

SISPROT® PlasmaG

Breaking the Low-Abundance Barrier to Unlock Comprehensive

>Plasma Data

Plasma proteomics is pivotal to clinical diagnostics, therapeutics, and biomarker R&D. Yet interference from high-abundance proteins and limited throughput render conventional methods inadequate for large-cohort studies. Powered by charge-selective magnetic microsphere enrichment and seamlessly integrated with a fully automated sample preparation workstation, the BayOmics SISPROT® PlasmaG Kit achieves 5,000+ protein groups identifications from fresh plasma—delivering a standardized, high-depth, and highly reproducible solution for large-scale cohort studies.

>Product Features

5000+

Proteins Identified
from Fresh Plasma

99%

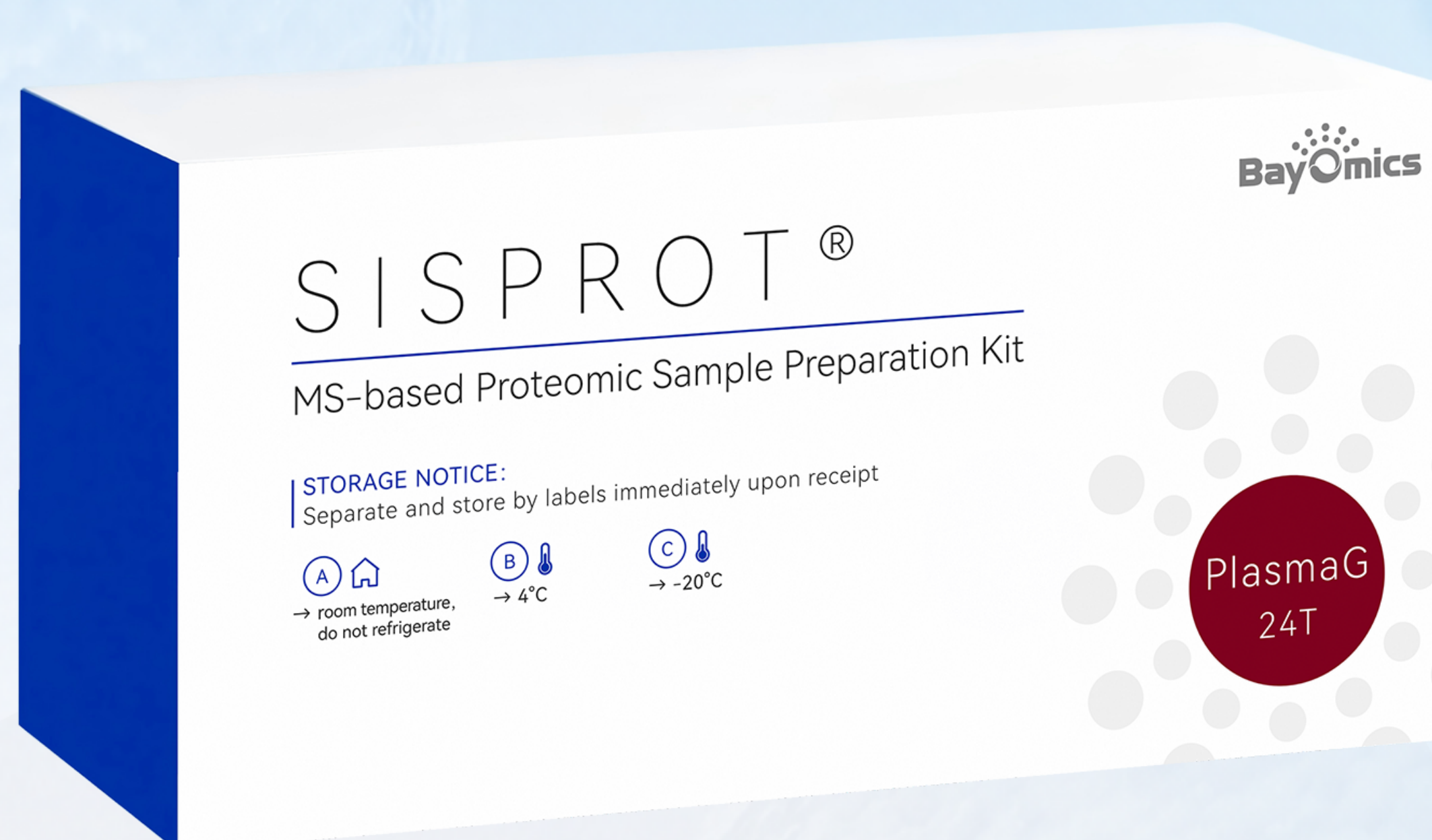
Efficient Removal of
High-Abundance Proteins

