SISPROT® PAC

Product introduction

The SISPROT® PAC kit is engineered for **Ultra-micro sample processing**, delivering stable performance at the **nanogram-level**. It is the ideal solution for **single-cell resolution** spatial proteomics and tissue microenvironment analysis. The system supports a wide range of inputs, specifically optimized for:

- **< 0.1 mm² & 500–100,000 cells:** Compatible with LCM tissue samples and ultra-micro cell counts, enabling single-cell resolution spatial proteomics.
- **Nanogram-level Sensitivity:** Specifically engineered for stable handling of nanogram-level samples in tissue microenvironment and exosome analysis.

1 ng	> 3,500	6h	CV < 10%	> 0.93
Protein Input	Proteins Identified (from 1ng input)	For 24 Samples	Reproducibility	Pearson Correlation

Product Features

Ultra-micro samples

1 ng Input: Capable of processing ultra-micro samples with as low as **1 ng** of protein.

High sensitivity & high coverage

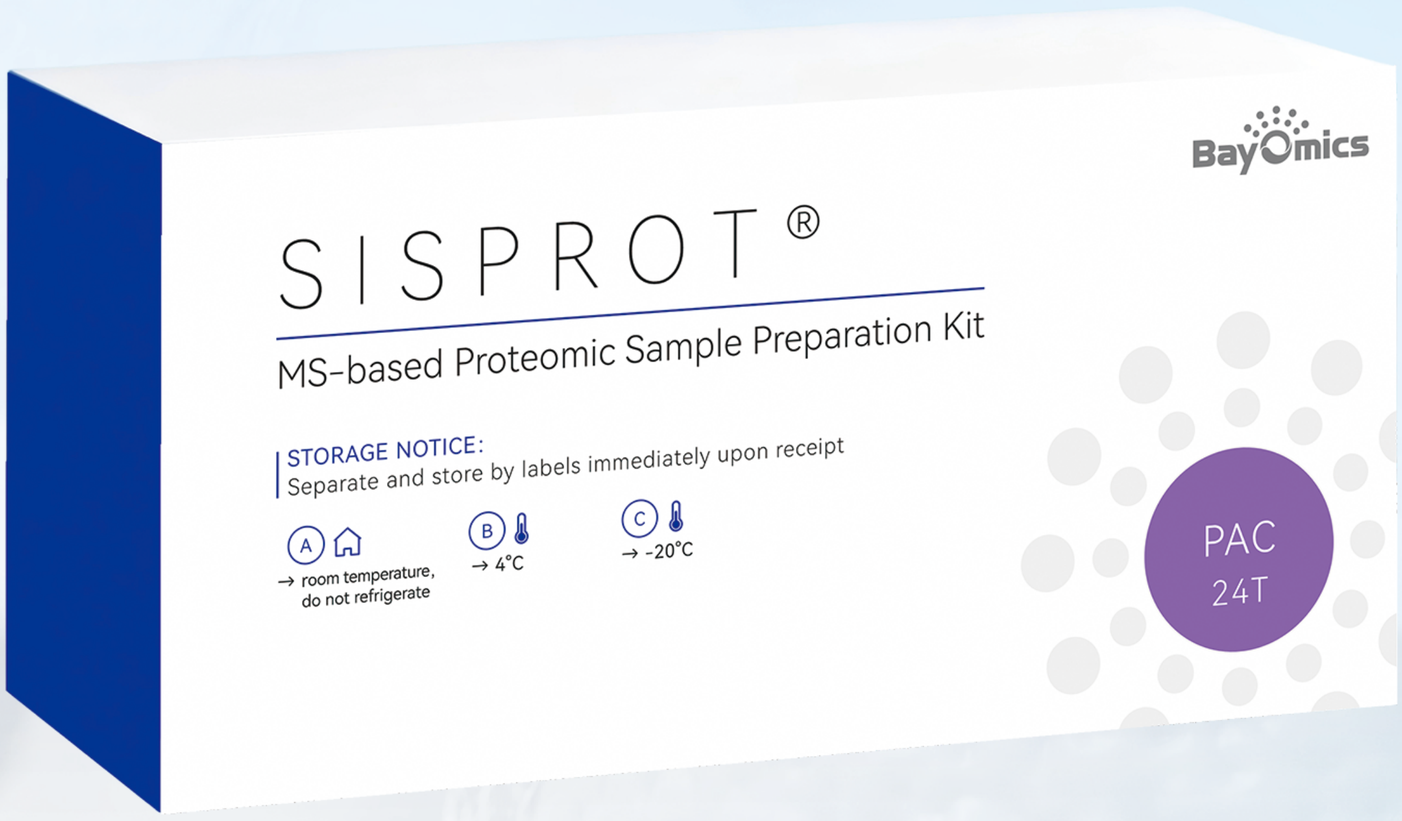
Approximately 3500 proteins can be stably detected from a 1ng protein sample

