SISPROT® FLEX

Unrestricted Sample Types, Making Proteomics More Accessible

SISPROT® FLEX Kit Introduction

Featuring an innovative design compatible with high-concentration lysis buffers, the SISPROT® FLEX Proteomics Sample Preparation Kit enables flexible and efficient processing of diverse sample types, including tissue specimens. With its streamlined workflow, the kit delivers simplified and efficient operation, significantly reducing both sample preparation time and sample input. This groundbreaking tool enhances research productivity and provides a practical solution for micro-sample analysis, making it an indispensable tool for researchers.

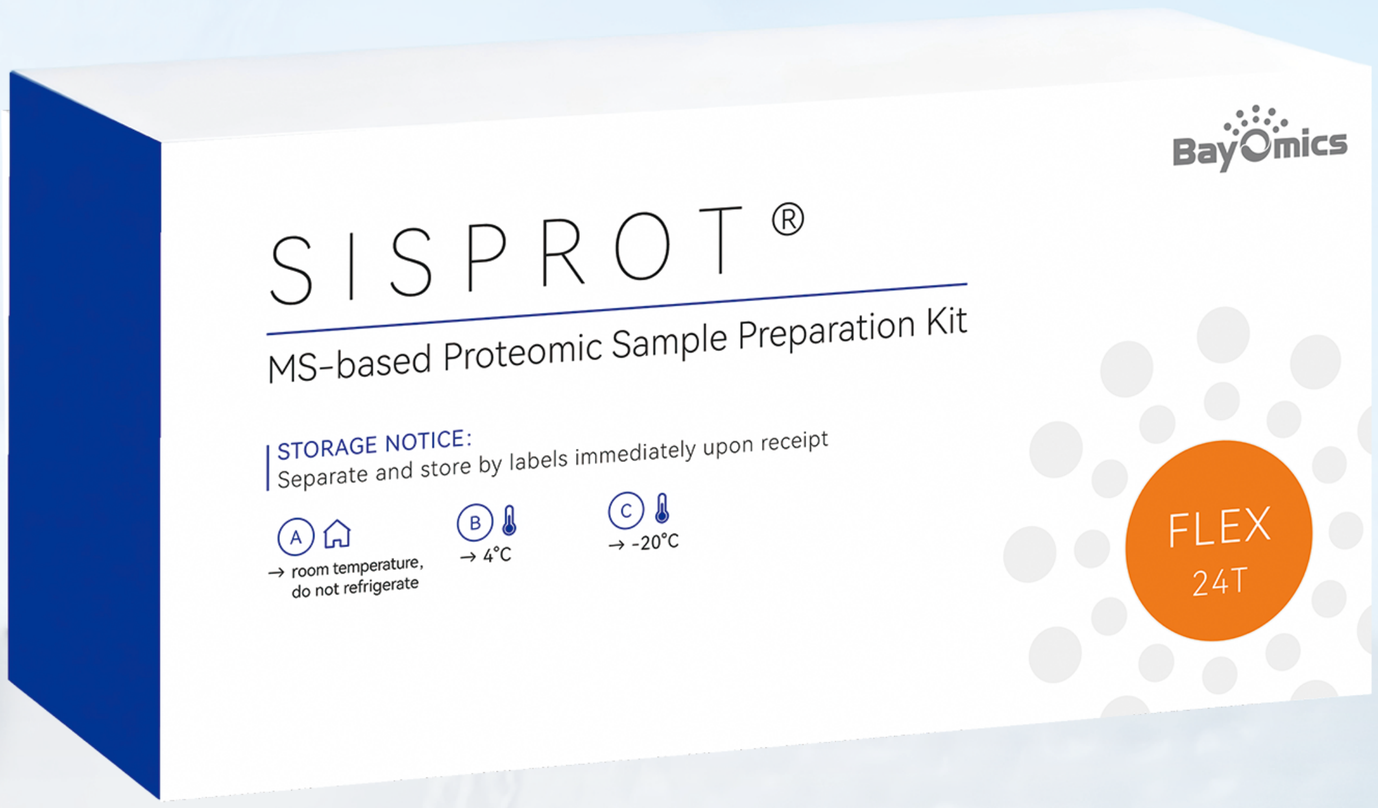
2.5 hours
Experiment duration

1–10 µg
Protein input

>7500
Proteins Identified
(from 4 µg input)

