SpectroDive™

powered by Pulsar

SIMPLIFY YOUR TARGETED PROTEOMICS ANALYSIS

Higher Accuracy with Minimal Effort for MRM, PRM, and SureQuant

ACCELERATING TARGETED PROTEOMICS

SpectroDive™ provides a fast, robust, and seamless targeted proteomics solution for an effortless experience and maximum productivity. Move past lengthy manual analysis and get faster results that you can trust.

Targeted proteomics focuses on the measurement of a selected set of proteins that need to be quantified with high sensitivity, quantitative accuracy, and reproducibility. In the past, the technique was hampered by two main bottlenecks: 1) the development of a target panel, and 2) the need to manually validate targets due to unreliable peak picking and identifications.

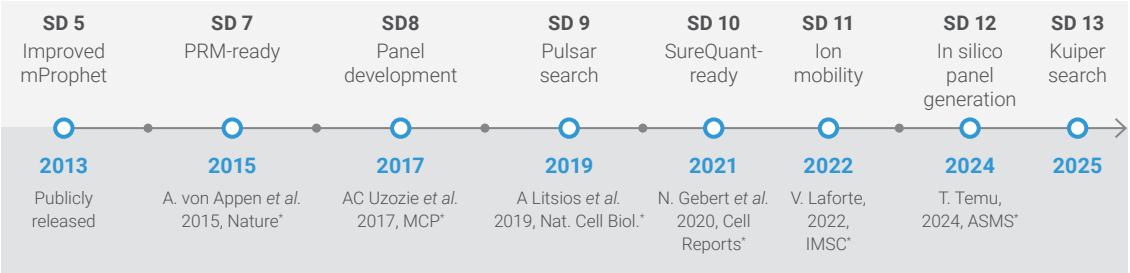
To overcome these limitations, **Biognosys** developed SpectroDive. With SpectroDive, custom panels can easily be generated from spectral libraries, FASTA files or peptide sequences. Powerful automatic peak picking algorithms allow for the streamlined parallel quantification of hundreds of proteins across large datasets, and FDR is automatically controlled for trusted results.

In addition, SpectroDive provides a complete and seamless solution for targeted workflows, from calibration curves to absolute quantification, all within the software.

SpectroDive brings targeted proteomics to its full potential with:

- **Seamless targeted workflows:** Analytical runs for integrated calibration curves and absolute quantification.
- **Advanced peak picking:** Improved mProphet algorithm for reliable identifications.
- **Custom panel generation:** Easy-to-use pipelines that take you from discovery to targeted analysis with Biognosys' embedded search engines: Pulsar and Kuiper supporting fast, unspecific digestion searches. Additionally, SD offers in silico panel generation from FASTA file or peptide sequence, which can optionally be enhanced through AI model optimization using empirical library data.
- **Optimized scheduling:** Increase your number of targets with High-Precision iRT® Calibration-assisted scheduling.
- **Complete analysis environment:** Targeted data analysis and detailed result review in a user-friendly interface.

Figure 1. **Milestones in SpectroDive's (SD) Development**



* Key publications using SpectroDive

Supported Instrument Vendors

- Bruker
- SCIEX
- Thermo Scientific
- Waters

Recommended System

- Windows 11 x64 / Windows Server 2016 or later
- Intel or AMD CPU with 16 cores or more
- 2 TB of free hard drive space or more (2x data set size)
- 16 GB of memory or more
- .NET 8.0 or higher

«SpectroDive 13, featuring the latest Kuiper algorithm and advanced AI models for in silico panel generation, streamlines the design and analysis of large-scale studies. It's optimized for precise quantitation, accurate measurement, and confident identification.»

