BIOGNOSYS
NEXT GENERATION PROTEOMICS

Spectronaut®

powered by Pulsar

TAKE YOUR DIA DATA TO THE NEXT LEVEL

The Most Complete and Versatile Solution for Quantitative Proteomics

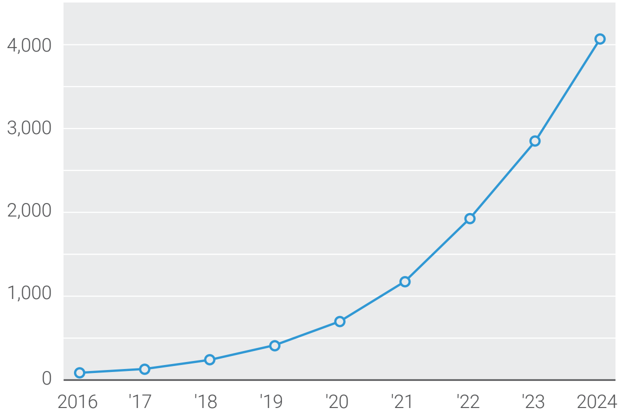
THE GOLD-STANDARD FOR DIA PROTEOMICS ANALYSIS

Spectronaut® provides a fast, robust and seamless proteomics solution for an effortless experience. Constantly at the cutting-edge of innovation, Spectronaut supports the newest technologies in data acquisition and is continuously improving.

Data-independent acquisition (DIA) has become the workflow of choice for discovery proteomics, enabling deep proteome coverage, excellent reproducibility and high precision across large numbers of complex biological samples.[1]

Since its first release in 2013, **Biognosys** have continuously updated Spectronaut, improving performance and supporting new mass spectrometry technologies. As a result, Spectronaut has become the most important vendor-independent analysis solution for DIA proteomics, making a growing impact in life sciences research.

Figure 1. **Total Mentions of Spectronaut in Scientific Publications** Source: Google Scholar "Spectronaut"



Boost your productivity in modern DIA proteomics with **Spectronaut** and its broad range of features:

- **Benefit from powerful directDIA™ workflows:** Quantify proteins directly without measuring additional samples for library generation.
- **Take advantage of the most AI-augmented DIA software:** With models trained on a wealth of data to cover a broad range of workflows and use-cases.
- **Analyze post-translational modifications (PTMs) with confidence:** Unlock unprecedented PTM depth and immunopeptidomics insights with the new Kuiper search engine!
- **Generate high-quality libraries with Pulsar:** Create DDA, DIA or hybrid libraries with full false discovery rate control.
- **Enjoy full support for ion mobility technologies:** Compatible with PASEF, diagonal PASEF and FAIMS Pro.
- **Experience the most powerful data visualization for DIA proteomics:** Now in an even more intuitive user interface.

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[1] Bruderer et al., MCP, 2017, 16, 2296-2309

Supported Instrument Vendors

- Bruker
- SCIEX
- Thermo Fisher Scientific
- Waters

Recommended System
for a library-free experiment with 200 DIA runs and typical search space settings

- Windows 10 x64 / Windows Server 2016 or Linux Ubuntu
- Intel or AMD CPU with 64 or more cores
- 2 TB of hard drive space or more (2x data set size)
- 128 GB of RAM

Spectro**naut**®
powered by Pulsar

«Spectronaut is an excellent addition to our informatics capabilities, especially its thorough analysis of large-scale DIA phosphopeptide data and advanced modification localization.»

Prof. Dr. Matthias Mann
Max Planck Institute of Biochemistry

«Spectronaut is our preferred DIA software due to its high performance and user-friendly interface, which makes analyzing complex, multiplex DIA datasets easy and reliable.»

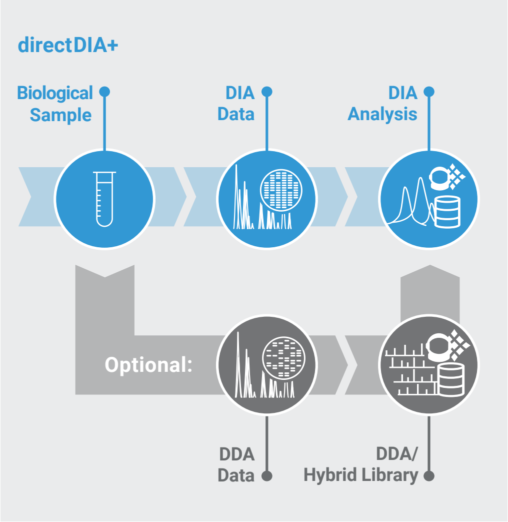
Prof. Yansheng Liu
Yale University School of Medicine

FEATURES	BENEFITS
Performance	**Unmatched accuracy and speed of Pulsar, amplified by the new Kuiper search engine to uncover the depths of unspecific searches.**
Scalability	**Large-scale projects made easy with directDIA™ and cloud support for Linux and Windows.**
Versatility	**Compatible with a wide variety of instruments and workflows including HRM™, SWATH™, FAIMS-DIA, dia-PASEF® and more.**
Simplicity	**From raw data to biological interpretation in one application.**
Reproducibility	**Robust, quantitative data across multiple samples with stringent false discovery rate control.**
Usability	**Effortless and robust analysis with automatic optimization of parameters.**

THE directDIA ROUTE TO THE PROTEOME

Skip straight to protein identification and quantification with Spectronaut®'s directDIA® analysis, the only library-free workflow that has native support for PTMs and labeling experiments. directDIA provides extensive proteome coverage comparable to using deep project specific libraries from highly fractionated samples.