3

Contamination indices
superior to competitors

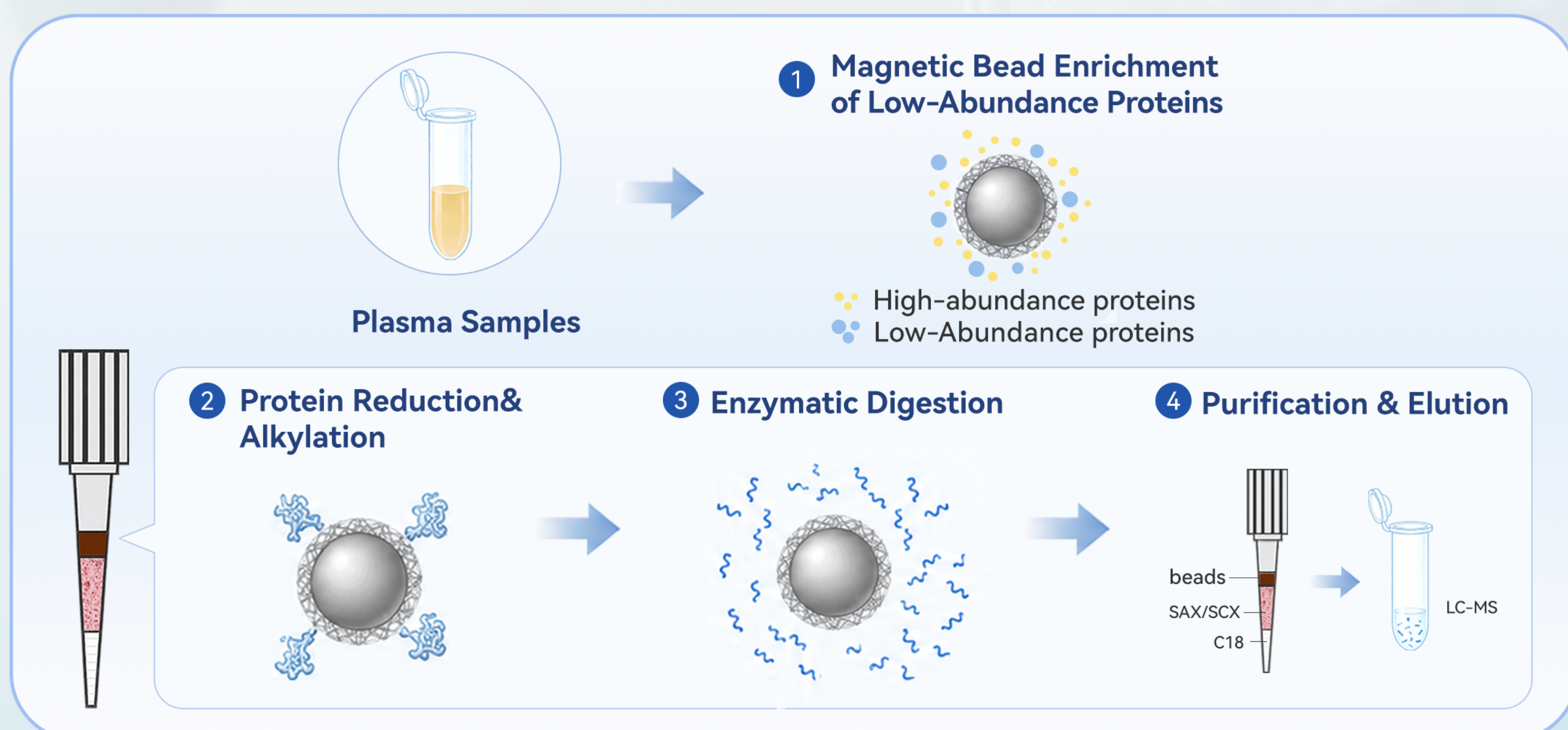
$r > 0.93$

Inter-Batch Pearson Correlation



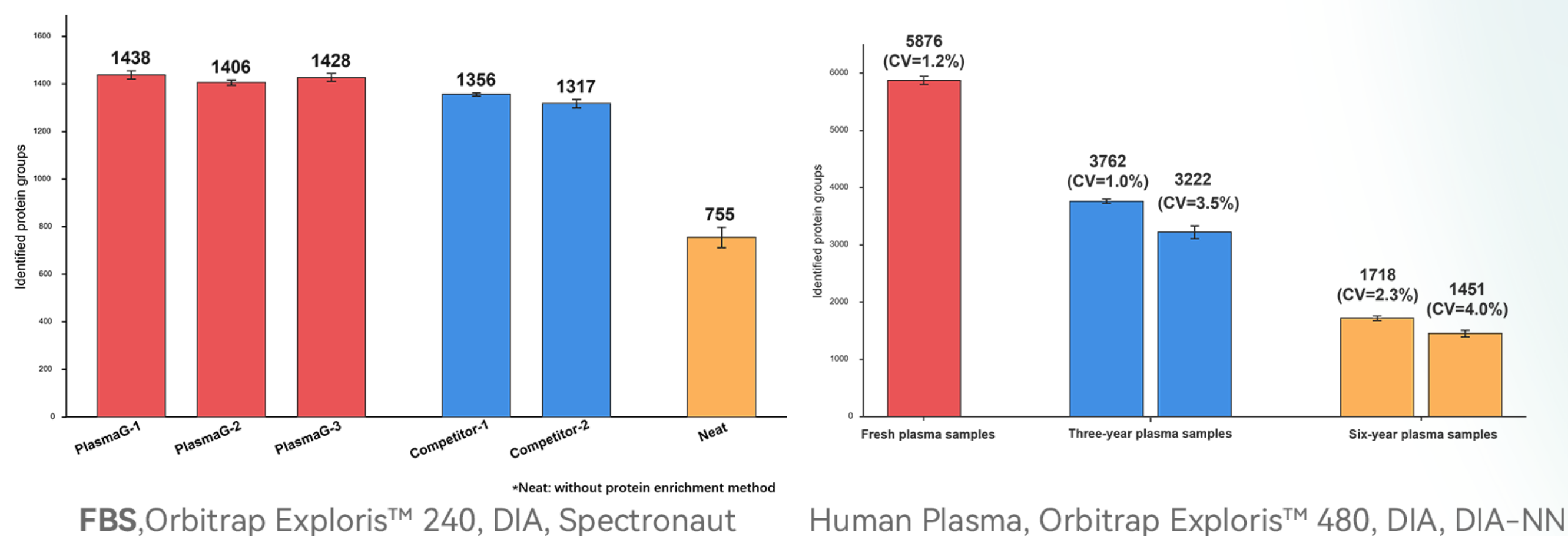
>Workflow

Leveraging magnetic microsphere-based enrichment, the workflow selectively captures low-abundance plasma proteins. On-bead digestion is performed throughout and integrated with our proprietary SISPROT® sample preparation technology, consolidating pre-enrichment, reduction, alkylation, digestion, and desalting into a single streamlined process to deliver purified peptides.



