

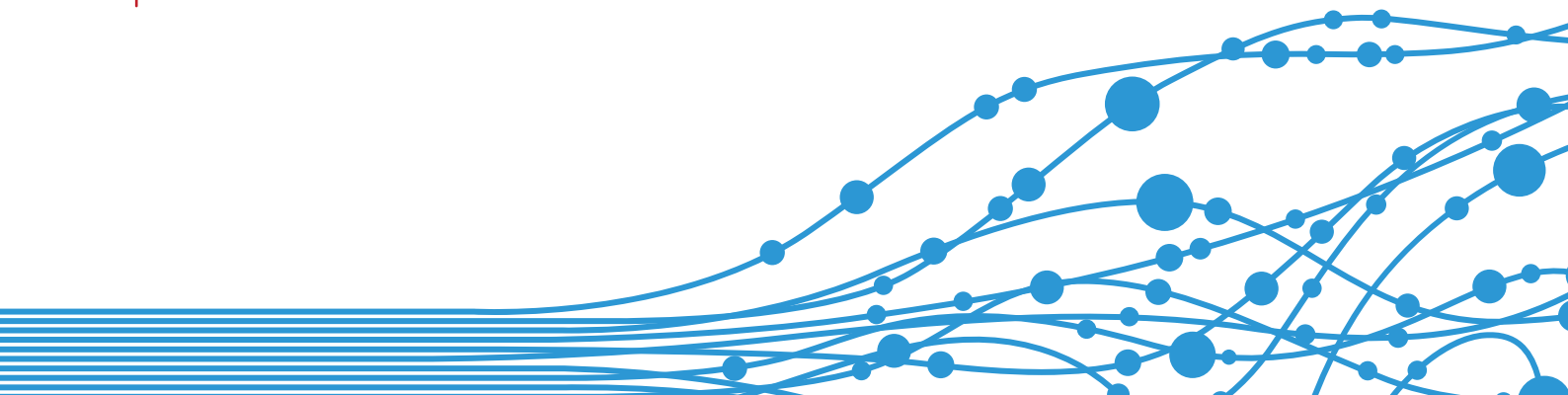


SpectroDive™

A COMPREHENSIVE TOOL FOR
TARGETED PROTEOMICS



- Library generation from DDA results and subsequent panel generation for MRM and PRM data acquisition
- Quick and easy setup of MRM and PRM measurements
- Smartest peak picking for fast data analysis with minimal bioinformatics resources
- Higher data confidence with complete workflow quality controls
- Integrated absolute protein quantification with stable isotope standards



UNDERSTANDING LIFE

TARGETED PROTEOMICS

Multiple and Parallel Reaction Monitoring (MRM and PRM)

Targeted proteomics is a mass spectrometry technology that targets specific peptides in a complex mixture and determines their presence and quantity.

In contrast to data independent acquisition where all peptides and fragment ions are recorded, targeted proteomics limits the number of peptides that will be monitored and only focuses on those peptides during acquisition to achieve the highest sensitivity and throughput for hundreds or thousands of samples.

Targeted proteomics currently relies on two main approaches: MRM and PRM. MRM is a well-established method for targeted proteomics and is primarily performed on triple quadrupole mass spectrometers, while its novel variant PRM was introduced only recently and is performed on the latest generation of high-resolution mass spectrometric instruments.

Both methods allow for highly specific and sensitive quantification of proteins from nearly any biological sample.

