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S-Trap™ Turbo: From Sample Prep to Analysis in Record Time

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INTRODUCTION

Recent advancements in proteomics enable rapid sample identification and quantification; this necessitates improved and simplified sample preparation workflows enhance throughput and robustness. The widely used S-Trap™ system has standardized sample preparation. Building on this, we introduce a further streamlined workflow with S-Trap™ Turbo to both simplify and speed up sample preparation **(Fig. 1).**

Workflow Simplification: S-Trap™ plates and columns efficiently capture proteins while removing various contaminants like buffers, salts, reducing and capping reagents, detergents, and small molecules. These impurities interfere with protein assays, digestion, and MS analysis.

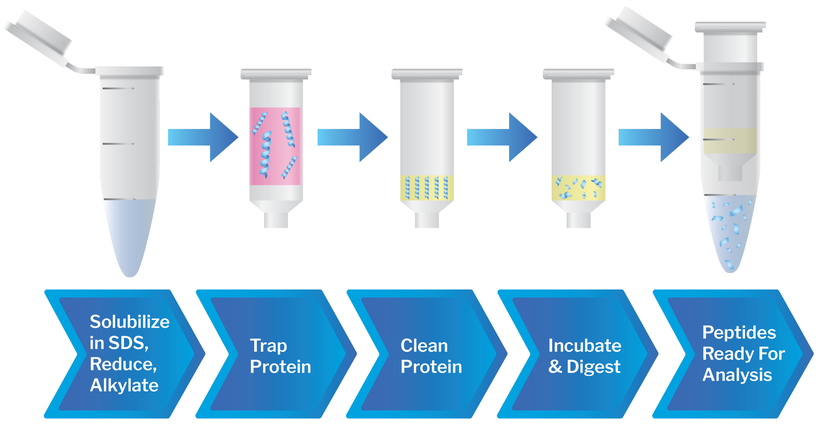

Fig. 1

The S-Trap™ Turbo 96-Well Mini Plate improves on the original S-Trap™ by employing polymeric materials with over 100 times greater surface capture density. The enhanced binding efficiency reduces the volume of capture matrix required and results in small elution volumes. Consequently, additional concentration steps are unneeded: elute and shoot! The S-Trap™ Turbo matches sample prep speed to new, very fast detection methodologies.

S-TRAP Turbo

METHODS

High-resolution mass spectrometry (Thermo Orbitrap Astral) was used to analyze samples. BCA and fluorescent assays were additionally used to assess sample yield and quality.

Samples of various hydrophobicities were evaluated using S-Trap™ Turbo 96-Well Mini Plate: rabbit tissue acetone powders including brain (most hydrophobic), muscle (moderately hydrophobic), and thymus (least hydrophobic).

Protein samples were prepared using S-Trap™ Turbo 96-Well Mini Plates following standard protocols for lysis, reduction, alkylation, denaturation, binding, and washing. A modified tryptic digestion and elution protocol enabled > 70% peptide recovery in a single low-volume elution step, eliminating the need for lengthy drying and significantly reducing reagent use.

RESULTS

Recovery of the S-Trap™ Turbo 96-well Mini Plate was evaluated using 60 µg input protein. A single 30 µL elution recovered > 70% of total peptides, 40% more recovery than standard S-Trap™ plates which need concentration prior to LC-MS. Workflows are streamlined with minimal handling and sample volumes **(Fig. 1, 2)**.

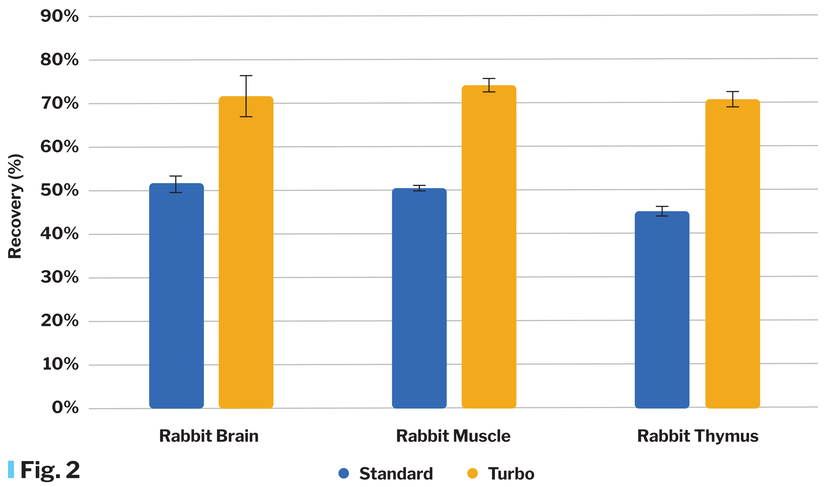

Fig. 2

Additionally, the S-Trap™ Turbo consistently produced a greater number of peptide and protein identifications. These gains were achieved using a single low-volume, dry-down free elution. The S-Trap™ Turbo format significantly reduces hands-on time and total workflow duration by approximately half while delivering equal or higher-quality data **(Fig. 3, 4)**.