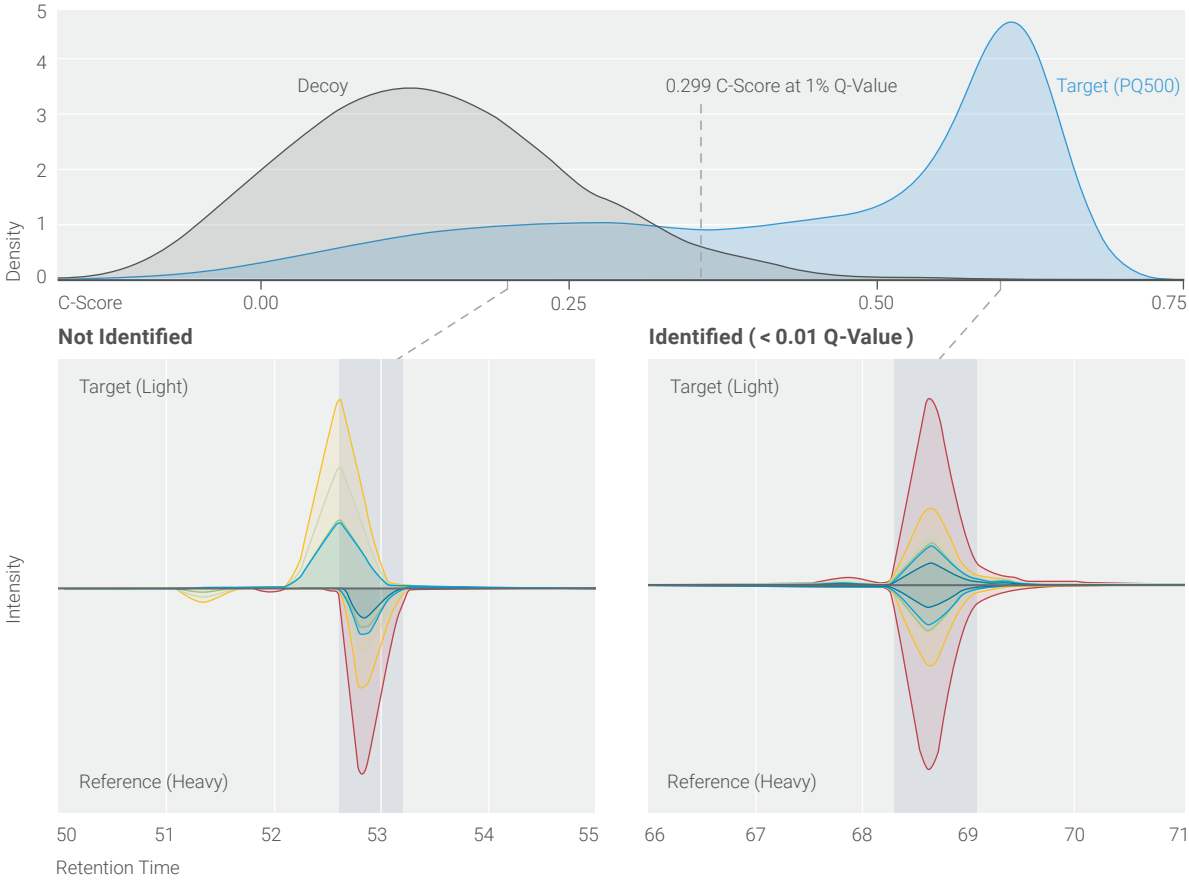
Simonas Savickas, PhD
Sr. Scientist Biognosys

FEATURES	BENEFITS
Performance	**Reliable peak picking and automated FDR-based identification.**
Scalability	**Analyze hundreds of samples in just one experiment.**
Versatility	**Compatible with a wide variety of instruments and acquisitions, including MRM, PRM, prm-PASEF, FAIMS PRM, and SureQuant.**
Simplicity	**Calibration curves for native absolute quantification read-outs, custom panel generation, and biological interpretation.**
Reproducibility	**Robust iRT®-based scheduling for both linear and non-linear chromatography.**
Usability	**Effortless analysis with automatic optimization of parameters for maximum productivity.**

DESIGNED FOR HIGH-THROUGHPUT ANALYSIS

SpectroDive™ provides optimized solutions for large-scale studies, including automated identification and quantification of targeted proteins via its cutting-edge peak picking algorithm and FDR control of the results.