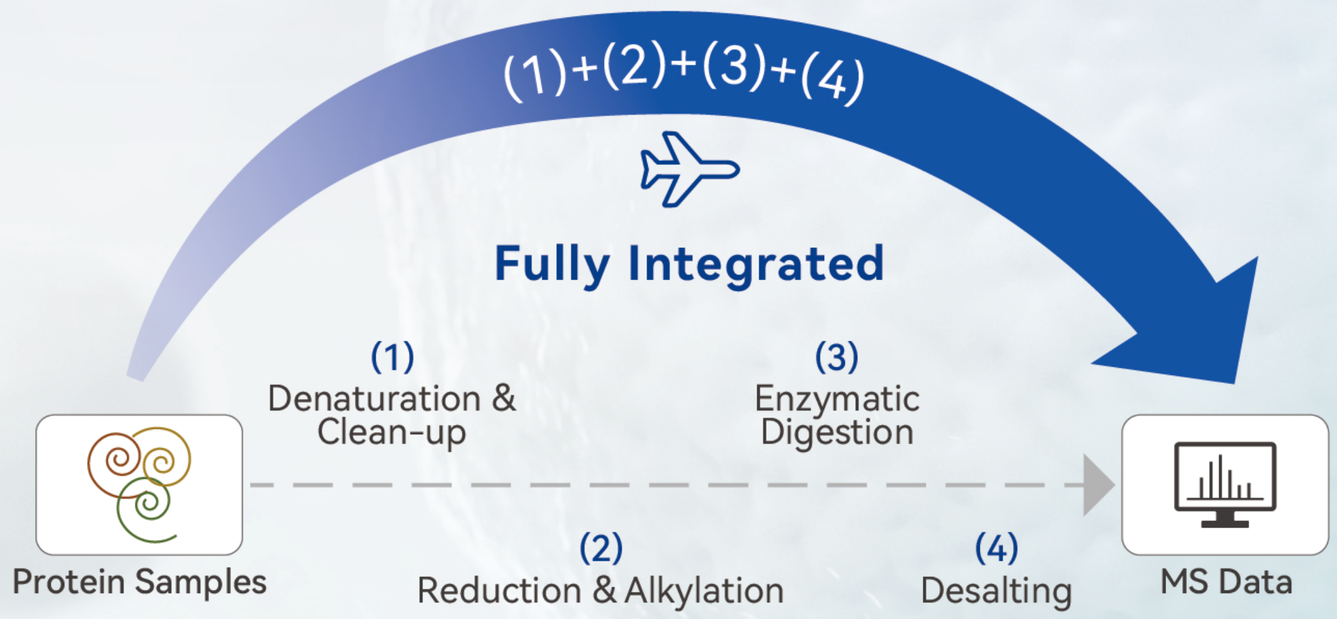
Easy operation

6 Hours/24 Samples: Integrates extraction, digestion, and desalting; pre-processing of 24 samples is completed within 6 hours.

