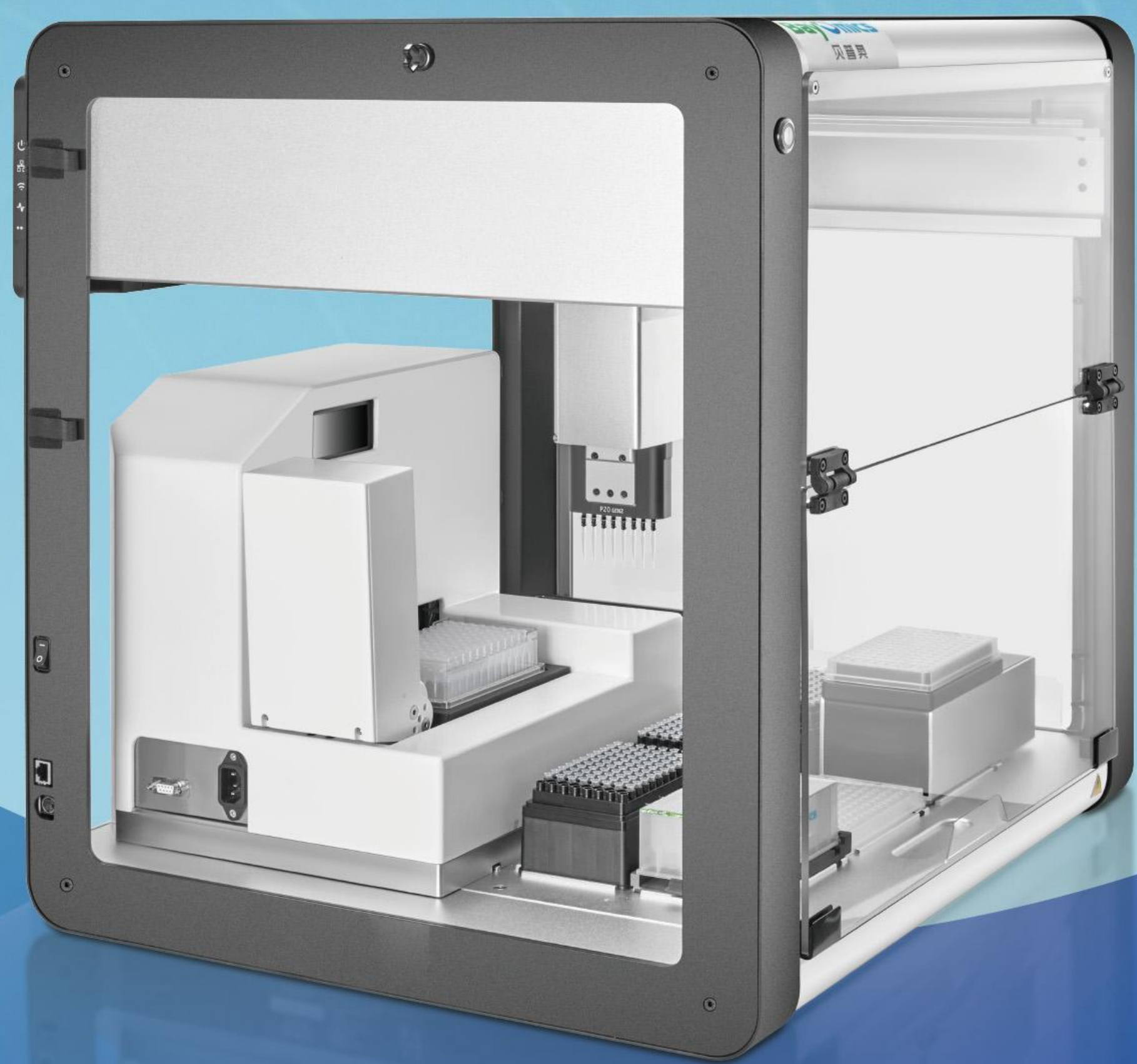


HTProX Automated Workstation for Proteomics Sample Preparation

HTProX Introduction

BayOmics HTProX and its supporting Auto SISPROT kit can achieve fully automated, standardized pre-processing of up to 96 samples with a detection limit as low as 0.1 μg within 4 hours. This includes steps such as protein enrichment, reduction, alkylation, enzymatic hydrolysis, and desalting.