Figure 2. **Score Distribution of Target and Decoy Identifications**



SpectroDive uses machine learning-based peak picking to robustly detect the correct peak in the data. This avoids the need to adjust the peak boundaries manually.[1] Once the correct peak is detected, target peptides are automatically identified based on false discovery rate (FDR) analysis using a target-decoy strategy. SpectroDive creates on-the-fly decoys during the analysis so that you do not need to explicitly measure them in your method. This gives you the flexibility to control the FDR without sacrificing acquisition time. It also means that you no longer need to validate all the targets in a given experiment manually. These crucial steps are invaluable in making SpectroDive the tool of choice for the high-throughput analysis of targeted proteomics data.

1 L. Reiter et al. 2011, Nat. Methods

APPLY LARGE PANELS TO LARGE DATASETS

SpectroDive™ offers optimized and time-efficient analysis of large protein panels, for instance with the ready-to-use PQ500 Reference Peptides kit for the quantification of 500+ plasma proteins.

Figure 3. **Differential Protein Abundances**
Elevated known cancer biomarkers,
e. g. C-reactive protein and protein S100-A9

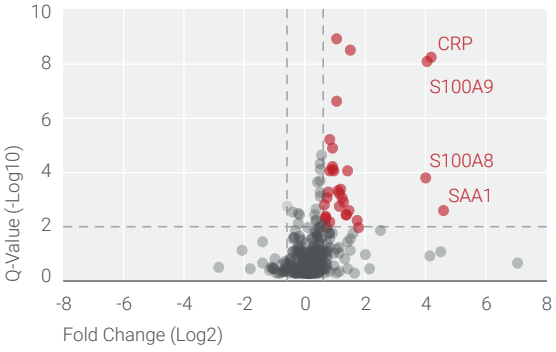
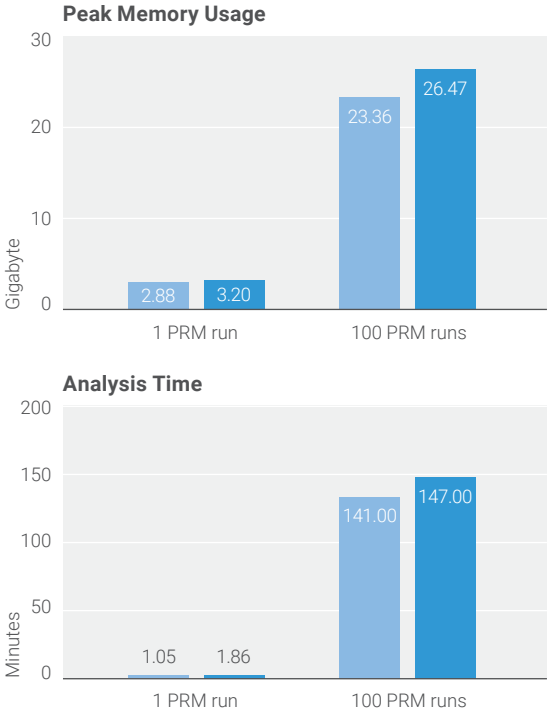


Figure 4. **Performance at Scale**
Resource requirements largely independent of panel size (2h high-resolution PRM runs)



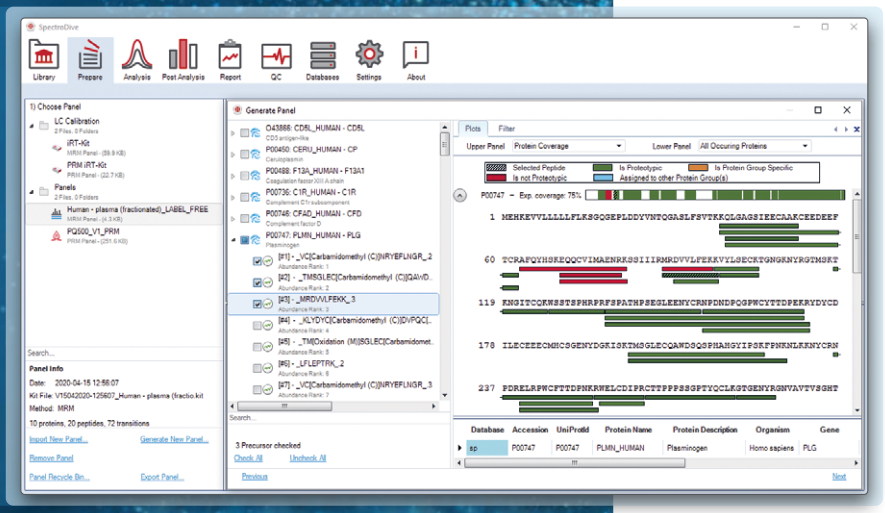
Human plasma is a widely used matrix in clinical and biological studies. It can provide comprehensive health insights and is readily available from patients and healthy individuals. SpectroDive makes it easy to explore plasma samples with our PQ500 Reference Peptides kit which contains stable-isotope standards that allow for the absolute quantification of more than 500 human plasma proteins. Whether you use PQ500 or your own panel, SpectroDive makes it effortless to obtain biological insights into your samples.