HIGH reproducibility

CV < 10% across different sample batches, with inter-batch Pearson coefficient **> 0.93**





Materials
Linkedin

Shenzhen BayOmics Biotechnology Co., Ltd

0755-2690-7483 www.bayomics.com contact@bayomics.com

Performance Evaluation

20ng protein loading, DDA mode, **n=3 batch**.

High Sensitivity

Average identification across three sample sets exceeds **3500**

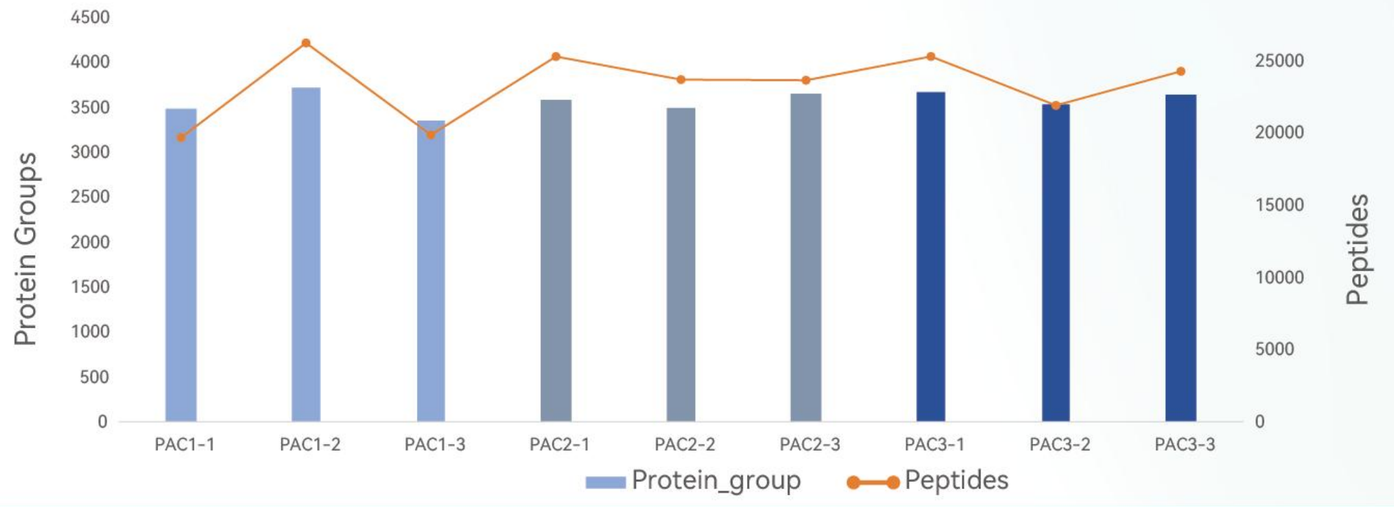


Figure 1. Statistics of 20ng peptide and protein identification

High Stability

Good reproducibility across three sample sets, with CV values all less than **10%**

