

# INTRODUCING DiscoveryEdge™ 600

The most comprehensive panel of  
internal standards for multiplexed  
absolute protein quantification

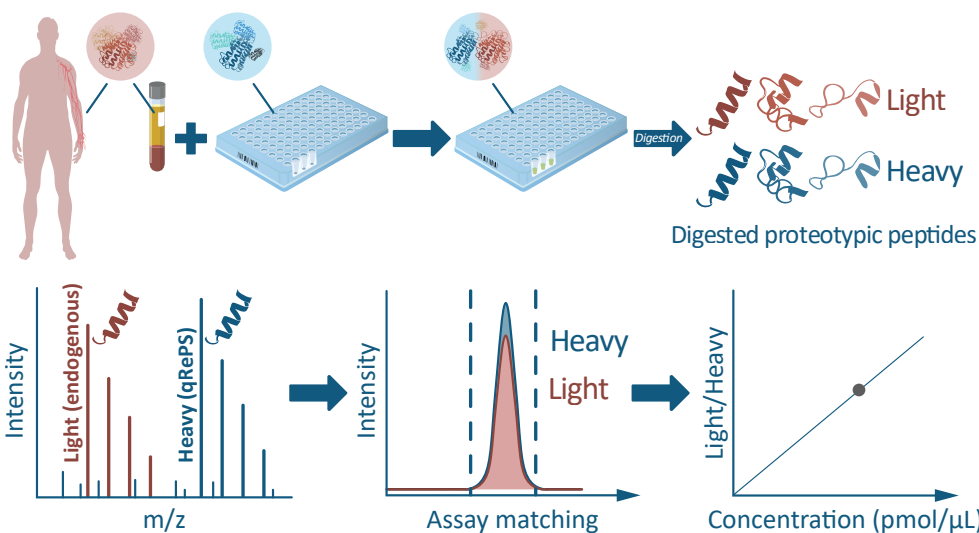


# THE CONCEPT

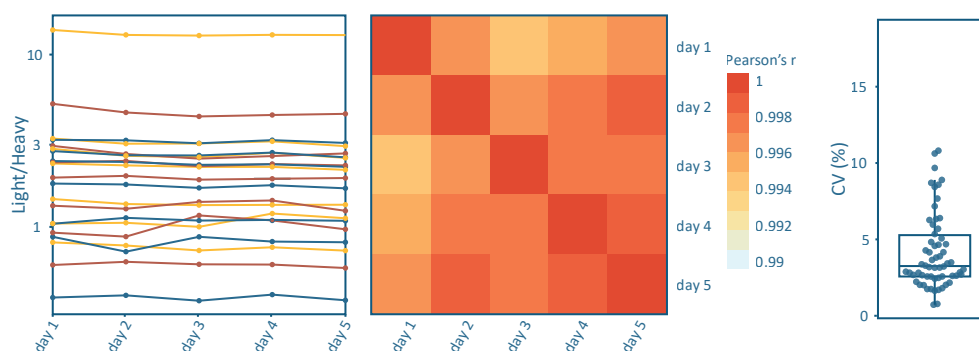
ProteomEdge is bringing precision into absolute quantification of blood plasma proteins with multiplex panels of qRePS (Quantitative Recombinant Protein Standards). The enzymatically cleavable internal standards are Lys and Arg <sup>13</sup>C and <sup>15</sup>N metabolically labeled proteins designed to serve as internal standards in MS-based proteomics experiments.



The products are designed for analysis of an equivalent of 1  $\mu$ L blood plasma and provided pre-aliquoted and dried in a 96-well plate for easy handling and seamless absolute quantification. Each well in the plate includes standards for all targets in the panel. Add your diluted plasma samples on top of the dry panel as the first step of sample preparation, followed by standard proteomics workflow and digestion ensuring accurate and precise quantification.



The qRePS are an excellent tool for precise protein quantification in liquid biopsies and other biological samples using MS as a read out. The sample preparation versatility and analysis allow for targeted and untargeted modes of operation such as SRM, PRM, DIA and DDA.



Day-to-day variability in absolute quantification using ProteomEdge's proprietary analysis platform.

