



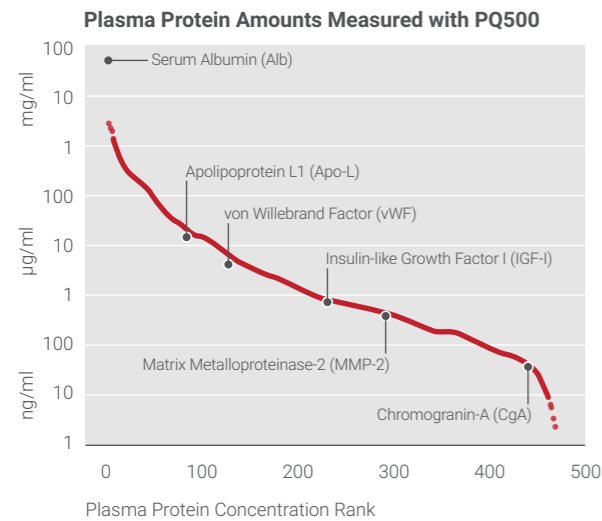
# THE KEY TO THE PLASMA PROTEOME

Accurate Quantification of >500 Plasma Proteins

# ACCURACY, COVERAGE & DEPTH

**Blood plasma is a rich and accessible source of biomarkers for clinical research and patient stratification. However, the low abundance of many plasma proteins makes it a challenging sample for protein quantification. PQ500 contains 804 carefully selected reference peptides for highly multiplexed measurements over six orders of magnitude in abundance.**

Blood plasma provides valuable insights into biological processes and therapeutic responses within the body, with plasma biomarkers emerging as important tools for biomedical research including biomarker discovery and patient stratification in clinical trials. However, more than 99% of the plasma proteome comprises the ten most abundant proteins, making it difficult to analyze lower abundance but biologically relevant molecules.



A solution to this analytical challenge is synthetic peptides that provide highly selective detection and quantification of low abundant endogenous peptides. PQ500 contains 804 carefully selected isotopically labeled reference peptides, enabling multiplexed measurement of more than 500 different plasma proteins over a wide range of expression levels.

## PQ500 is the best choice for plasma proteomics in pre-clinical research:

- Identify and quantify 500+ plasma proteins with unprecedented accuracy and specificity
- Detect 6 orders of magnitude in protein concentration from nano- to micrograms when using targeted mass spectrometry. Figure (left) shows results from a single PRM experiment on a typical blood plasma sample
- Achieve high reproducibility between samples and sample batches over time, allowing reliable comparisons between different timepoints and trials

PQ500 is compatible with various standard workflows including discovery proteomics with **Data-Independent Acquisition (DIA)** and **Multiple or Parallel Reaction Monitoring (MRM/PRM)**, supported by Biognosys' **Spectronaut** or **SpectroDive** software.



*«We developed PQ500 to solve the biggest challenge in plasma proteomics – identifying and quantifying low abundance biomarkers in a reliable, reproducible way across multiple samples and studies.»*

**Dr. Lukas Reiter,**  
Biognosys AG

## FEATURES

Biology

Coverage

Usability

Standardization

Repeatability

Versatility

Quality

## BENEFITS

**Covers hundreds of relevant proteins, including FDA approved clinical markers**

**Detects more than 500 targets in native and depleted plasma samples**

**Detailed protocols, plug-in panels, personalized support**

**One kit for all your plasma projects**

**Comparable results across different platforms and laboratories**

**MRM, PRM and DIA compatible, native and depleted plasma, tissue biopsies, urine, CSF**

**AAA quantified peptides of highest grade, iRT peptides are included**



# MEET OUR PQ500 REFERENCE PEPTIDES

PQ500 contains a smart combination of more than 800 reference peptides, each carefully selected to ensure they are representative of their parent proteins in variable experimental conditions. This ready-to-use peptide pool is compatible with a wide variety of mass spectrometry methods and instrumentation.



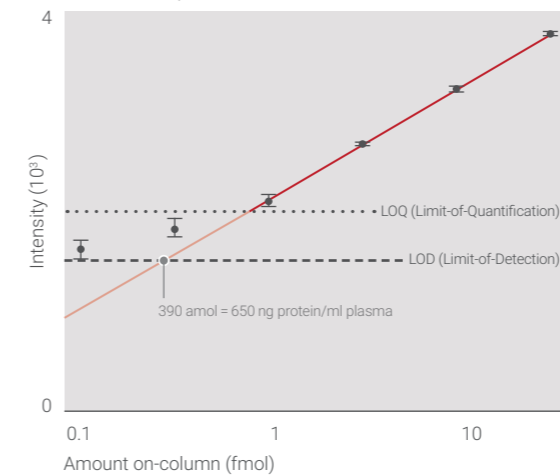
## PQ500 Reference Peptides

- Are primarily derived from experimental data
- Are selected across multiple parameters, including experimental variability and detectability
- Are well-distributed across the whole elution range of the most common LC set-ups
- Have a balanced intensity to ensure detectability on almost any MS system
- Contain Biognosys' iRT peptides for quality control and retention time calibration

# VALIDATION & CHARACTERIZATION

The PQ500 peptide pool has been tested and validated across a variety of settings and instruments, and comes with an optimized assay panel to ensure reliability across any set-up.

