



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.

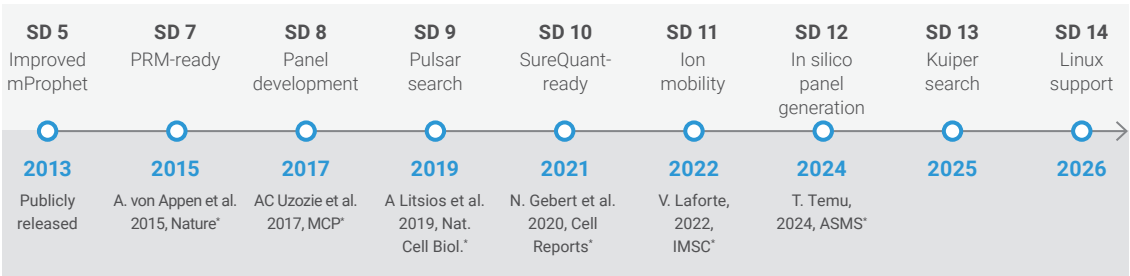
To overcome these limitations, **Biognosys** developed *SpectroDive*. With *SpectroDive*, custom panels can easily be generated from spectral libraries, FASTA files or peptide sequences. Powerful automatic peak picking algorithms allow for the streamlined parallel quantification of hundreds of proteins 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 / Ubuntu 22.04 LTS • Intel or AMD CPU with 16 cores or more • 2 TB of free hard drive space or more (2x data set size) • 128 GB of memory or more • .NET 8.0 or higher / .NET 8.0 for Linux
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«*SpectroDive*, 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

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.

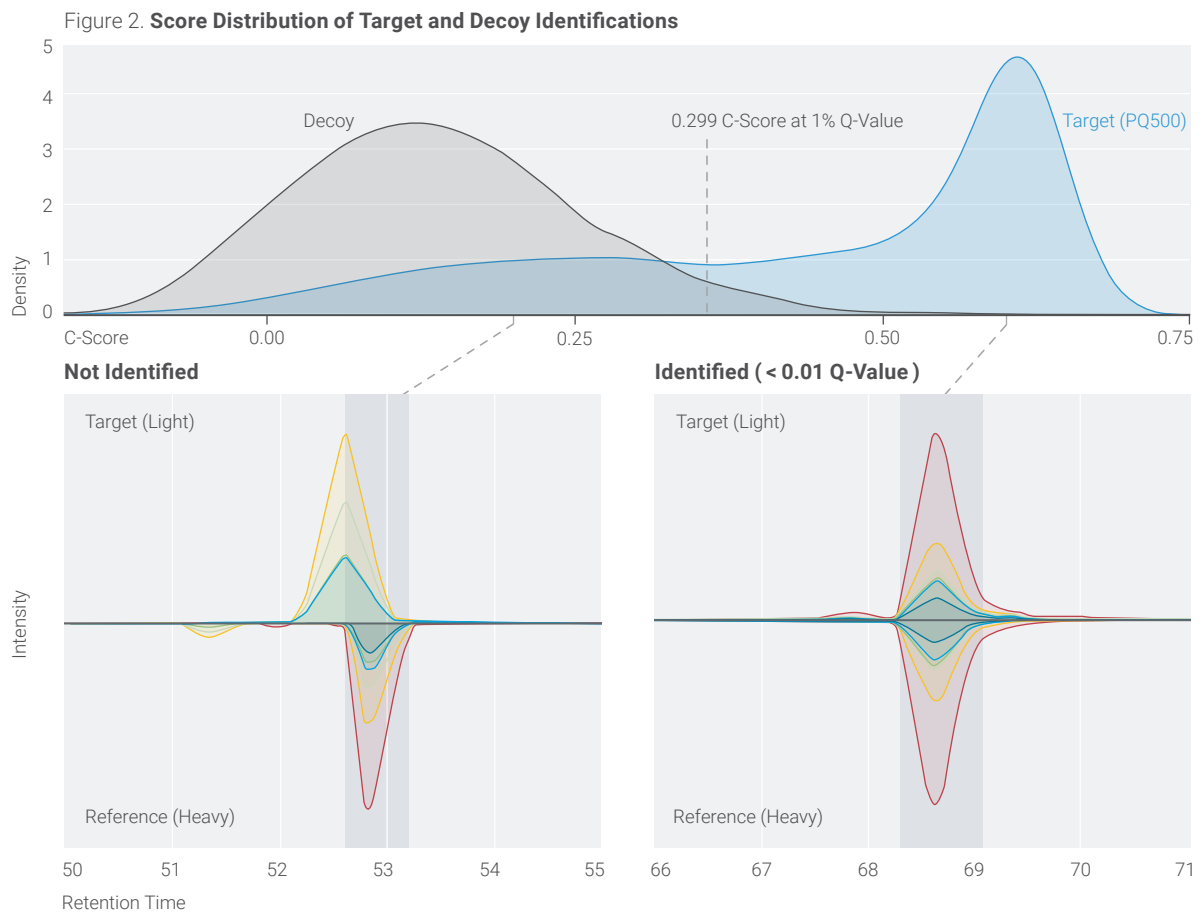
Usability

Effortless analysis with automatic optimization of parameters for maximum productivity.