>99.99%
SDS removal rate

Product Features



Broad Sample Compatibility

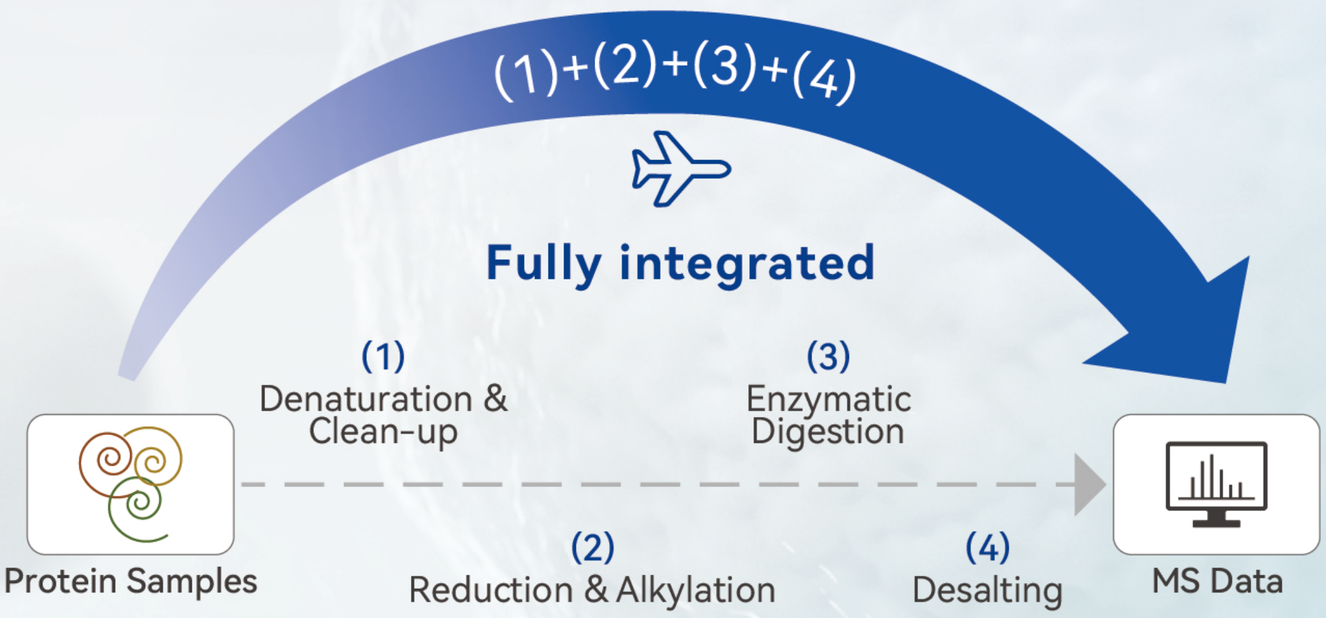
Compatible with SDS lysis buffer, applicable to various sample types with high result.

Miniaturized Samples

1– 10 µg Input: Single-run processing requires only **1–10 µg** protein from conventional samples, substantially reducing sample input while allowing multiple analyses from a single specimen.

Simplified and Efficient Workflow

2.5h experiment duration: All-in-one processing completes proteomics sample preparation within **2.5 hours**, with an intuitive protocol accessible even to novice.



Materials

Linkedin

Shenzhen BayOmics Biotechnology Co., Ltd

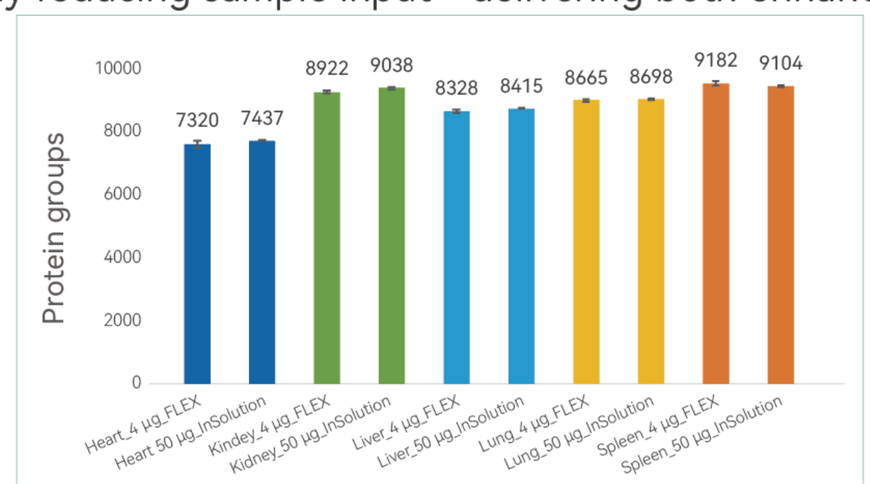
0755-2690-7483 www.bayomics.com contact@bayomics.com