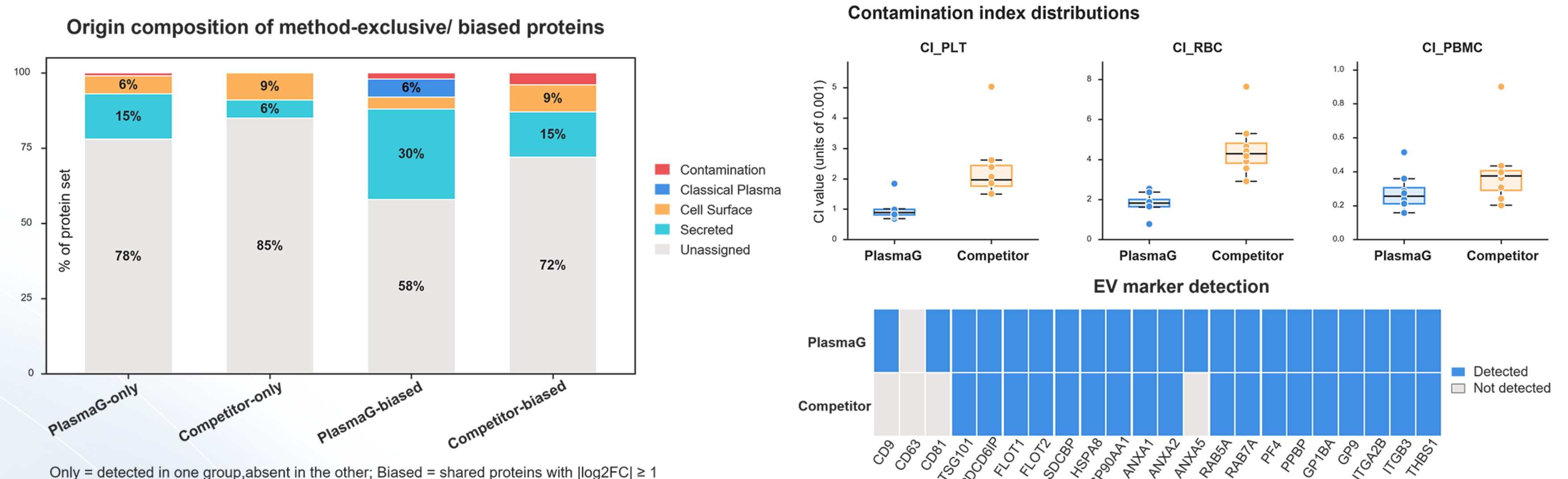
> Broad Proteome Coverage

- ~**100%** higher protein groups identifications than conventional methods;
~**10%** higher than competing products.
- **5,000+** proteins from fresh plasma; **3,000+** proteins after 3 years of frozen storage.



> Low Contamination and High Functional Protein Enrichment

- The detection of secreted proteins and extracellular vesicle (EV) markers is **far superior to that of competing products**.
- Contamination indices for platelets (PLT, CI < 0.009), red blood cells (RBC, CI < 0.050) and peripheral blood mononuclear cells (PBMCs, CI < 0.005) **are below safety thresholds and outperform competing products**. This minimizes background interference from contaminating proteins at the sample-preparation stage, ensuring authentic and reliable data.