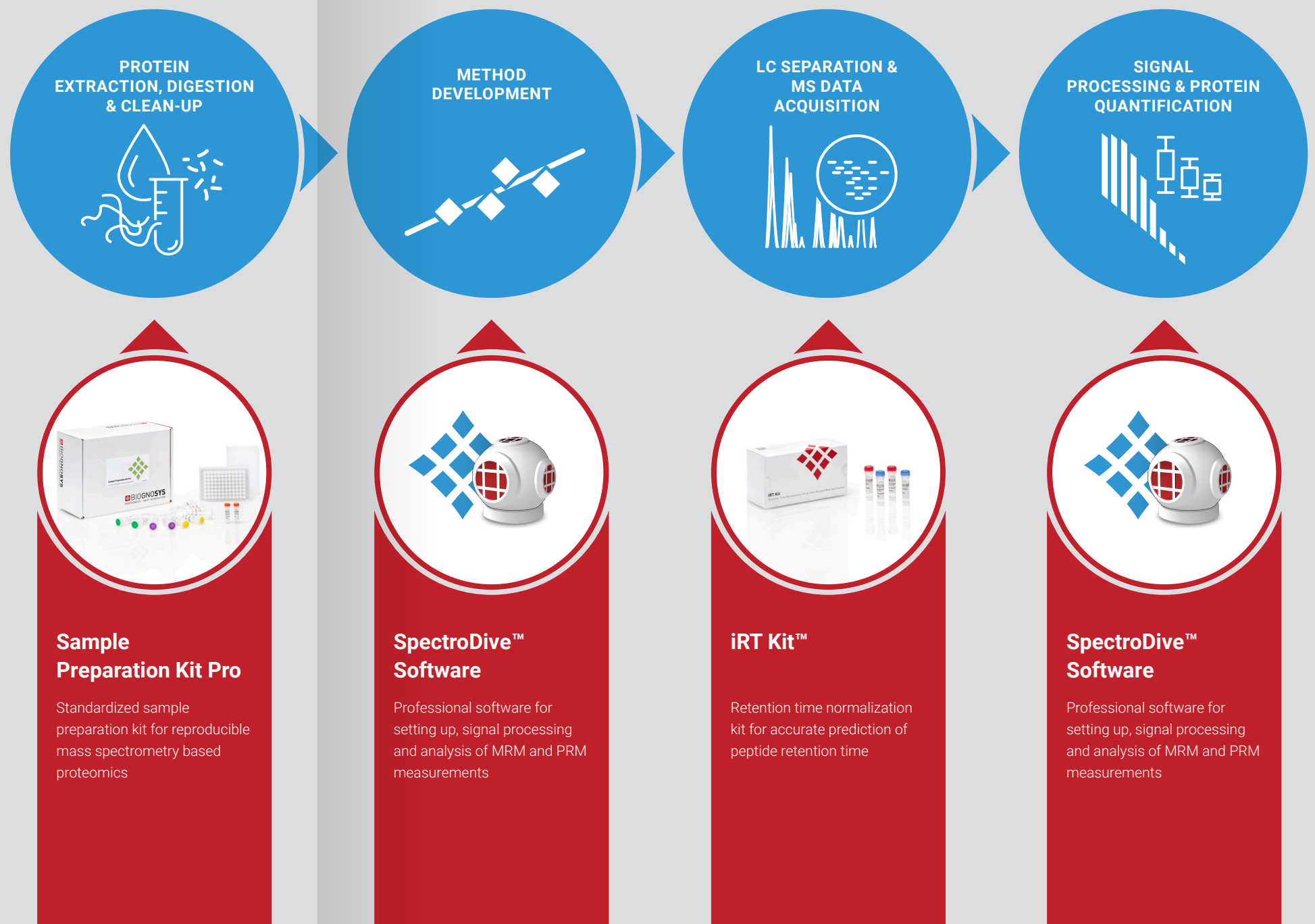
Biognosys' targeted proteomics workflows with the integrated **iRT** concept allow the quantification of hundreds of proteins in a single run covering a dynamic range of 6 magnitudes with high precision and reproducibility. Panel generation, method set-up, signal processing and data analysis is handled by **SpectroDive™**, a professional software for MRM and PRM measurements that enables fast analysis of large datasets. Biognosys targeted proteomic workflows also offer the possibility to include stable isotope standards into the analysis to obtain absolute quantities of the proteins of interest.

“SpectroDive™ is easy to use. It streamlines the process from assay development to validation to peptide quantification. The good graphical interface allows for an easy manual inspection to assess data quality and the software is very robust from a statistical point of view.”