Free your hands, focus on research
Efficient proteomics sample preparation accelerates new scientific discoveries.



> HTProX



Compact footprint, powerful performance



High throughput



Simple and efficient



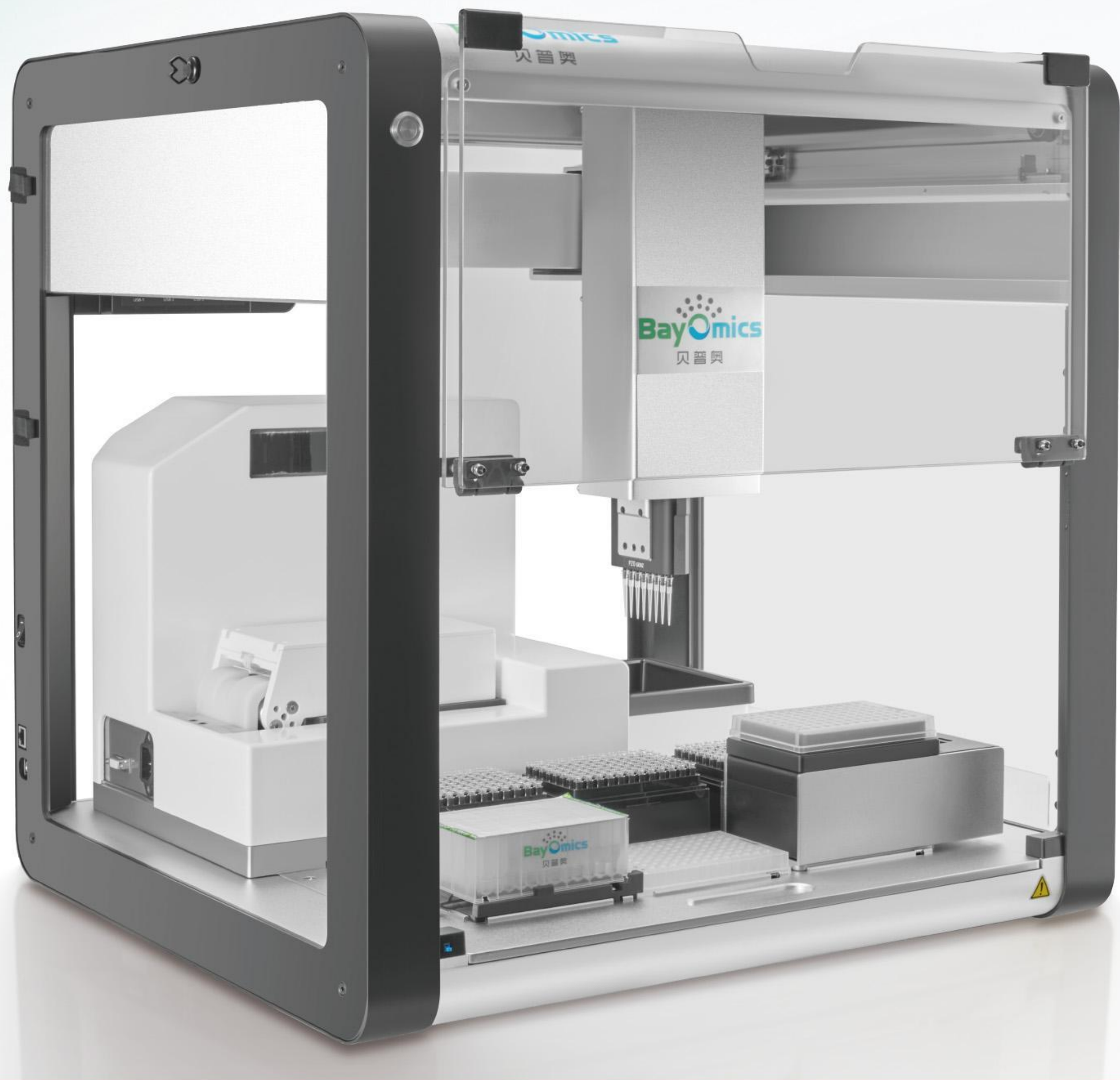