Taking just under two minutes to process a single measurement run, SpectroDive can analyze large datasets, irrespective of how many peptides are targeted in the panel. At the same time, SpectroDive features powerful experiment-wide visualizations, and quality control parameters commonly used in discovery proteomics to increase identification confidence. Highly efficient algorithms coupled with reliable identification makes SpectroDive an ideal tool for high-throughput analysis of targeted proteomics data.

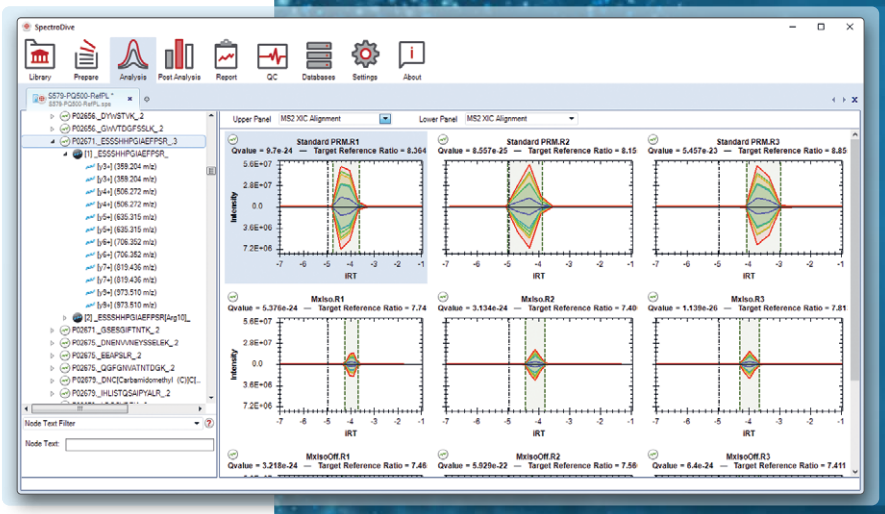
FROM PANEL DEVELOPMENT TO BIOLOGICAL INTERPRETATION

SpectroDive™ takes the hassle out of targeted proteomics by offering integrated calibration curve calculation and optimization for custom panels, High-Precision iRT® Calibration-assisted scheduling, and ready-to-publish results without manual revision.

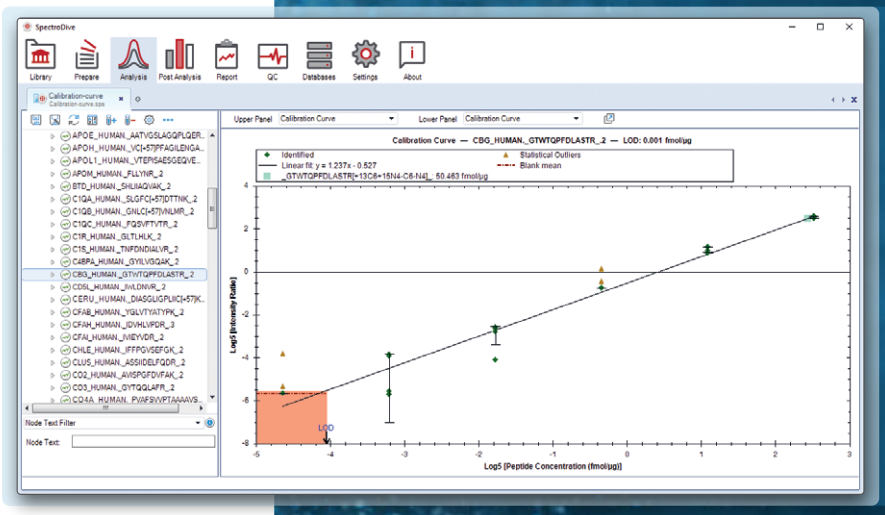
Seamless Panel Generation
Use Pulsar and Kuiper search engine built libraries to generate custom panels for your target proteins with refined precursor and fragment ion selection or generate taget panels in silico directly from a FASTA file or peptide sequence.