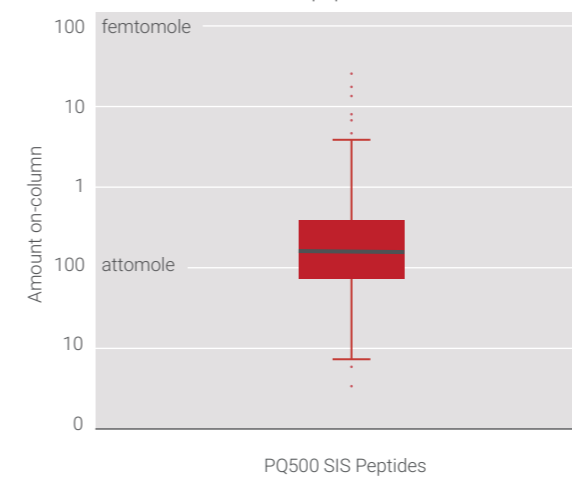
**Assay for Pigment Epithelium-Derived Factor (PEDF)**  
P36955 - Peptide: ELLDTVTAPOK



All PQ500 peptides and corresponding assays have been tested to perform to the highest analytical standards. This graph (left) shows MRM analysis of a dilution series of peptides in plasma, demonstrating linear quantification across the analytical range of the instrument and estimated limit-of-detection (LOD).

LODs for the whole set of PQ500 reference peptides, as determined by MRM. The results demonstrate excellent sensitivity with the median LOD in the atto-mole range, utilizing mass spectrometry to the best of its capabilities.

**Overview of LODs for PQ500 Assays**  
Median LOD: 163 amol peptide on-column

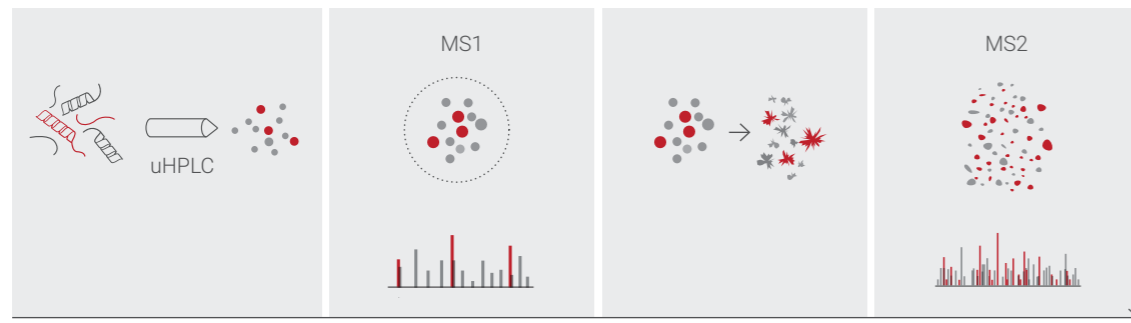


We have tested and validated our PQ500 reference peptides in a large variety of targeted and discovery set-ups, drawing on years of experience in targeted and discovery proteomics. We are committed to enhancing your specific applications and instruments to make sure you get the best results possible.

# USING PQ500 WITH DATA-INDEPENDENT ACQUISITION (DIA)

**Data-Independent Acquisition (DIA) is a perfect match for Biognosys' PQ500 reference peptides kit. It adds up to an easily applicable workflow for the standardized routine analysis of plasma samples without any additional requirements or prior knowledge.**

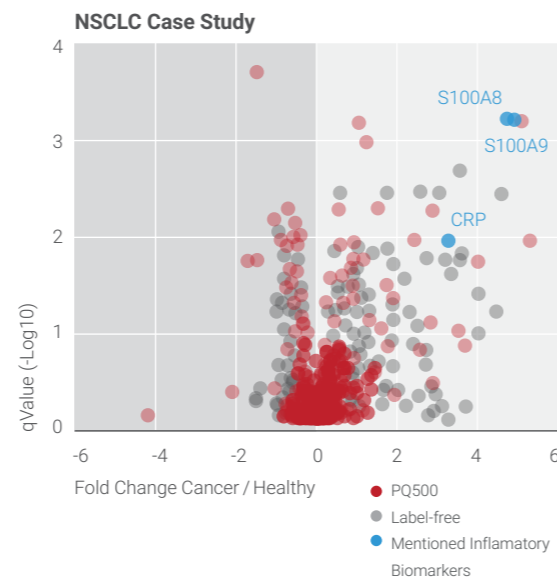
## DIA Mass Spectrometry (DIA)



Combining PQ500 with **DIA acquisition** and data analysis in Spectronaut allows identification and quantification of the targeted peptides without the need for prior method development. In addition, the DIA workflow also provides label-free quantification of all background proteins, making up for a combined targeted-discovery approach.