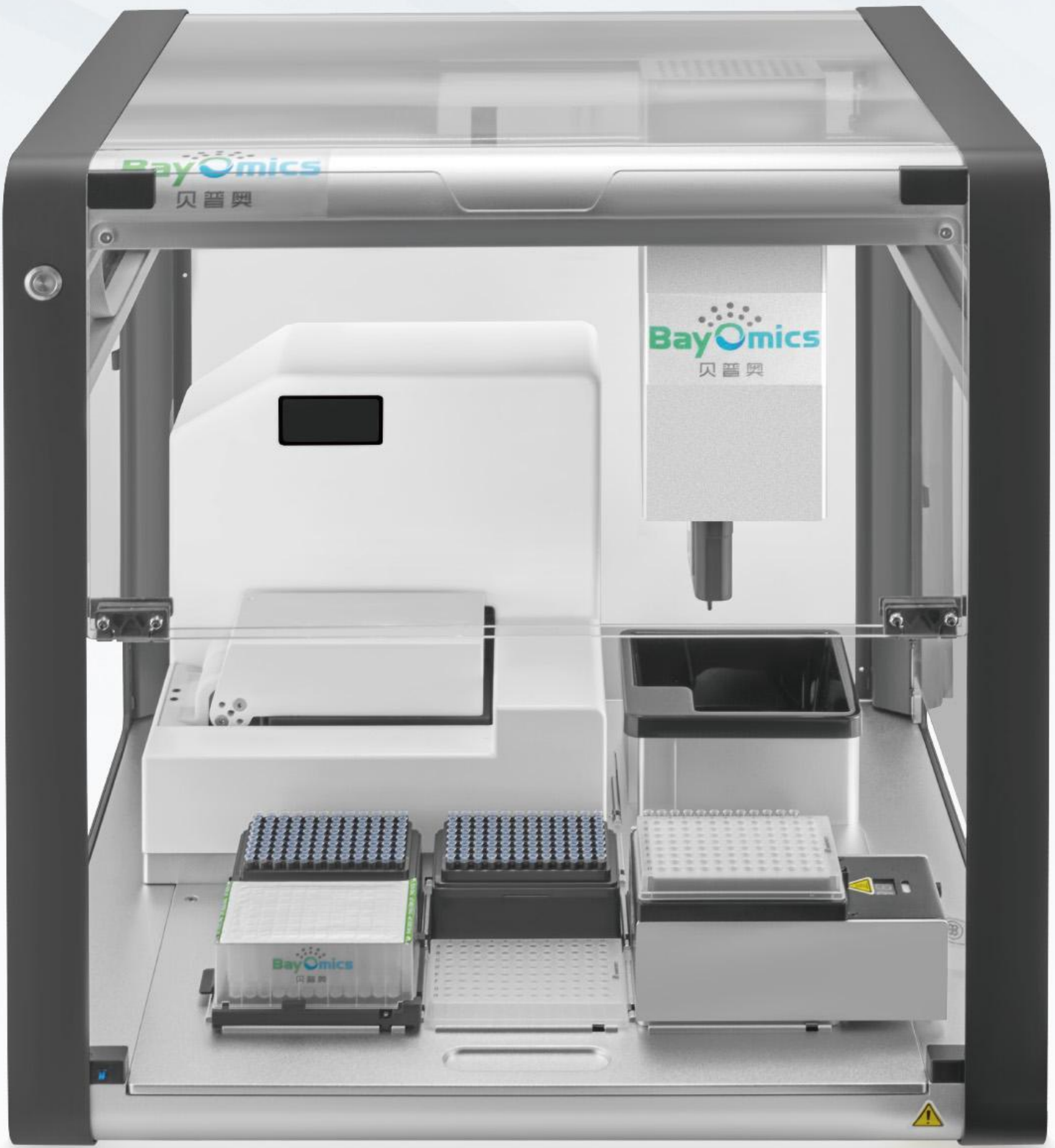
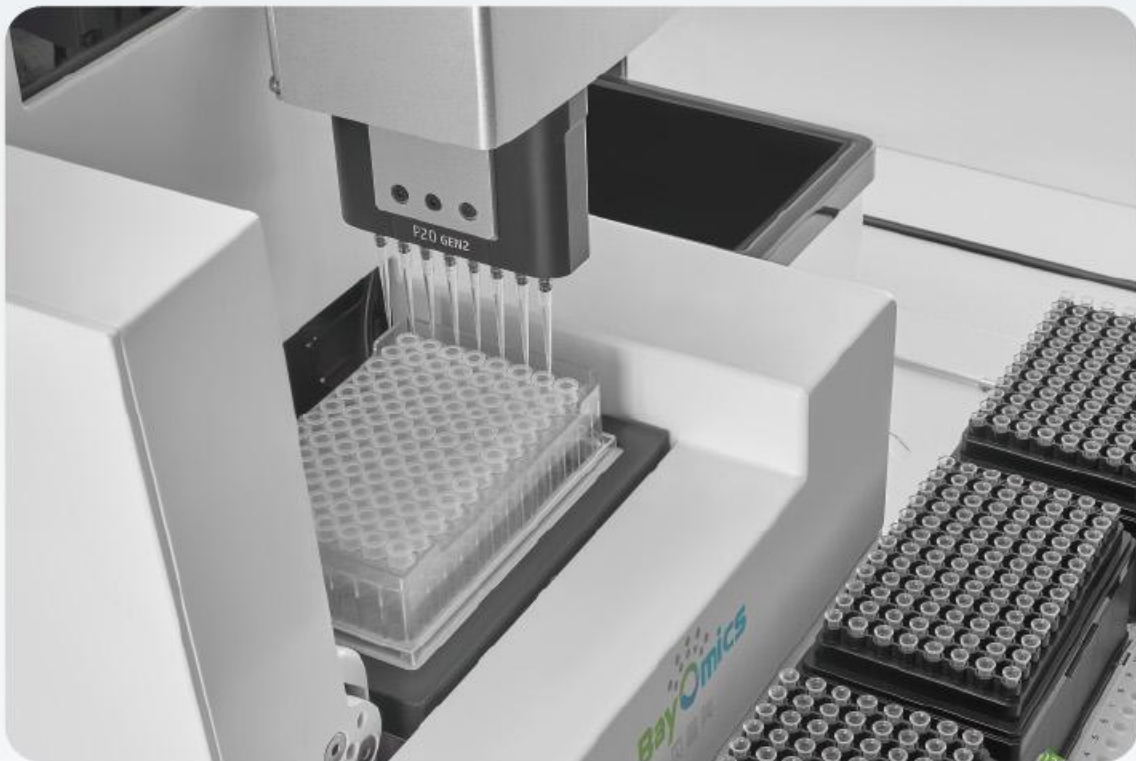
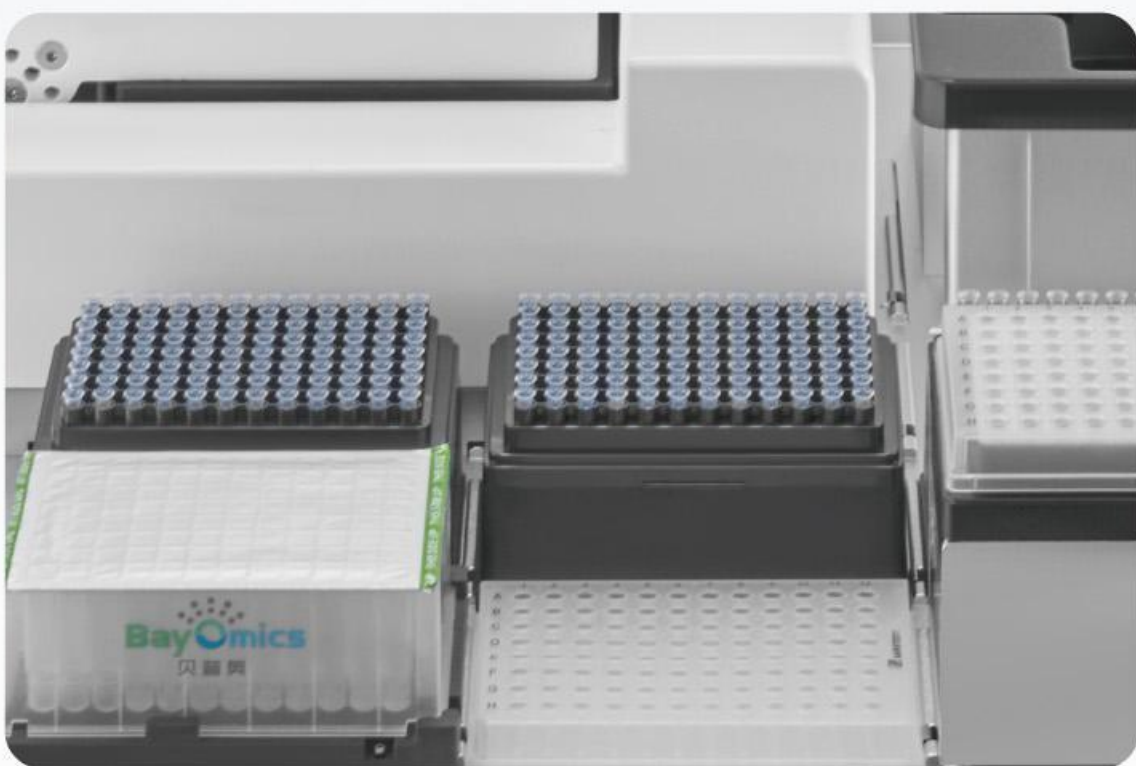
High stability