Alessandro Ori, PhD
Leibniz Institute on Aging (FLI) Germany

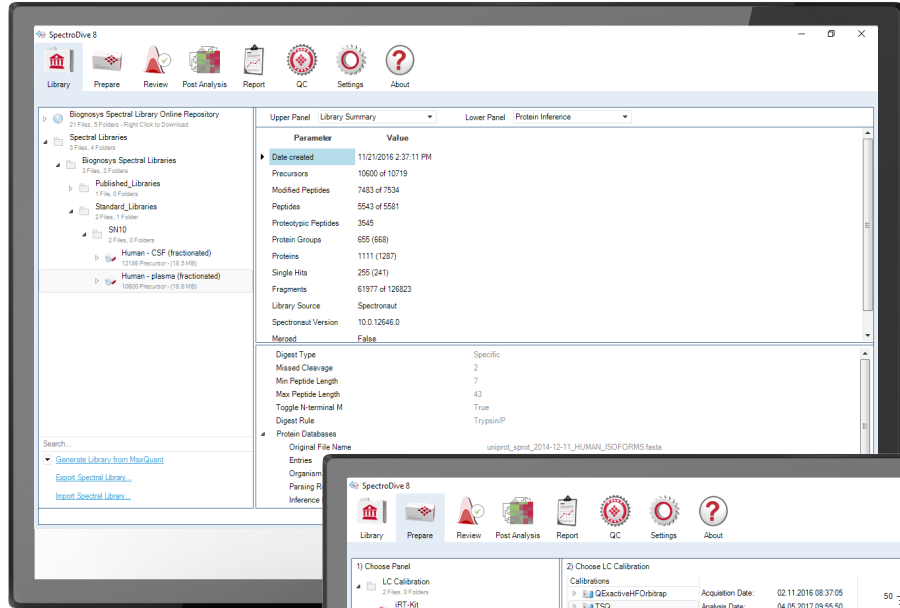
Targeted proteomic workflows

Biognosys solutions support each step in the MRM and PRM workflow



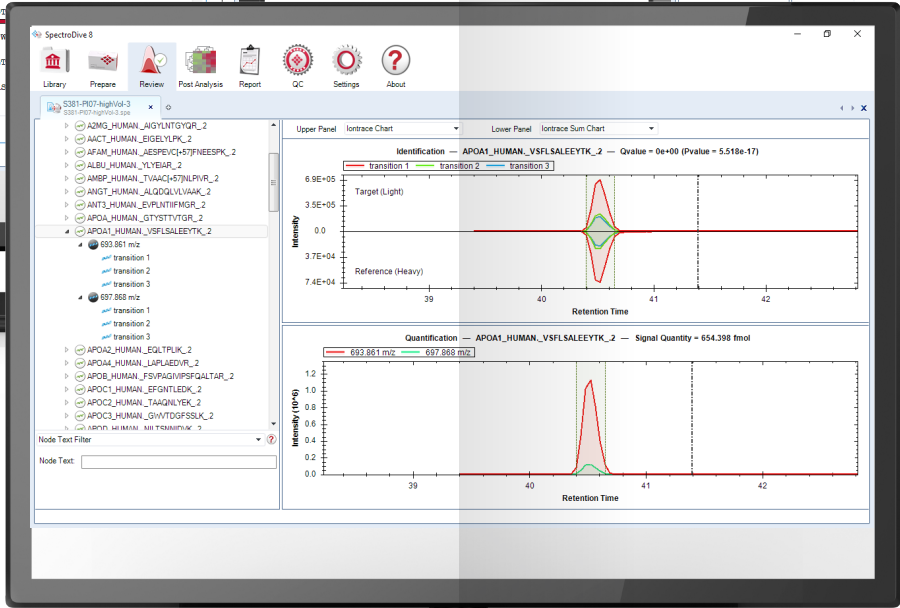
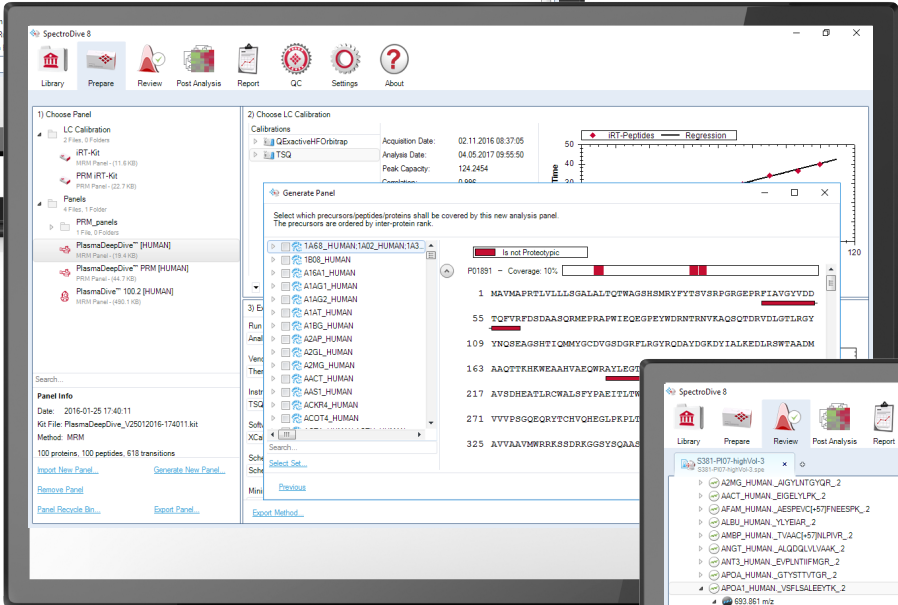
SOFTWARE FEATURES

