

# COMBINED PROTEOMICS AND METABOLOMICS ANALYSIS

**Proteomics** is an intermediate bridge technology for systems biology in the postgenomic era. As the executor of the functions of life activities, proteomics studies the composition and activity patterns of intracellular proteins and protein-protein interactions at a holistic level.

**Metabolomics**, as a nascent histological technology in the post genomic era, explores key scientific questions related to cellular metabolism in organisms by qualitatively and quantitatively characterizing changes in small molecule metabolites (metabolites with molecular masses of 1,000 Da or less) in different organisms. Metabolomics is a portrayer of phenotypic states and a functionally regulated active metabolite. Its ability to modulate protein-protein interactions and alter enzyme activity leads to changes in protein stability, which in turn feed-back regulates the metabolic state of the organism.

The **combined analysis of proteome and metabolome** is an effective research strategy to systematically characterize the metabolic regulatory network of biological organisms. By normalizing and statistically analyzing the bulk data from proteome and metabolome, together with metabolic pathway enrichment and correlation analysis, molecular models of downstream metabolite changes and metabolic enzyme regulation mechanisms can be constructed. Rapidly screen the data to find differential proteins and differential metabolites that share a certain type of metabolic pathway or have the same change trend, systematically describe the molecular regulation mechanism in the organism, and provide data basis for subsequent experimental validation and analysis.



## Pathway-Based Approaches

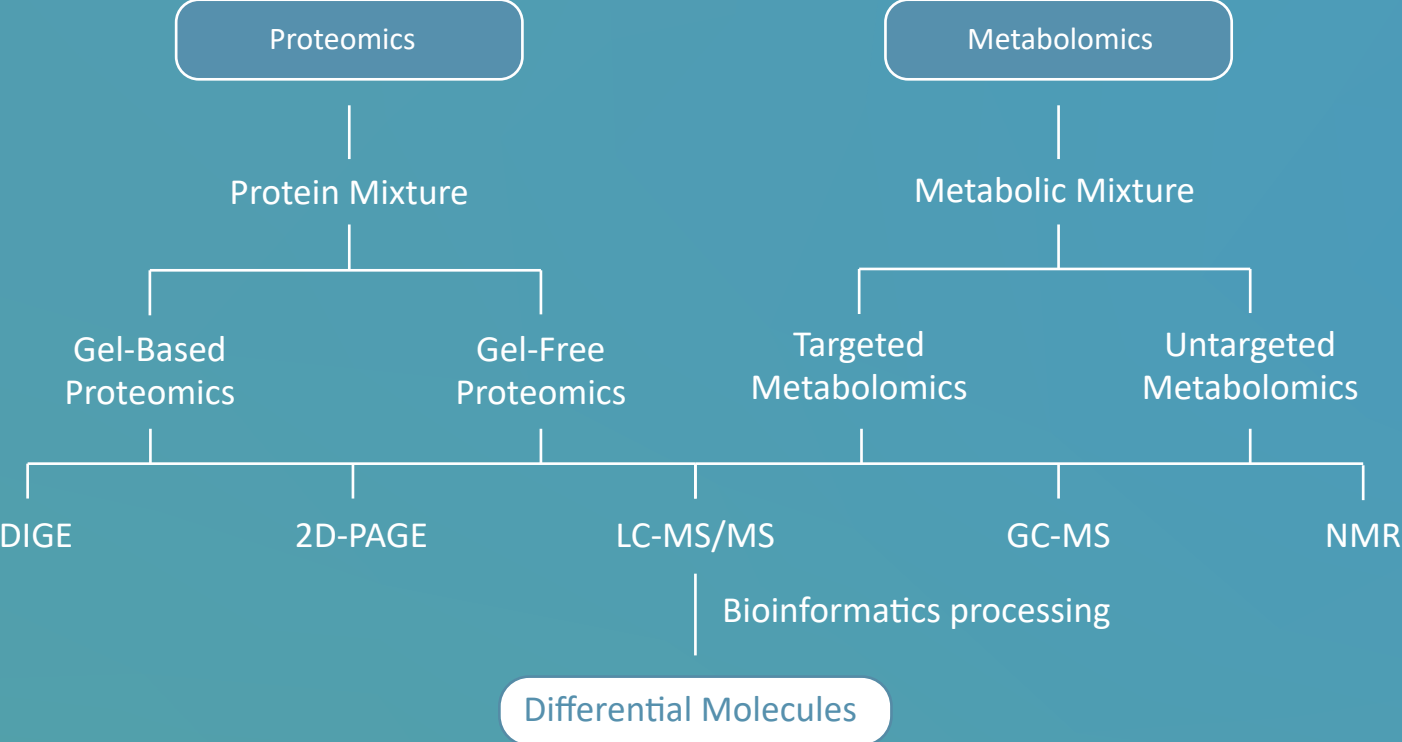
The KEGG metabolic pathway unites proteomic and metabolomic data to find proteins and metabolites that undergo significant changes in the same biological process, and quickly targets key proteins and metabolites. This is then combined with enrichment analysis and KEGG Pathway color coding to visualize the relevant results.



## Expression-Based Approaches

The expression data of differentially expressed proteins and metabolites are jointly analyzed to identify differential proteins and metabolites with synchronous change patterns. Combine with correlation coefficient matrix heat map, correlation analysis clustering heat map, and correlation coefficient regulatory network map for personalized analysis.

## Research Process for Metabolomic Proteomic Conjoint Analysis



## Applied Research Fields



### Agriculture and Forestry

Stress resistance mechanism, growth and development mechanism, breeding protection research, etc.



### Preclinical Research

Research on biomarkers, disease mechanism, disease typing



### Biomedicine

Drug mechanism of action, drug efficacy evaluation, drug development, etc.



### Microbiology

Infection immunity, pathogenesis, drug resistance mechanism, pathogen-host interaction research, etc.



### Marine Aquaculture

Fisheries resources, mariculture, fisheries environment and aquatic product safety, etc.



### Environmental Science

Fermentation process optimization, biofuel production, environmental risk assessment research, etc.



### Food Nutrition

Food component and quality identification, functional food development, food safety monitoring and testing.



### Livestock Industry

Meat and milk quality research, pathogenic mechanism research, etc.

## Data Analysis

Analysis Type	Analyze Content
Weighted gene co-expression network analysis	KEGG annotation, KEGG enrichment analysis, KEGG pathway visualization.
Correlation analysis	Correlation coefficient matrix heat map. Correlation analysis hierarchical clustering heat map. Correlation coefficient regulatory network analysis
PCA comparative analysis	Comparative proteomic and metabolomic PCA analysis
Multivariate statistical integration analysis	O2PLS correlation analysis. Screening of OPLS correlation variables.
WGCNA analysis	Weighted gene co-expression network analysis

Equipped with Orbitrap Fusion Lumos mass spectrometry coupling nanoUPLC platforms, Creative Proteomics is able to provide qualitative and quantitative proteomics services, targeted and untargeted metabolomics services, and customizable bioinformatics analysis. We provide one-stop integrated proteomics and metabolomics analysis solutions from experimental design, sample detection, to data analysis to meet your research needs.

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