High sensitivity

HTProX: Automated Workstation for Proteomics Sample Preparation

	Initial Sample Input	Processing Time	Automation Level
Traditional Protocol	Microgram Level	> 24 Hours	Semi-Automation
BayOmics Solution	Nanogram Level	Only 3 Hours	Full Automation



01 Independent Innovation with Patented Technology

HTProX is equipped with proprietary TPP modules (Temperature-Pressure Integration) and is based on the SISPROT® patented technology. It integrates sample loading, on-bead protein digestion, and desalting steps, boasting leading-edge technology and user-friendly operation.

02 Precise Temperature Control for Stability and Reliability

The TPP module enables a constant temperature of 37°C, with a temperature accuracy of $\leq 0.5^{\circ}\text{C}$ and stability of $\leq 0.5^{\circ}\text{C}$, ensuring experimental stability and repeatability. The positive pressure module of HTPProX features a CV value of $< 7.5\%$, guaranteeing stable and uniform airflow for applications such as solid-phase extraction.

03 Low Sample Requirement for High-Efficiency Processing

As a leading domestic automated sample preparation workstation, HTPProX requires only 0.1–10 μg of sample. It is suitable for the efficient processing of both routine and trace samples.

Seven Core Product Features

04 Excellent Technical Reproducibility

- Inter-batch and intra-batch Pearson correlation coefficient: > 0.95
- Intra-batch protein quantification CV: $< 5\%$
- Peptide quantification CV: $< 10\%$
- Zero missing cleavage rate: $> 80\%$
- Alkylation efficiency: $> 99\%$

05 Leading Processing Throughput and Automation Level

HTProX completes the pre-processing of 96 samples within 4 hours. It features high automation with no manual intervention required, significantly improving processing throughput and efficiency.

06 Eco-Friendly Pioneer with 50% Reduction in Waste

While maintaining high processing efficiency, HTPProX generates only 1/10 of the waste compared to similar products, leading the new trend of eco-friendly scientific and technological innovation.

07 Open-Source Software for Unlimited Expansion

HTProX features open-source software with reserved empty slots, allowing users to customize workflows to meet personalized research needs with strong scalability.

Applicable Sample Types