SpectroDive™ was developed for data processing generated with targeted proteomics methods (MRM and PRM). It covers a complete workflow starting from panel generation, automated mass spectrometry method set-up and signal processing to quantitative and qualitative data analysis. SpectroDive™ is organized in modules called perspectives that follow the analysis flow.



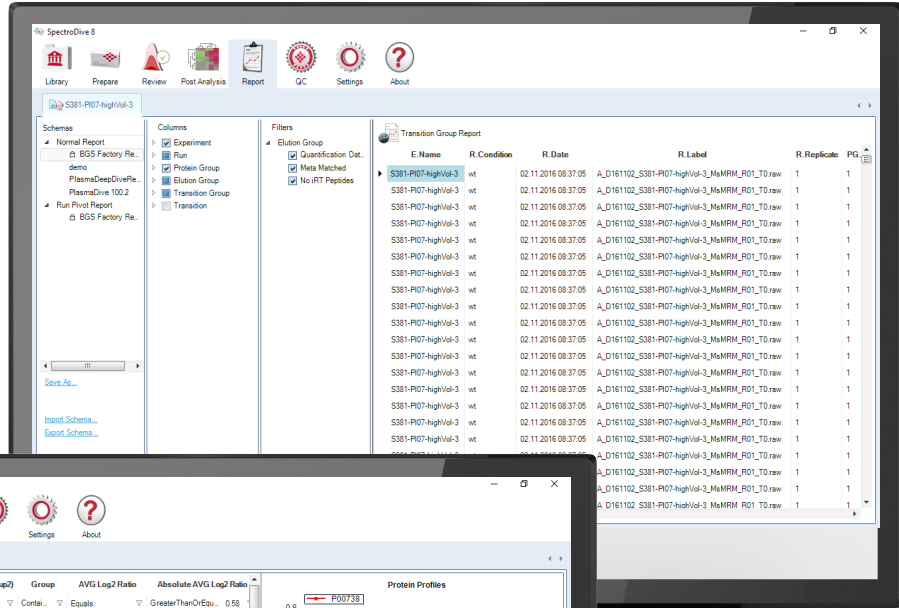
Library perspective:
the spectral library generation perspective supports main database search engines such as: MaxQuant, Proteome Discoverer and ProteinPilot. SpectroDive™ automatically converts searched shotgun runs into a ready-to-use spectral library.

Prepare perspective:
generates MRM or PRM panels from spectral libraries and exports ready-to-use method files (transition lists). SpectroDive™ also features flexible panel management, automated LC calibration and IRT refinement of PRM panels.

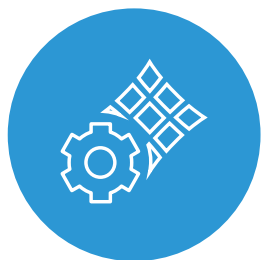


Review perspective:
the data analysis in SpectroDive™ is based on the powerful mProphet peak picking algorithm. The review perspective also allows manual reviewing of your MRM or PRM data with a variety of visualization options for different levels of the experiment review tree.

