Technology Introduction

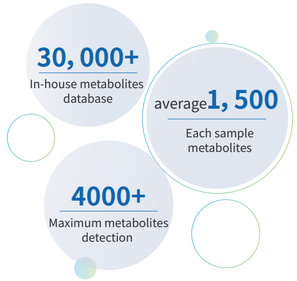
The LC-MS/MS metabolomics is used for unbiased detection of metabolites to obtain their qualitive and quantitative information, combined with APTBIO' s in-house metabolite database to identify different metabolites. Compared to GC-MC detection, LC-MS/MS provides a more comprehensive metabolic profile, which can provide clues and directions for the research of metabolic key pathways, disease biomarker screening and drug pathological development.

INOMIXO has been providing untargeted metabolomics services and curated an in-house database for over a decade, and we can provide analysis results using integrated public database as our clients need.

Technical Features

Large in-house database

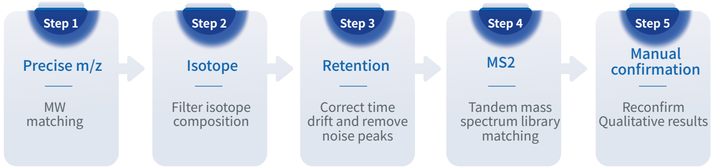
- INOMIXO database contains over 30,000+ metabolites
- Each sample can typically identify 1000-2500 metabolites, with an average of 1500 metabolites
- Maximum detection capability reaches 4000+ metabolites



Rigorous identification standards

- Four-step filtering method

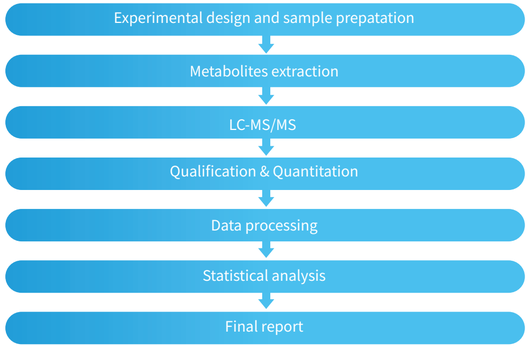
Compliance with Metabolomics Standards Initiative (MSI) standards



- Strict tandem mass spectrum library matching standards

We will retain the results with high similarity score and provide customers with all matching results from a tandem mass spectrometry database for all identified qualitative metabolites.

Project Workflow



Sample Requirements

Sample type	sample	Recommended	Biological duplication
Body fluid	Seminal plasma. serum, urine, saliva, sperm, secretions……	⩾200 μL	Clinical ⩾30 samples/group Animal ⩾10 samples /group Plant ⩾6 samples /group Cell ⩾6 samples /group
Animal tissue	Cancer and adjacent non-tumor, brain, liver tissues……	⩾200 mg	
Plant	Roots, stems, leaves	⩾200 mg	
	Nectar, * root exudates	⩾200 μL	
Stool	Feces, intestinal contents	⩾200 mg	
Cells	Suspension and adherent cells	⩾10^7	
Culture medium	* Cell supernatant * Fermentation broth	⩾200 μL	
Bacteria	Microbes (bacterial precipitate)	⩾200 mg	
Others	Environmental samples or others	Customized	

★ Prefer to be sent in the concentrated form.

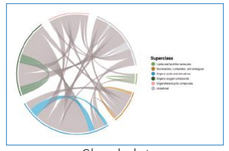
Boinformatics Analysis

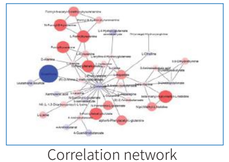
INOMIXO offers standard, advanced and customized analysis services to meet various research requirements.

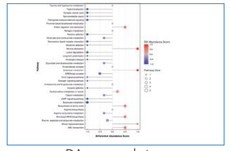
Standard analysis	
Identification results	Metabolites quality and chemical classification
Inter-group variance analysis	Univariate analysis (T-test, Volcano plot)
	Multivariate analysis (PCA, OPLS-DA)
Differential metabolite analysis	Fold-change analysis (Butterfly plot)
	Abundance analysis (Bar chart, Violin plot, Box plot)
	Venn analysis (Venn diagram)
	Cluster analysis (Dendrogram, Cluster heatmap)
	Correlation analysis (Heatmap, Chord plot, Correlation network)
	KEGG pathway annotation and analysis
	MetPA analysis (Bubble plot)
	MSEA analysis (Bar chart)
	ROC analysis
Advanced analysis	
Biomarker screening	Integrated machine learning system
Metabolite screening	OPLS regression analysis
Metabolite expression and phenotypes correlation	WGCNA
Two-omics analysis	Transcriptomics/proteomics/PTM omics + metabolomics
Three-omics analysis	Transcriptomics + proteomics + metabolomics

Analysis Content Display

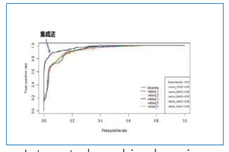
Standard analysis

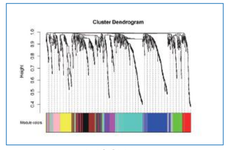

Chord plot


Correlation network

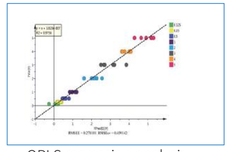

DA score plot

Advanced analysis


Integrated machine learning



WGCNA


OPLS regression analysis

Selected Publications

Year	Journal	Paper
2023	Cell	Light modulates glucose metabolism by a retina-hypothalamus-brown adipose tissue axis
2023	Cell Metabolism	Thymidine kinase 1 drives hepatocellular carcinoma in enzyme-dependent andindependent manners
2023	Journal of Clinical Investigation	Gluconeogenic enzyme PCK1 supports S-adenosylmethionine biosynthesis and promotes H3K9me3 modification to suppress hepatocellular carcinoma progression
2022	Cell Host & Microbe	Gut microbiome dysbiosis contributes to abdominal aortic aneurysm by promoting neutrophil extracellular trap formation
2021	Cell Metabolism	Pharmacological inhibition of arachidonate 12- lipoxygenase ameliorates myocardial ischemia reperfusion injury in multiple species
2020	CirculationResearch	Intestinal Flora Modulates Blood Pressure by Regulating the Synthesis of IntestinalDerived Corticosterone in High Salt-Induced Hypertension

ABOUT US

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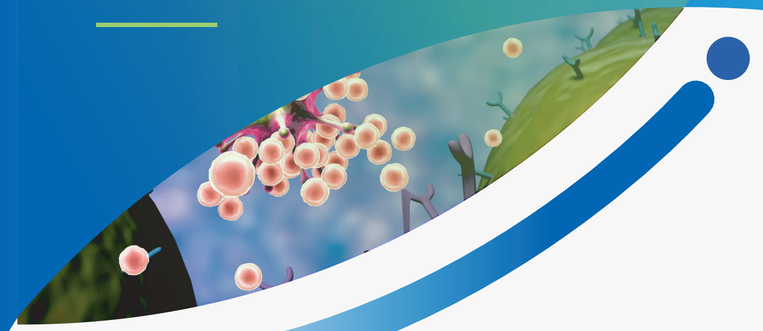
Untargeted Metabolomics Services



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