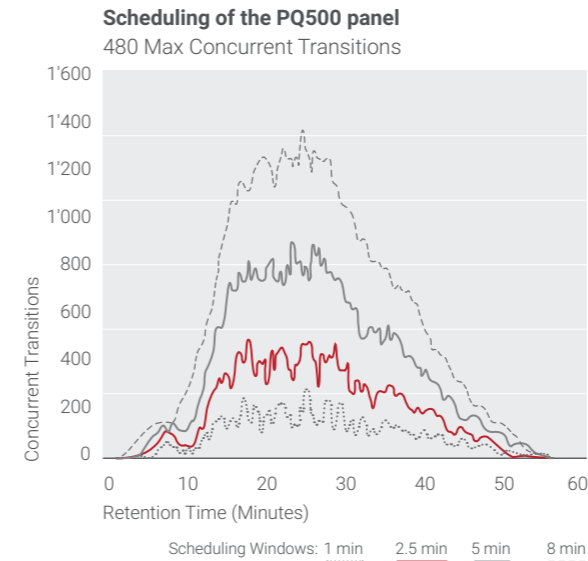
This combined workflow was applied to a proof-of-concept study of depleted plasma samples from patients diagnosed with non-small cell lung cancer (NSCLC). Samples were spiked with PQ500 before injection into the mass spectrometer. On average, 400 proteins were quantified based on the ratio of endogenous to reference peptides, with 600 additional proteins detected label-free. We could see significant up regulation of inflammatory biomarkers such as C-reactive protein (CRP), and S100-A8 and S100-A9 (figure on the right).

PQ500 coupled with DIA combines the accuracy of targeted proteomics with the depth of discovery proteomics, without the need for extensive method development. It is the easiest way to detect all reference peptides and corresponding sample proteins within the dynamic range of your instrument and acquisition method.



# USING PQ500 WITH MRM & PRM ACQUISITION

**Conventional targeted proteomics techniques can only measure a few selected proteins in a sensitive and reproducible way. PQ500 is pushing this concept to the next level by achieving discovery scale coverage with targeted methods.**

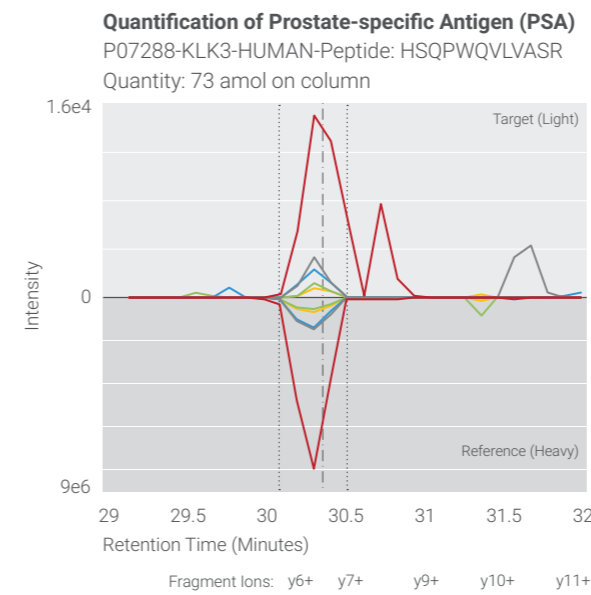


## Multiple Reaction Monitoring (MRM)

usually focuses on a limited number of target peptides. With PQ500, this scope is dramatically widened. The high number of reference peptides act as calibration points for scheduled acquisition, leading to narrow scheduling windows. Therefore, the whole PQ500 panel can be scheduled in a targeted analysis, making full use of the capabilities of the latest generation of triple quadrupole mass spectrometers.

PQ500 also dramatically enhances the capability of **Parallel Reaction Monitoring (PRM)** acquisitions. Our SpectroDive software enables scheduled PRM analysis with non-linear gradients, increasing resolution and achieving sensitive quantification of targets down to the atto-mole range.

PQ500 reference peptides are well suited for use in novel smart targeted acquisition strategies such as **SureQuant™** from Thermo or **MaxQuant.Live**, which rely on stable detection of reference peptides to effectively target endogenous peptide counterparts.





## HOW TO GET PQ500

If you are interested in learning more about PQ500, visit our webshop at [biognosys.com/shop](https://biognosys.com/shop) or contact us at [order@biognosys.com](mailto:order@biognosys.com). For in-depth discussions, we can also arrange personal meetings to support you in implementing next-generation proteomics in your research facility. The Biognosys Team is looking forward to learning more about your specific research questions.

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At Biognosys, we believe that deep proteome insights hold the key to breakthrough discoveries that transform science for better lives. We make the proteome actionable to empower research, drug development, and clinical decision-making with our versatile portfolio of mass spectrometry-based proteomics research services, software, and kits. These solutions provide a multi-dimensional view of protein expression, function, and structure in all biological species and sample types.

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