# DiscoveryEdge™600

Includes 620 protein standards generating 6,000+ verified peptides, enabling exceptional depth in multiplexed absolute quantification of plasma proteins.



Drug Targets



Cancer Markers



Inflammation & Immune Response



Cardiovascular Health



Clinical Diagnostics



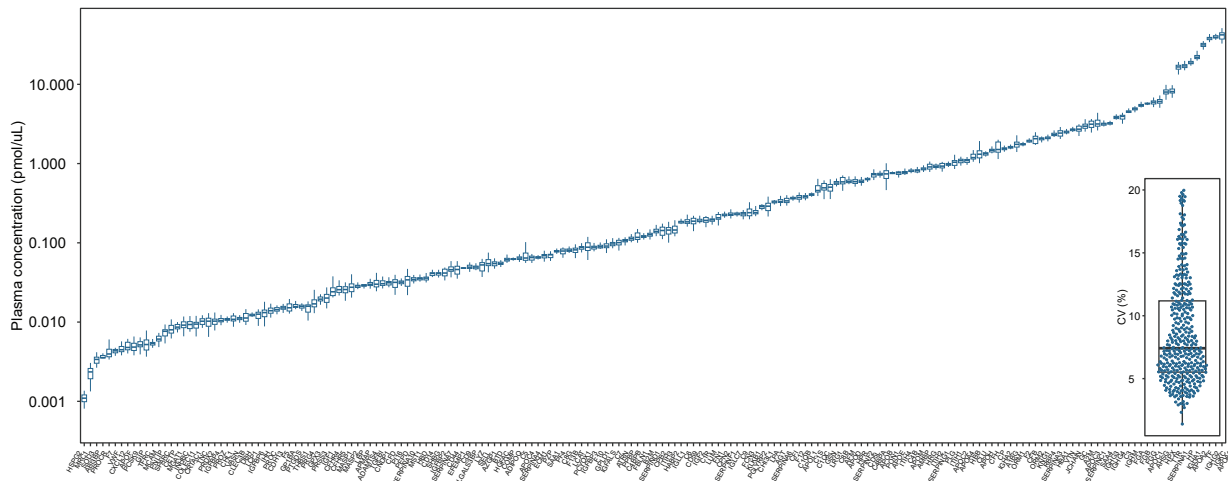
Renal Function



Coagulation

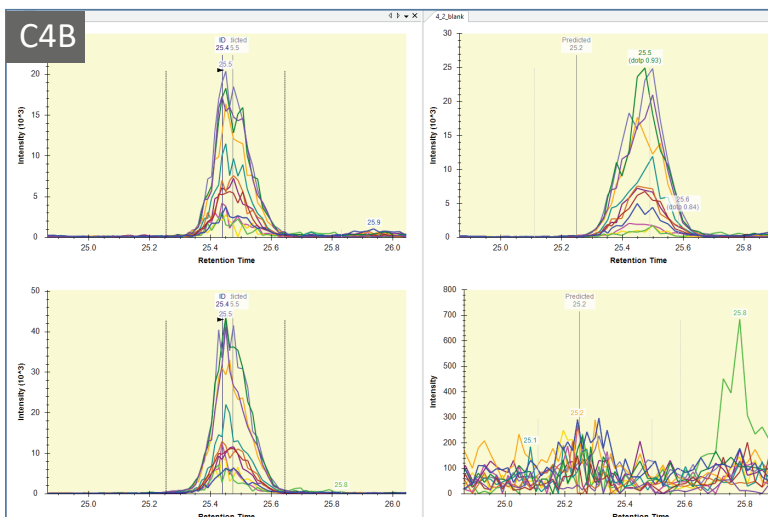


Metabolic Diseases



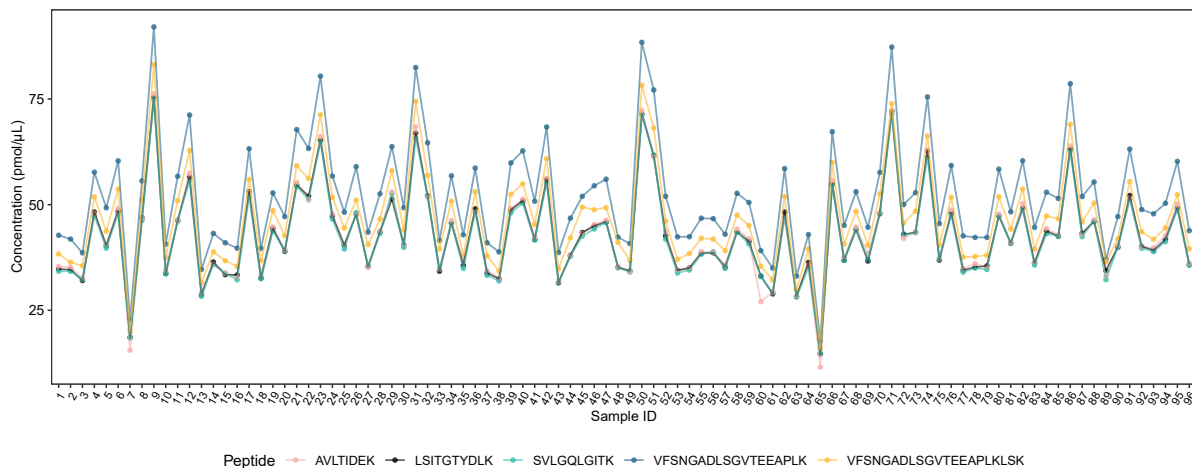
Dynamic range of concentrations for proteins quantified with Stellar MS (Thermo) coupled to Evosep One (Evosep) at 40 SPD with CV < 20% (median CV = 7.4%) across 24 biological replicates and 3 different DiscoveryEdge600 product plates.

