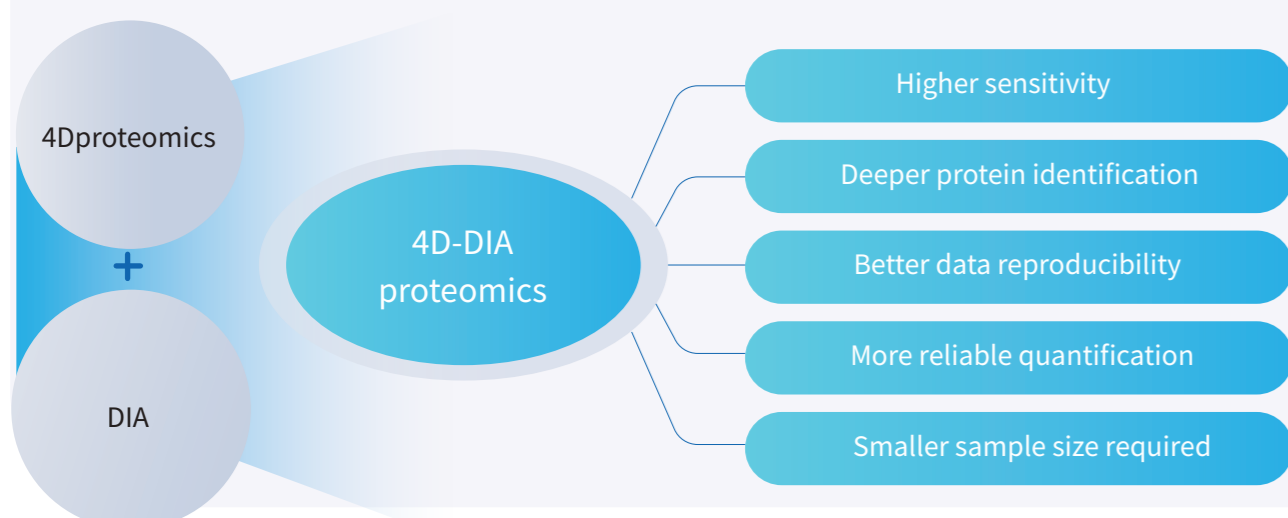


# Proteomics Service

Conventional proteomics research relies on three dimensions post proteolytic digestion: retention time, mass-to-charge ratio (m/z), and peptide ion intensity. With the development of Trapped Ion Mobility Spectrometry (TIMS) and Parallel Accumulation Serial Fragmentation (PASEF) techniques, ion mobility dimension was added as the fourth separation dimension, making 4D proteomics technology the latest quantitative approach.

Based on Bruker timsTOF Pro2 platform, 4D-DIA significantly improves the scanning speed and detection sensitivity, as well as enhances proteomic analysis performance in terms of identification depth and quantitative accuracy with less sample input. INOMIXO is a leading omics service provider with decades of experience in the field of proteomics, we are committed to delivering the highest quality 4D-DIA services for researchers worldwide.

## The optimal choice for proteomic analysis of large-cohort samples



### ► High sensitivity

Nearly 100% ion utilization, greatly improving detection sensitivity.

### ► Deeper protein identification

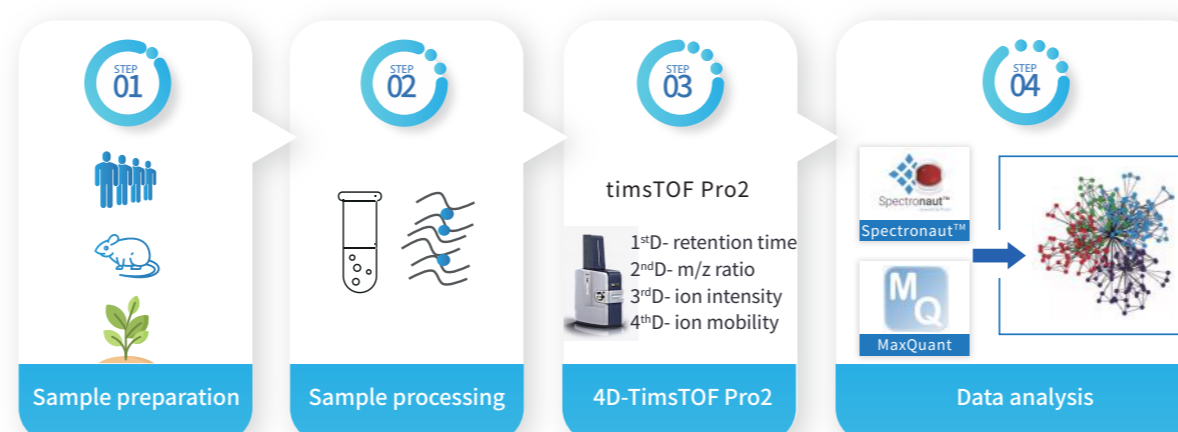
Protein identification level has increase by 20%, 6000+ cells per needle (200 ng 293T cells).

### ► Higher integrity and reproducibility of protein area

### ► Smaller sample size required

Suitable for rare and minimal samples: FFPE, tissue biopsies, immune cells.....