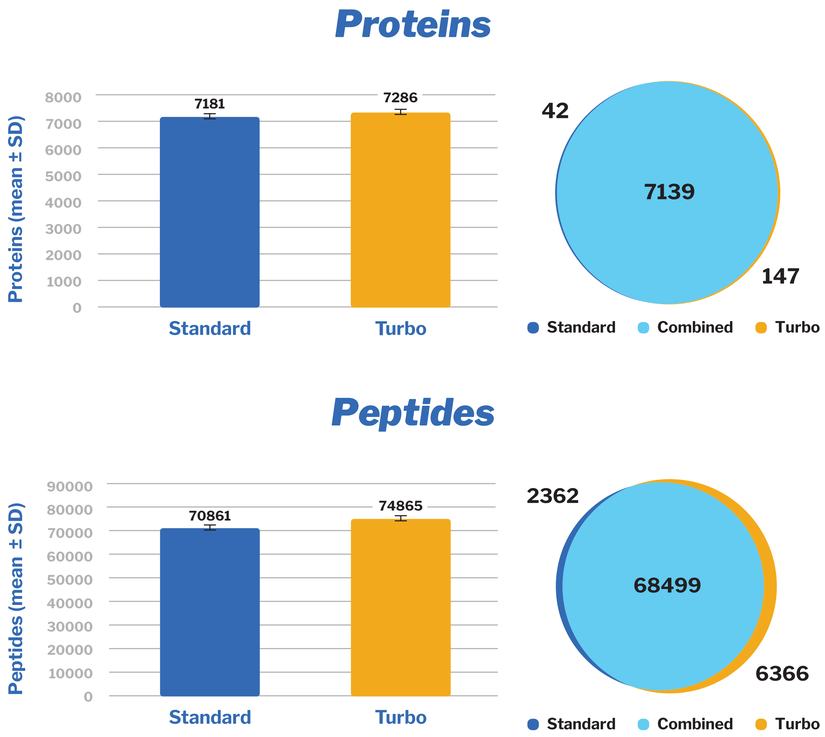

Fig. 3

CONCLUSIONS

The S-Trap™ Turbo 96-well Mini Plate provides the same high-quality data as the standard S-Trap with a significant reduction in the time from sample receipt to analysis readiness. Its time efficiency, combined with improved accuracy and throughput make it perfect for high-throughput proteomics analysis **(Fig. 3, 4)**.

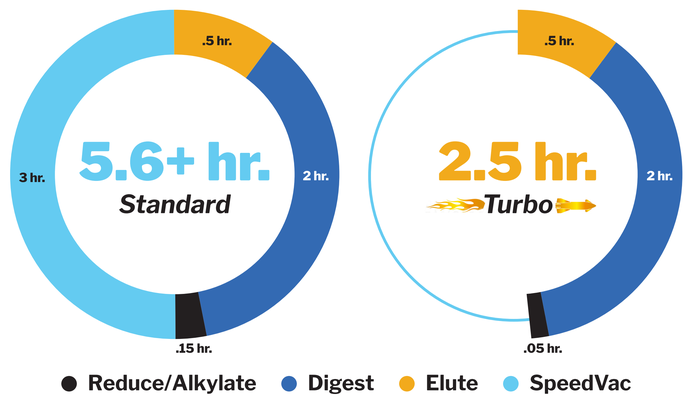

Fig. 4

Enhanced Efficiency & Time Savings: The S-Trap™ Turbo 96-well Mini Plate format streamlines sample preparation and reduces total processing time from > 5 hours to ~2.5 hours including digestion. A single elution replaces multiple high-volume steps, removes the need for concentration, minimizes sample handling, decreases opportunities for sample loss, and affords higher throughput. Despite the shorter workflow, analytical results remain comparable or superior to the standard format **(Fig. 4).**

Immediate Analysis Readiness: The S-Trap™ Turbo generates highly concentrated peptides in one low-volume elution, eliminating the need for SpeedVac concentration and allowing direct LC-MS injection. Removing this bottleneck simplifies processing and accelerates turnaround time without compromising performance.

Optimal Recovery: The S-Trap™ Turbo delivers high peptide recovery (> 70% in a single elution), reducing or eliminating the need for additional elution steps. Most sample material is captured immediately, enhancing digestion efficiency and supporting strong downstream detectability.

Sample Integrity: High recovery is maintained across tissues of varying hydrophobicity, preserving balanced representation of both hydrophilic and hydrophobic peptides. This broad capture performance ensures confident protein identification and quantification across complex sample types.

Broad Sample Compatibility: Robust performance was demonstrated across multiple sample kinds spanning diverse hydrophobicities. Similar proteome coverage with increased identifications highlights the versatility of the S-Trap™ Turbo format for diverse sample sources.

High-Throughput Ready: The S-Trap™ Turbo workflow integrates seamlessly into 96-well processing and automated platforms. Its streamlined format supports efficient processing of large sample cohorts to make it well-suited for discovery studies, comparative screens and other high-demand proteomic applications.

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