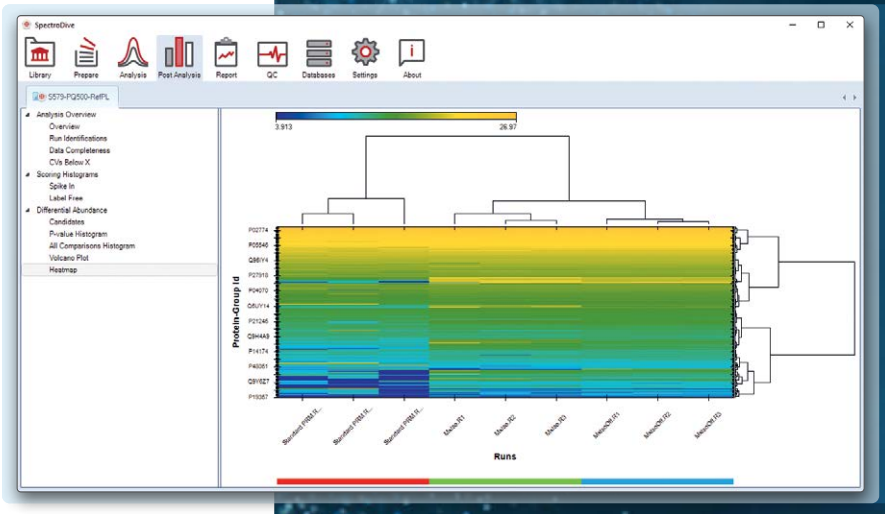
Method Development and Refinement
Generate unscheduled and scheduled methods that can be exported and directly used on the instrument for acquisition. SpectroDive's High-Precision iRT Calibration allows for scheduling method refinement and also increases target multiplexing.



Analysis Review
Easily review the target peptides across all runs. If necessary, you can adjust extraction boundaries and reject assignments manually.



Absolute Quantification with Calibration Curves
Calculate your calibration curve, linear range, and limits of detection and quantification all within SpectroDive™. Use multiple calibration curves to select the best read outs for specific precursor of your panel. Absolute quantification has never been this easy.



Results Visualization and Export
View differential protein abundance candidates, explore results with intuitive plots, and export your results with fully customizable reports. Save your reporting schemas to reuse them in future exports.

HOW TO GET SPECTRODIVE™

Here at Biognosys, we are committed to making our next-generation proteomics solutions widely available to researchers. Therefore, we offer flexible licensing options to best fit your personal and organizational needs.

If you are interested in a SpectroDive demo, a free trial license, or you would like to proceed to purchase, contact us at **order@biognosys.com.**

FIRST CLASS SUPPORT

We are proud to offer you extensive advice and support to help you integrate our software and kits into your workflow. Our support team is here to ensure a great user experience.

If you would like to have your own personal meeting with us, please feel free to contact us by emailing **support@biognosys.com.** Our average response time is less than 24 hours.

At Biognosys, we believe that deep proteome insights hold the key to breakthrough discoveries that can dramatically improve human health. We enable life science researchers and drug hunters to look at the proteome from every angle with our versatile portfolio of proprietary proteomics services, software, and kits. These solutions provide a multi-dimensional view of protein expression, function, and structure in all biological species and sample types. Through advanced data analytics, Biognosys translates data into actionable insights for R&D and clinical research.

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