BENEFITS

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.



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

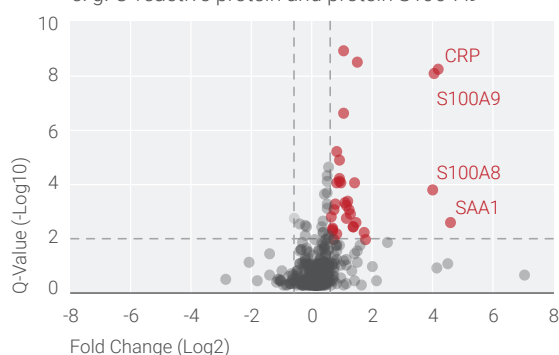
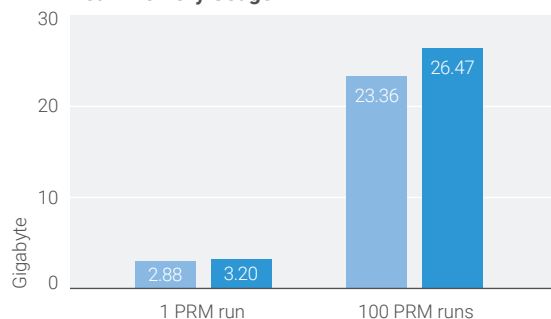
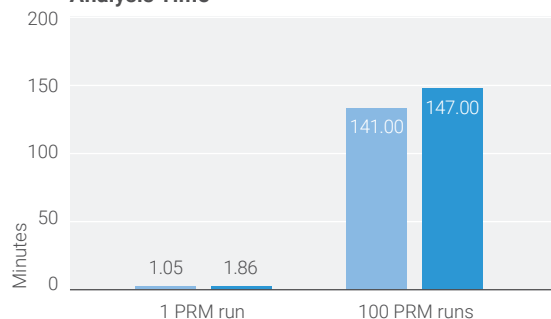


Figure 4. **Performance at Scale**
Resource requirements largely independent of
panel size (2h high-resolution PRM runs)

Peak Memory Usage



Analysis Time



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.

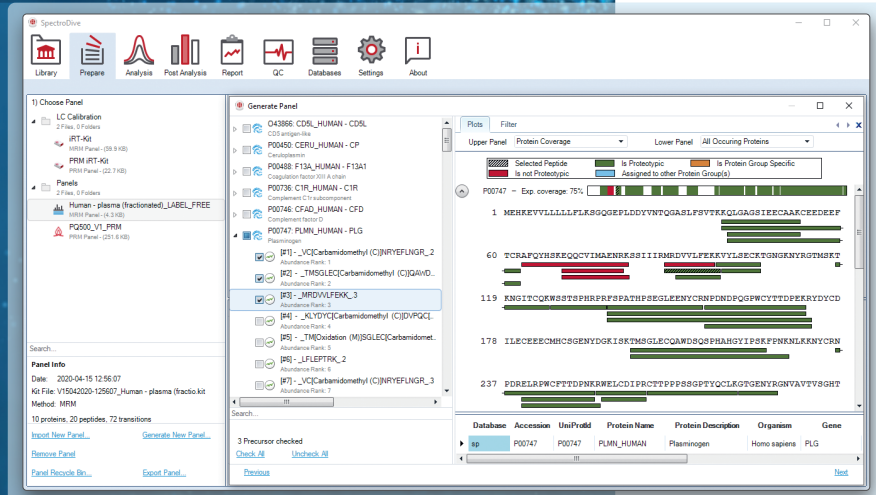
■ PQ500 Subset (100 peptides)
■ PQ500 (804 peptides)

