BIOGNOSYS
GROUP

iST Technology

iST-S High Throughput Sample Preparation for Low Input Proteomics

- **Affordable sample preparation** with optimized lysis and digestion, delivers reliable performance for **1–10 µg protein inputs** from cells and pelleted proteins.
- **Built on proven *iST* technology**, enables deep proteome coverage & low variability in the low-input range.
- **Standardized 96x plate-based workflow** supporting high-throughput applications and seamless integration into lab automation.
- **Ideal for** compound screening, chemo-proteomics, and large-scale cell profiling.

01 **Sample Collection**
Cells, Pelleted Protein (1–10 µg)

02 **Sample Preparation**
iST-S Kit

03 **LC-MS Analysis**
timsTOF HT

04 **Data Analysis**
Spectronaut 21

Figure 1. Workflow overview for low-input proteomics. *iST-S* sample preparation is combined with *Bruker's timsTOF HT* mass spectrometer and *Biognosys' Spectronaut 21* software package.

Protein Preparation Solutions

iST-S

Ramp-up Comparison Study

A ramp-up comparison experiment using *iST-S* and *standard iST* (Std-iST) kits across 1–10 µg protein input from the HeLa cells, analyzed on a *timsTOF HT* (40 SPD method).

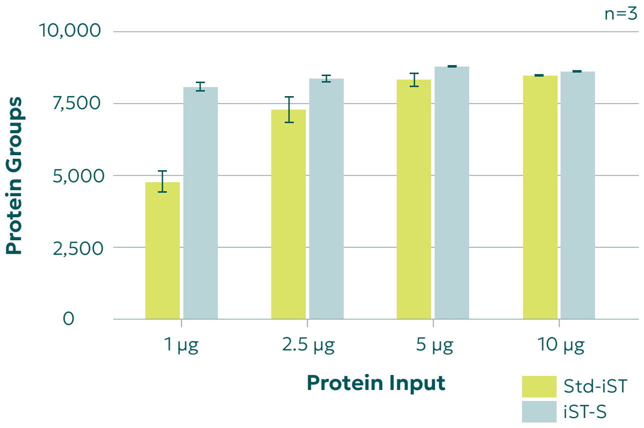

Figure 1. Comparison of protein groups identified with *Std-iST* and *iST-S* across 1–10 µg protein inputs.

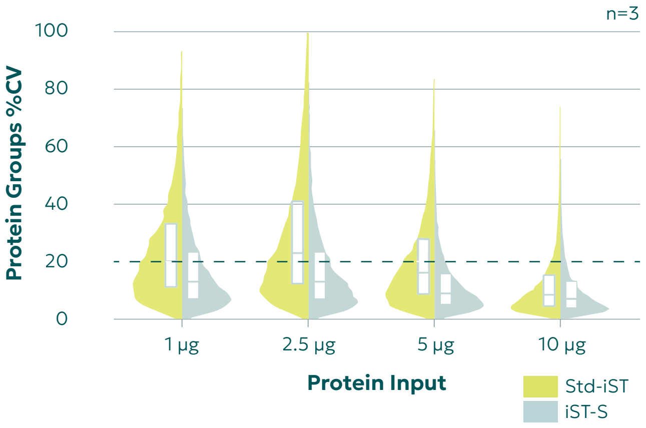

Figure 2. Protein CV distributions for samples processed with *Std-iST* and *iST-S* workflow across 1–10 µg protein inputs.

iST-S delivers higher protein IDs from the low-input samples

- Deep proteome coverage across tested low inputs.
- Designed for low-input, scalable proteomics studies.

iST-S shows the reduced variability in the low-input samples

- Consistent quantitative performance across low-input samples, the majority of protein CVs below 20%.
- Suitable for high-throughput screening and longitudinal studies.

Learn more
about iST-S

biognosysgroup.com

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