Metabolomics	Lipidomics	Our Expertise
35,000+ plant related metabolites	591+ metabolites	4,000+ lipids database	100+ patents
3,000+ mammalian metabolites			700+ publications
			20,000+ projects

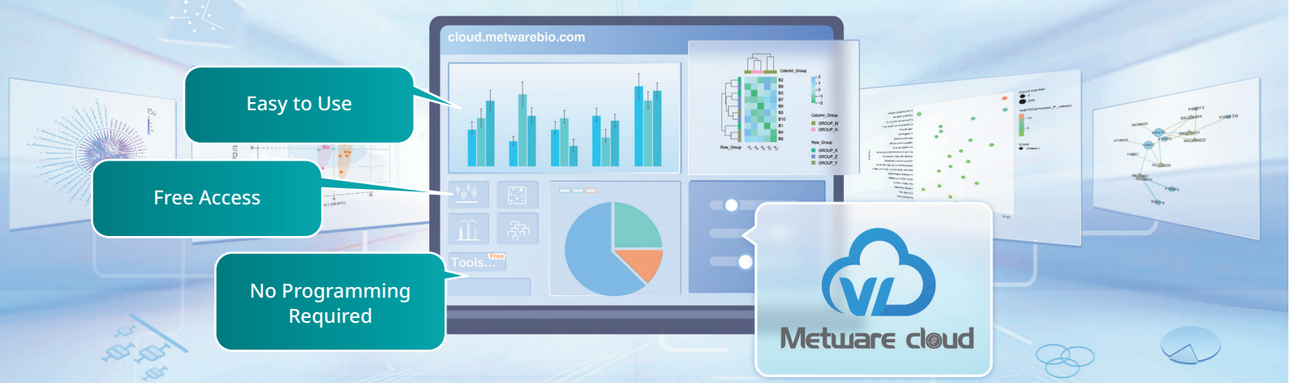
Joint Analysis


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

Sample Type	Sample	DIA / DDA Quantitative Proteomics		Phosphoproteomics	
		Recommended	Minimum	Recommended	Minimum
Animal Tissue	Normal tissues (heart, liver, spleen, lungs	50 mg	5 mg	5 mg	30 mg
	intestines, kidneys, etc.)	200 mg	100 mg	1 g	500 mg
	Brain tissue	50 mg	5 mg	100 mg	50 mg
	Bone	1 g	200 mg	1 g	500 mg
	Hair	500 mg	200 mg	1 g	500 mg
	Skin	200 mg	100 mg	/	/
Liquid Samples	Serum/Plasma	20 μl	5 μl	/	/
	Serum/Plasma (low-abundant proteinsenrichment)	200 μl	100 μl	/	/
	Joint fluid, Lymph fluid, Cerebrospinal fluid	200 μl	100 μl	1 ml	500 μl
	Aqueous humor, Vitreous body	300 μl	200 μl	/	/
	Ascites, Follicular fluid	100 μl	50 μl	/	/
	Alveolar lavage fluid (BALF)	1 ml	500 μl	/	/
	Amniotic fluid	1 ml	500 μl	5 ml	2 ml
	Milk	20 μl	5 μl	/	/
	Urine	10 ml	5 ml	50 ml	20 ml
	Saliva (mammals)	1 ml	500 μl	/	/
	Fermentation broth, Bacterial solution	10 ml	5 ml	/	/
	Cellular supernatant	25 ml	10 ml	/	/
Cells	Primary Cells	3×10^6	1×10^6	2×10^7	1×10^7
	Transmissible cells	2×10^6	1×10^6	1×10^7	5×10^6
	Sperm, Platelets	2×10^7	1×10^7	5×10^7	2×10^7
Plant Tissue	Young tissue (young leaf, seedling, petal, etc.)	200 mg	100 mg	500 mg	200 mg
	Mature tissue (root, stem, fruit, pericarp, etc.)	1 g	500 mg	2 g	1.5 g
	Pollen	40 mg	15 mg	/	/
Microorganisms	Bacteria	200 mg	100 mg	/	/
	Fungi	300 mg	150 mg	1 g	500 mg
Protein	Protein	100 μg	30 μg	1000 μg	500 μg

Biological duplicates: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 700 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.

METWARE BIO

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