## Project workflow



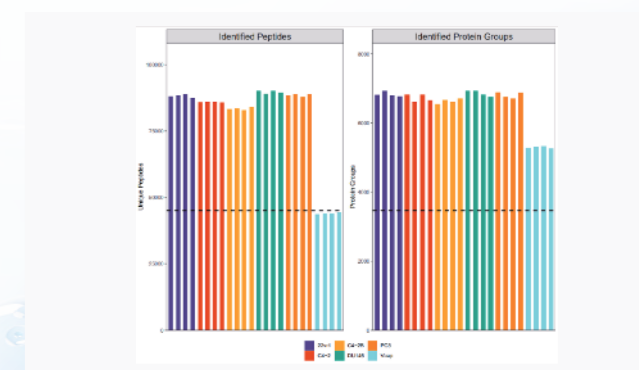
## Sample Requirements

Sample type	sample	Recommended volume
Body fluid	Plasma. serum	0.05~0.2 mL
	Urine	5~50 mL
	Cerebrospinal fluid, synovial fluid, ascites.....	0.05-3 mL
	Animal or human milk	2-50 mL
Animal tissue	Brain, heart, liver, spleen, lungs, kidneys, muscles, skin, or other tissues	15 mg~2 g
Plant tissue	Soft tissues of woody and herbaceous plants	50 mg~2 g
Cells	Cells	0.5 × 10 <sup>7</sup> ~1 × 10 <sup>7</sup>
Special sample	FFPE	5-10 μm thick, 50 mm <sup>2</sup> size, ≥10 slices
	Biopsy or puncture tissue	1 needles, visible to the naked eye, the size of millet grains

- ★ Please ensure proper pre-processing and storage methods for the samples.
- ★ Please feel free to contact us if you have any questions regarding the samples.

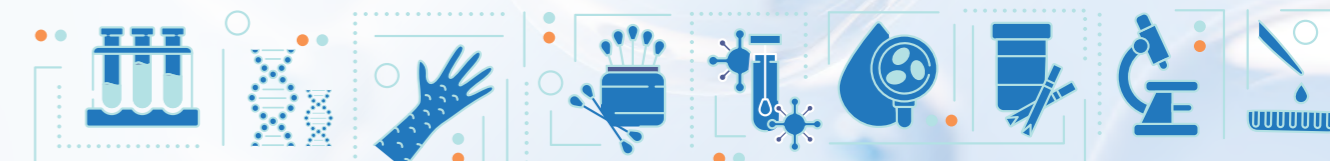
**80,000+**  
the peptides  
identification for  
samples

**6,000+**  
while the protein  
identification

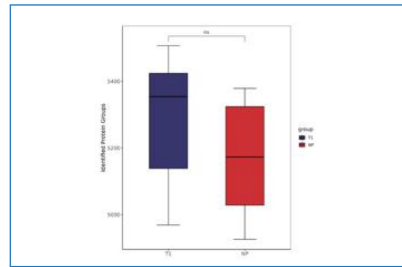


Typically, the peptides identification for samples can reach 80000+, while the protein identification can reach 6000+

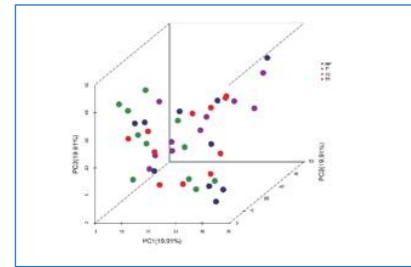
Protein and peptides identification Column chart



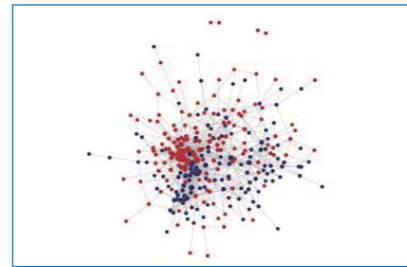
## Analysis Content Display



Identified protein box plot



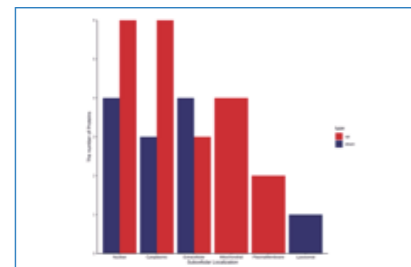
3D-PCA



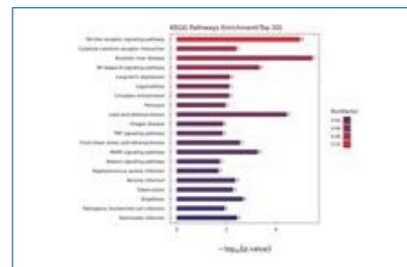
PPI network



GO circo



Subcellular localization bar plot



KEGG pathways enrichment

INOMIXO can provide a variety of bioinformatics and customized analysis services in addition to the charts mentioned above. For more analysis needs, please contact [info@inomixo.com](mailto:info@inomixo.com)



## Selected Publications

Year	Journal	Paper
2023	British Journal of Pharmacology	Icariside II preconditioning evokes robust neuroprotection against ischaemic stroke, by targeting Nrf2 and the OXPHOS/NF-κB/ferroptosis pathway
2023	European Journal of Pharmacology	Melatonin ameliorates atherosclerosis by suppressing S100a9-mediated vascular inflammation

## ABOUT US

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