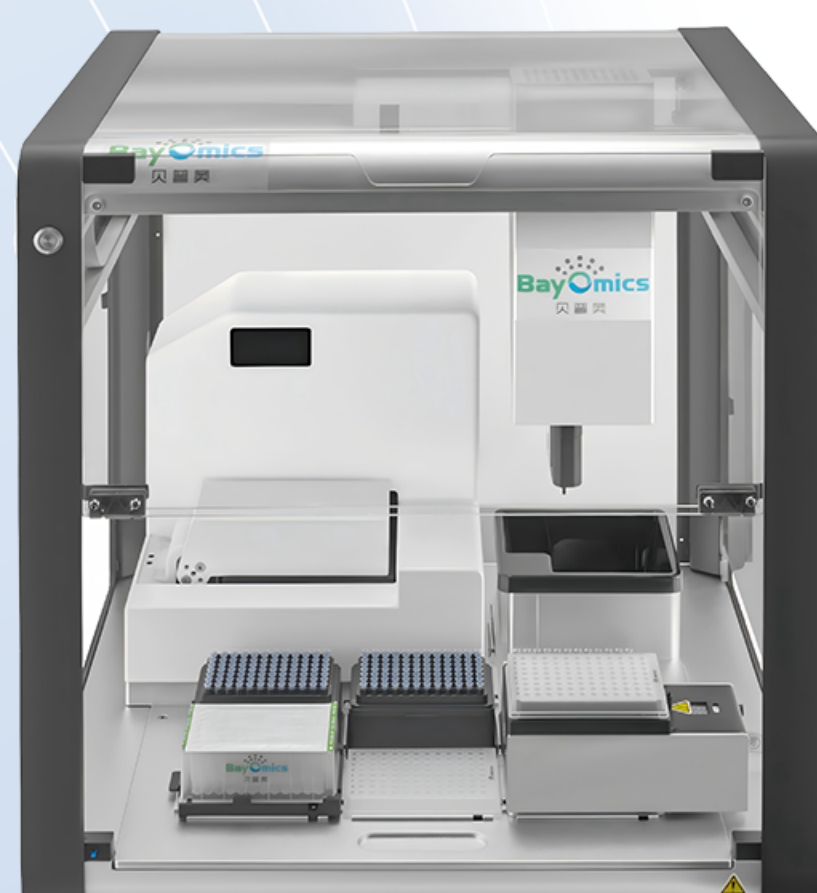
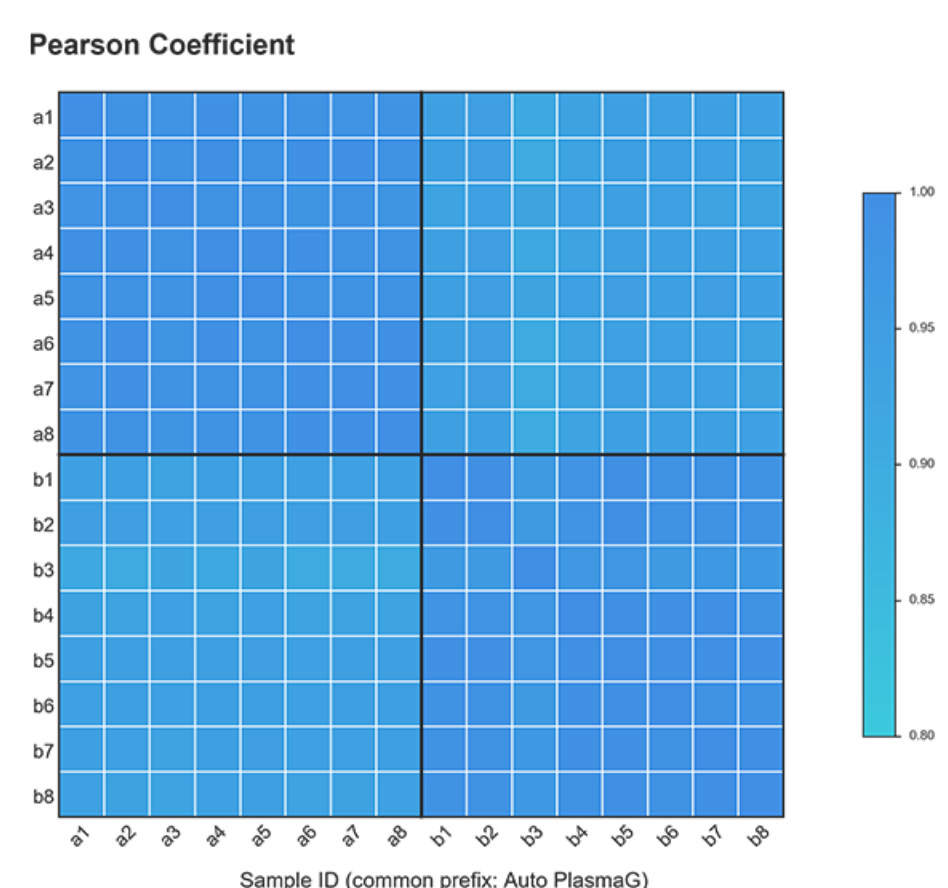


Human Plasma, Astral zoom, DIA, Spectronaut

*Contamination index (CI): calculated using the quantitative formula proposed by Geyer et al. (2019, EMBO Molecular Medicine).

> High Stability and Reproducibility

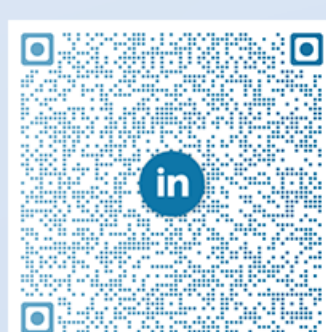
- Paired with the **HTProX automated sample preparation system** for fully automated 96-sample processing—scalable to thousand-participant cohorts.
- Excellent quantitative reproducibility: **intra-batch $r > 0.96$; inter-batch $r > 0.93$** .



FBS, Orbitrap Exploris™ 240, DIA, Spectronaut



Materials



LinkedIn

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