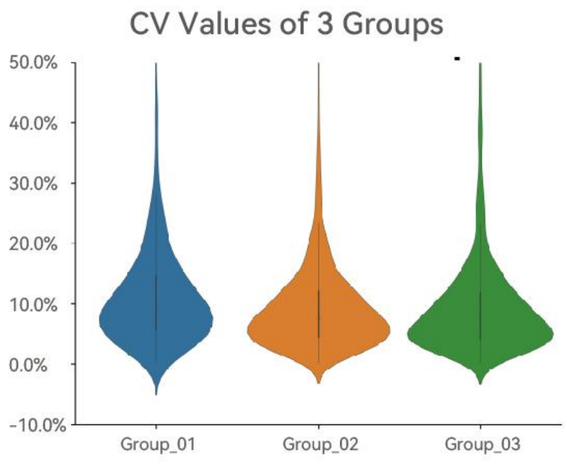


Figure 2. CV value box plot

High Repeatability

Repeatability across three sets is greater than **0.93**

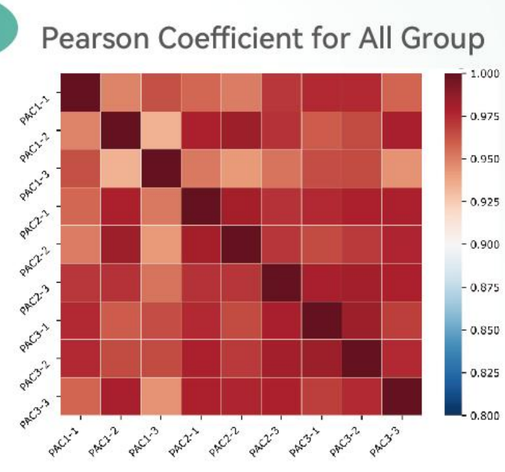


Figure 3. Repeatability heatmap

Actual Data Showcase

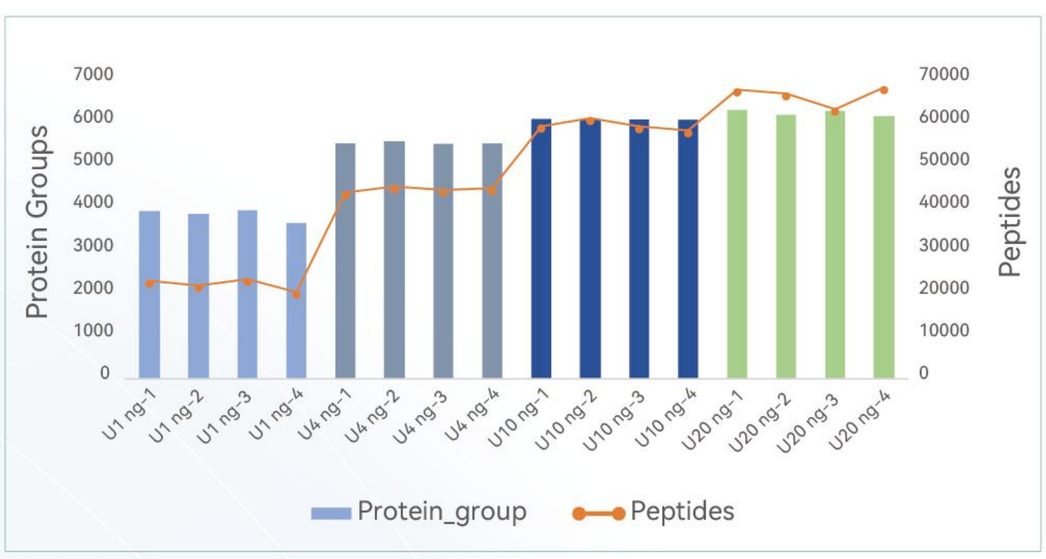


Figure 4

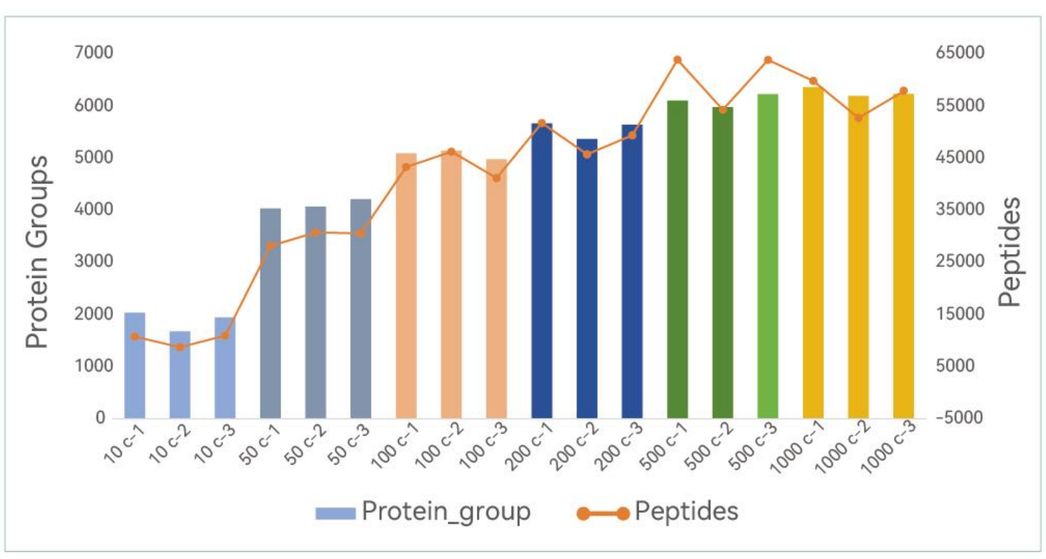


Figure 5

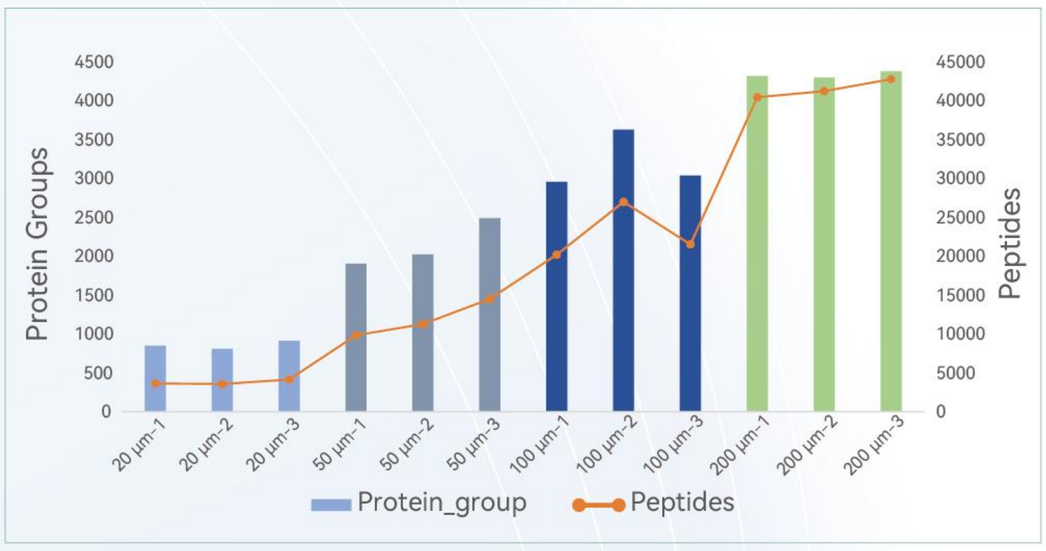


Figure 6

Figure 4. Peptide and protein identification statistics for **1~20 ng** protein samples (timsTOF Ultra)

Figure 5. Peptide and protein identification statistics for **10~1000 cell samples** (timsTOF pro)

Figure 6. Peptide and protein identification statistics for **20~200 μm** tissue sections (timsTOF pro)

Relevant Literature

- Deep spatial proteomics reveals region-specific features of severe COVID-19-related pulmonary injury, Cell Rep., 2024, 43(2):113689.
- Multimodal single cell-resolved spatial proteomics reveals pancreatic tumor heterogeneity, bioRxiv, 2023, 565590.
- Mixed-mode ion exchange-based integrated proteomics technology for fast and deep plasma proteome profiling, J. Chromatogr. A, 2018, 1564:76-84.
- 3D-SISPROT: A simple and integrated spintip-based protein digestion and three-dimensional peptide fractionation technology for deep proteome profiling, J. Chromatogr. A, 2017, 1498:207-214.
- Simple and integrated spintip-based technology applied for deep proteome profiling, Anal. Chem., 2016, 88(9):4864-71.