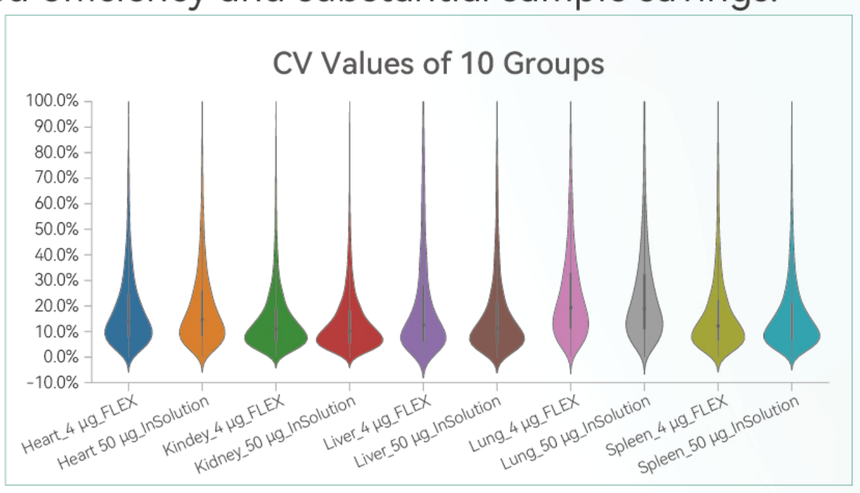
Experimental data

Miniaturized samples

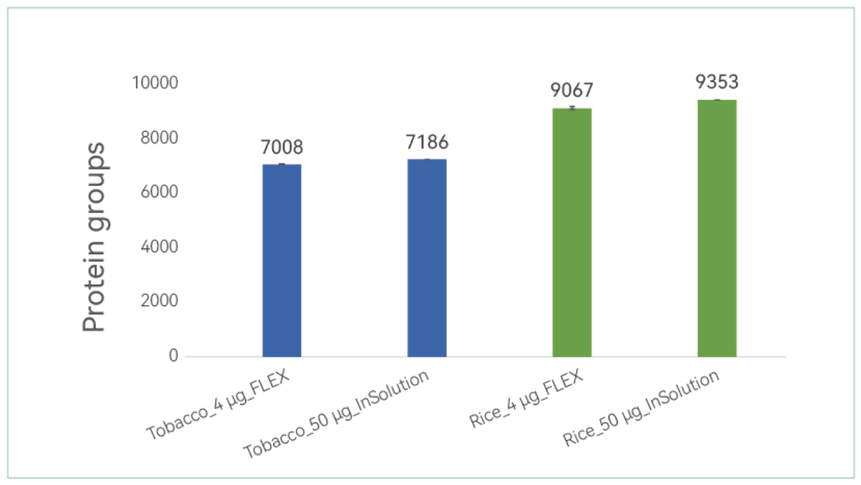
The SISPROT® FLEX Kit achieves protein identifications comparable to conventional methods across diverse tissue samples, while significantly reducing sample input—delivering both enhanced efficiency and substantial sample savings.