High multiplexing in the DiscoveryEdge600 panel improves both confidence in endogenous signal detection and analytical sensitivity. We evaluated the effect of panel spiking by analyzing neat blood plasma digests side-by-side with spiked samples and confirmed that highly multiplexed absolute quantification can be achieved without compromising sensitivity.



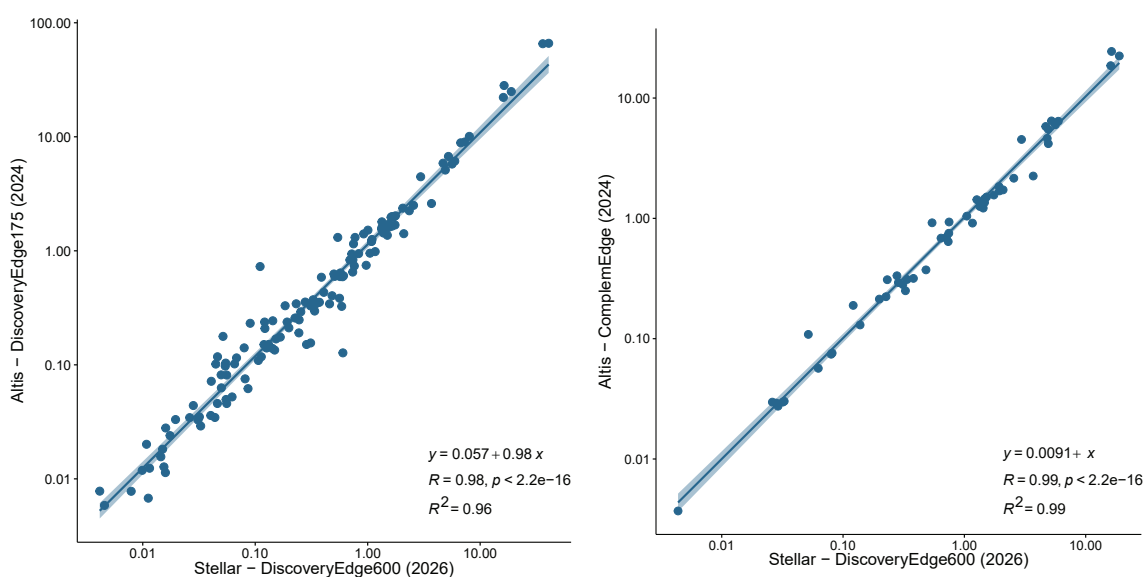
Extracted peptide ion chromatograms originating from protein C4B. The left pane shows results of plasma sample spiked with DiscoveryEdge600, the right of neat blood plasma only. The top pane shows signals of the endogenous peptide and bottom of qRePS.