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

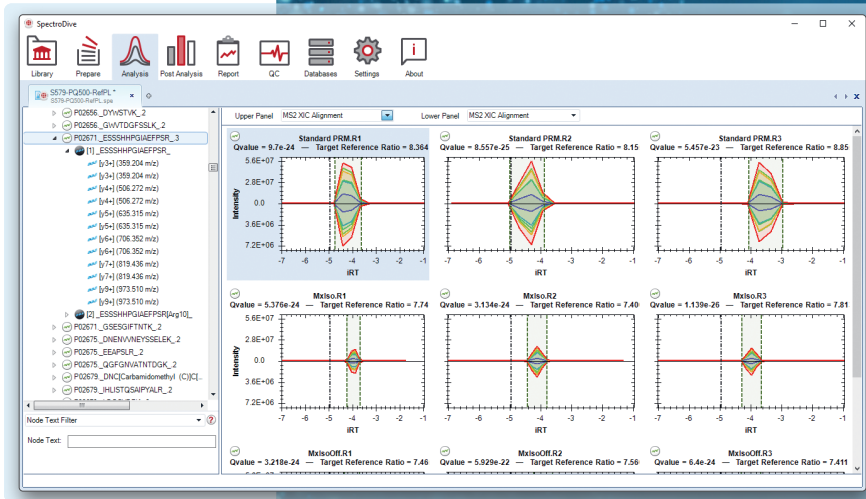
Use Pulsar and Kuiper search engine built libraries to generate custom panels for your target proteins with refined precursor and fragment ion selection or generate target panels in silico directly from a FASTA file or peptide sequence.



Method Development and Refinement

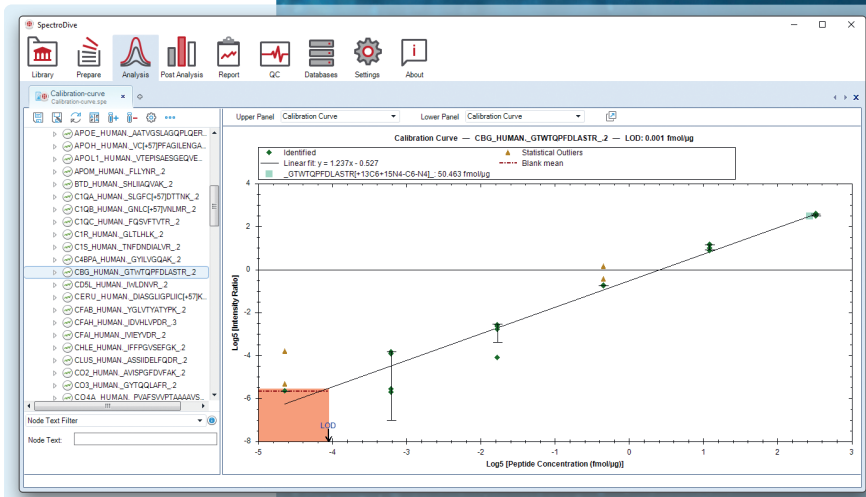
Generate unscheduled and scheduled methods that can be exported and directly used on the instrument for acquisition. *SpectroDive's* High-Precision iRT Calibration allows for scheduling method refinement and also increases target multiplexing.





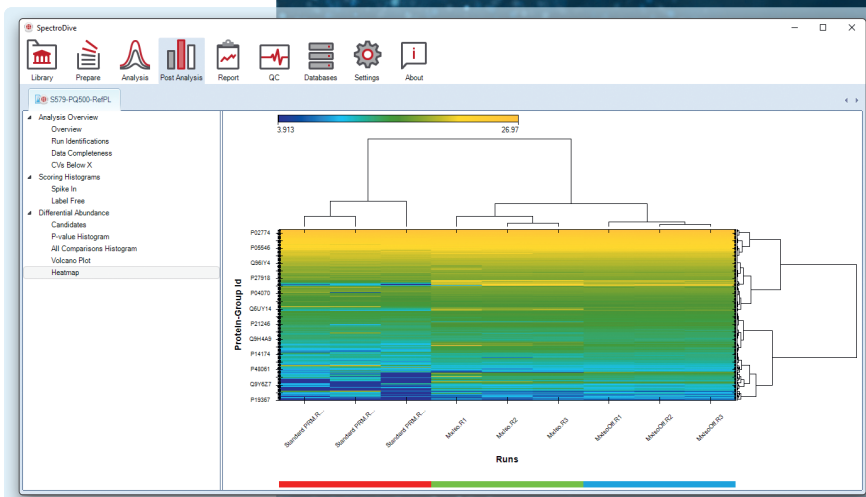
Analysis Review

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.

The *Biognosys Group* brings together the Bruker Corporation affiliates Biognosys, biocrates, and PreOmics to deliver integrated solutions across proteomics, metabolomics, and lipidomics. Its ecosystem spans high quality consumables, software, and contract research services. The Group enables seamlessly connected mass spectrometry workflows, making advanced multiomics technologies accessible to laboratories worldwide.

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