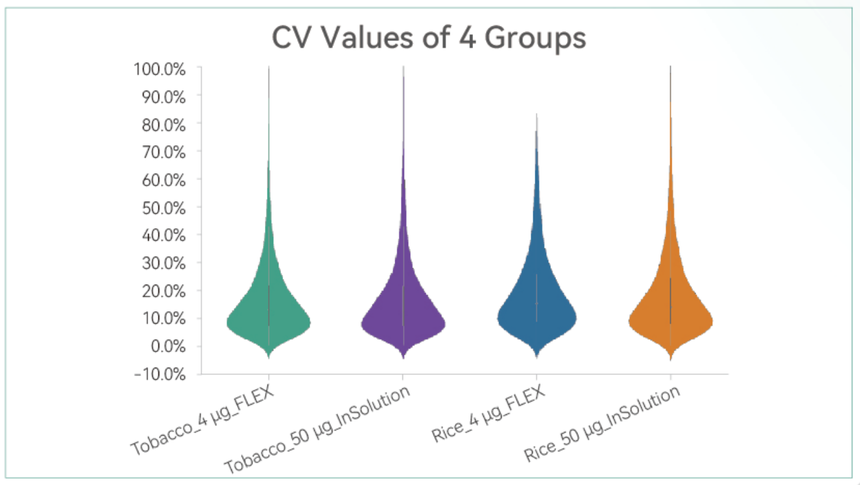
Animal tissue samples





Plant tissue samples

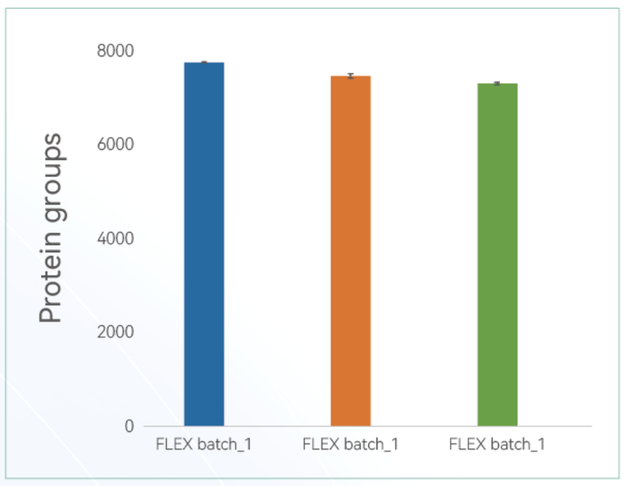


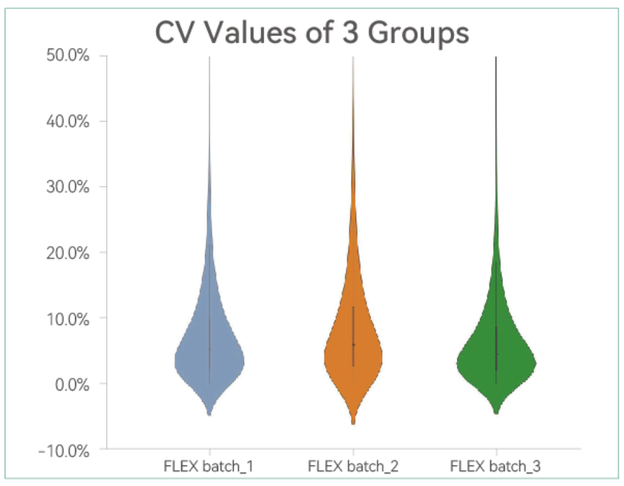


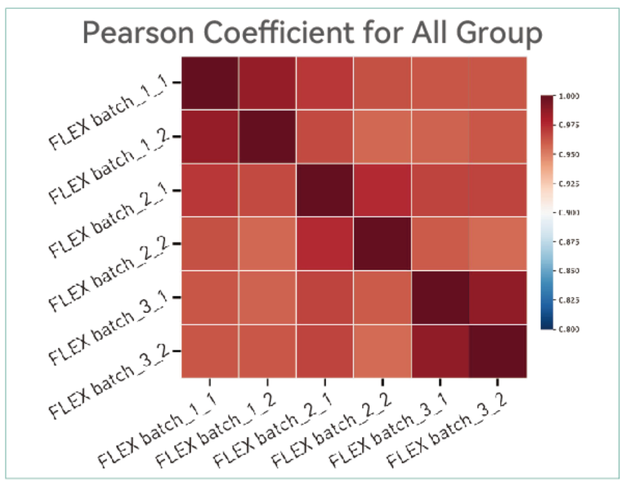
High Sensitivity and Stability

More than 7,500 proteins were reliably identified from **4 µg cell samples** using the SISPROT® FLEX Kit. The results demonstrate a **CV of <5%**, with both intra-batch and inter-batch **Pearson correlation coefficients >0.96**. These results confirm that the kit provides exceptional efficiency, sensitivity, consistency, and reproducibility.

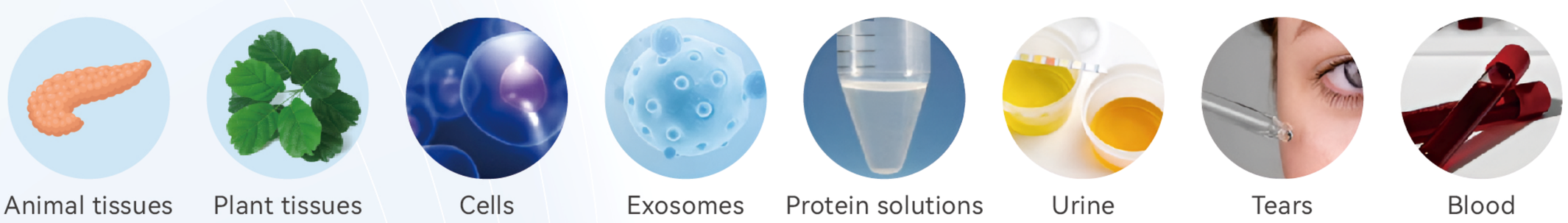
Cell Samples







Applicable sample types



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.