Co-digestion of qRePS with endogenous proteins generates multiple quantitative peptides, strengthening measurement accuracy and enabling deeper understanding of how peptide signals reflect true protein abundance. This bridges the gap between biomarker discovery and real-world application by ensuring analytical robustness across research and clinical settings. qRePS are spiked in to increase sensitivity, provide built-in quality control, and deliver clinical-grade precision.



Multi-peptide quantification of protein SERPINA1 with all 5 peptides correlating and showing the same pattern as an additional verification of quantified protein abundance.

Reproducible quantification is essential for longitudinal and cross-platform proteomics studies, and qRePS facilitates robust harmonization of methods across different MS instruments and analytical platforms while maintaining highly consistent performance across the entire ProteomEdge product portfolio over time. Using qRePS, we obtained highly concordant results across multiple products, diverse LC-MS configurations, and biological replicates prepared more than two years apart, demonstrating both analytical stability and long-term reproducibility.



Comparison of blood plasma protein concentrations in pmol/μL based on quantification using DiscoveryEdge175 (left) and ComplemEdge (right) with DiscoveryEdge600. DiscoveryEdge175 and ComplemEdge results were acquired in 2024 using Thermo Fisher Scientific's triple quadrupole MS Altis while the Stellar platform was used for quantification with DiscoveryEdge600 in 2026. The results show very strong correlation and demonstrate the robustness and stability of the qRePS panels.

## WHAT IS IT?

Heavy-labelled protein standards, pre-aliquoted and calibrated for the analysis of 1  $\mu$ L blood plasma using mass spectrometry.

## WHAT DO I GET?

Unmet precision and depth in multiplexed absolute quantification of human proteins.

## HOW DO I USE IT?

Provided in a 96-well plate, each well including all proteins in the standard, enabling the analysis of up to 96 samples in parallel.

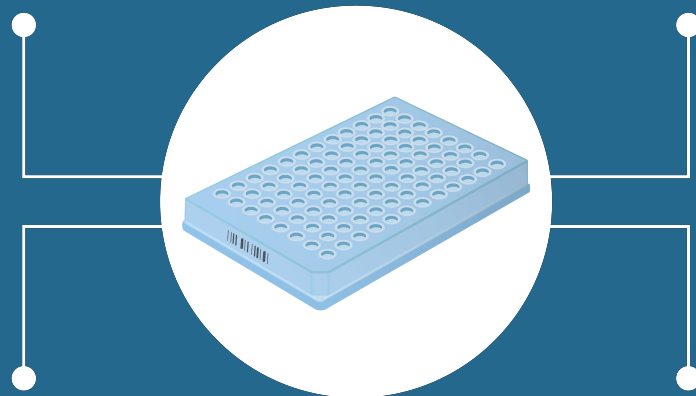
Add your diluted plasma samples to the wells and digest your samples together with the ready-to-use panel for reproducible, high-precision workflow and results.

### Cleavage-dependent Standards

Multipепptide quantification  
Unmet precision and accuracy

### Protein Panel in Every Well

Designed for plasma analysis  
Multiplex absolute quantification



### Standardized Plate Format

Easy to automate  
Highly scalable

### Pre-aliquoted and Dried

Stable at room temperature  
Seamless sample processing

## References:

Kotol D, Hober A, Strandberg L, Svensson AS, Uhlén M, Edfors F. Targeted proteomics analysis of plasma proteins using recombinant protein standards for addition only workflows. *Biotechniques*. 2021;71(3):473-483.  
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Zeiler M, Straube WL, Lundberg E, Uhlen M, Mann M. A Protein Epitope Signature Tag (PrEST) Library Allows SILAC-based Absolute Quantification and Multiplexed Determination of Protein Copy Numbers in Cell Lines. *Molecular & Cellular Proteomics*. 2012;11(3):O111.009613.  
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