Report perspective:
flexible data export capability meets the design of your experiment. SpectroDive™ automatically reports absolute protein quantities when using a method with stable isotope standards.



Post-analysis perspective:
differentially expressed proteins are displayed immediately after the analysis. SpectroDive™ performs a t-test pairwise comparison of all conditions in your experimental setup.



TECHNICAL INFORMATION

MRM SUPPORTED INSTRUMENTS

- Thermo Scientific™ TSQ™ Series (Vantage, Quantum, Quantiva)
- SCIEX API 4000™
- SCIEX Triple Quad™ 5500
- Agilent 6400 Series

PRM SUPPORTED INSTRUMENTS

- Thermo Scientific™ Q Exactive™ Series
- Thermo Scientific™ Orbitrap Fusion™ Series
- SCIEX TripleTOF® Series (5600, 5600+, 6600)

RECOMMENDED SYSTEM REQUIREMENTS

Windows 7 x64 or higher, CPU Intel Core i7 4770, 3.4 GHz (octa core) or more, HDD 500 GB free space (SSD), Memory 16 GB or more, Software .NET 4.5 or higher.



FREQUENTLY ASKED QUESTIONS

HOW DO I BENEFIT FROM USING THE iRT KIT TOGETHER WITH SPECTRODIVE™?

Using SpectroDive™ with the iRT Kit translates into better results:

- Easy setup of scheduled methods on your LC system
- Smart in-run parameter calibration guarantees quick and robust analysis
- Higher quantitative accuracy by supporting optimized ion current extraction in PRM
- Automated quality control by monitoring LC and MS performance

WHAT ARE THE MAIN DIFFERENCES BETWEEN TARGETED PROTEOMICS (MRM AND PRM) AND HRM WORKFLOWS?

HRM provides precise quantification for thousands of proteins in a single sample and is ideal for unbiased discovery applications focused on proteome profiling such as: drug and target discovery, biomarker discovery, pathway modeling etc. On the other hand, MRM and PRM are used to quantify selected proteins with better sensitivity and higher throughput. Targeted proteomics is especially powerful for monitoring the quantities of a selected set of proteins in hundreds or thousands of samples.

HOW IS THE ABSOLUTE QUANTIFICATION OFFERED IN BIOGNOSYS' ASSAY PANELS (E.G. PLASMA DIVE™) INTEGRATED IN SPECTRODIVE™?

The MRM or PRM Assay Panel such as PlasmaDive™ comes with a reagent kit and stable isotope standards that are synchronized with the sample preparation protocol. Also included in the kit is a SpectroDive™ plug-in that contains the method (transition list) and quantitative information about the standards. SpectroDive™ uses this plug-in to automatically calculate the exact concentration of the endogenous proteins and reports the quantities (in ug/ml) in the review perspective as well as in the final report, which can be exported in the tab separated file.

PlasmaDive™

Everything you need in one box!

MRM and PRM Assay Panel for multiplexed absolute quantification of 100 proteins in human plasma / serum samples

PlasmaDive Panel Kit contains

- Reagents and optimized protocol for reproducible sample preparation
- Stable isotope standards for accurate quantitation
- iRT Standard for transfer to virtually any LC setup
- MS Method for optimized measurements

“We offer various MRM and PRM Panel kits including customized solutions that can be transferred to your laboratory or analyzed in our state-of-the-art facility.”



How to order

Biognosys offers SpectroDive™ **free for individual academic researchers** and can be obtained directly from Biognosys' online shop. Government, core labs and industrial researchers can send their inquiries for SpectroDive™ licenses to order@biognosys.com.

OUR PROTEOMICS EXPERTS CLOSE TO YOU

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ABOUT BIOGNOSYS

Biognosys was founded in 2008 as a spin-off from the lab of Prof. Ruedi Aebersold at the ETH Zurich. Biognosys provides innovative services and products for protein quantification using next-generation proteomics technology.