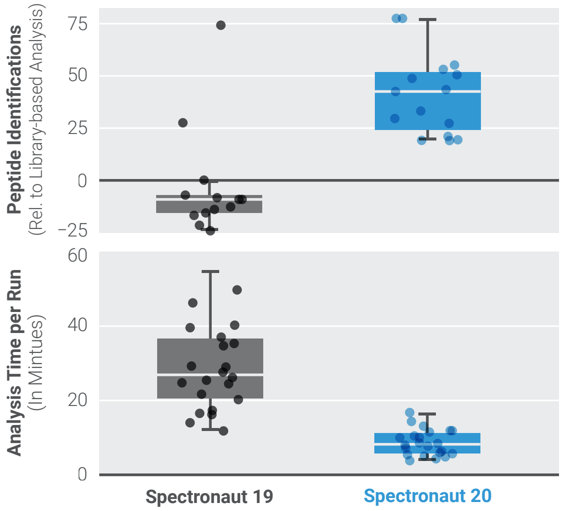
Figure 2. **DIA Analysis Using directDIA+ or a Project-specific DDA Library**



In the past, data-independent acquisition (DIA) analysis has depended on spectral libraries generated from separate data-dependent acquisition (DDA) runs, requiring additional instrument run time (Figure 2). Spectronaut's industry-leading library-free DIA analysis (directDIA) offers a fast, cost-saving alternative with identification performance comparable to the more conventional project-specific DDA library approach (Figure 2). With Kuiper on board, Spectronaut delivers deep, lightning-fast directDIA coverage for challenging applications like immunopeptidomics — eliminating the need for traditional library-based workflows.

For cases where spectral libraries are still preferred, we allow a combination of DDA data with directDIA. This hybrid workflow is easily accessible and supported: Spectronaut takes care of details including differences in chromatgoraphy and controlling for false discovery rates at the library level. To help you jump-start your proteomics projects, Spectronaut comes pre-loaded with a selection of high-quality, species-specific search archives.

Figure 3. **directDIA Outperforms Library-based Analyses in Spectronaut 20**



HIGH PERFORMANCE AND RELIABILITY AT SCALE

Spectronaut® is the comprehensive solution for robust and reliable data analysis in DIA proteomics.[2] Innovative data handling and false discovery rate control solutions allow efficient processing of large proteomics data sets with confidence.

Figure 4. **Score Distribution of Target, False and Decoy Identifications**

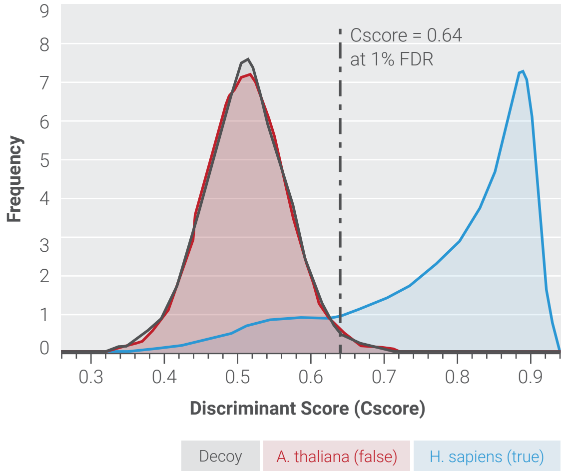
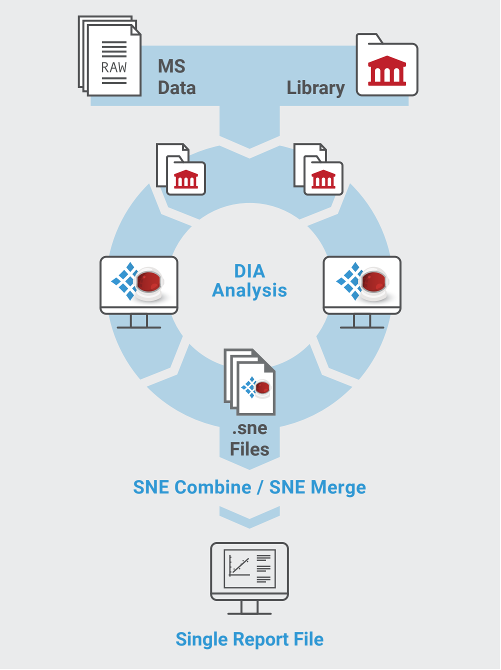


Figure 5. **Parallel Processing in the Cloud or High-Performance Cluster**



For reliable proteomics analysis, it is essential to correctly estimate the proportion of false positive identifications (false discovery rate, FDR) in a dataset at both the peptide and protein level. Identification scores are calculated for all peptides in the target protein database. To estimate FDR, 'decoy' peptides are generated in-silico, and scores calculated for them from the data. FDR is estimated by means of the fraction of decoys in the total identified features. Ideally, the score distribution for synthetic decoys should resemble that for peptides from species that are unrelated to the biological sample, while scores for truly present target peptides should be higher (Figure 4). We rigorously test our software, for instance through so called two species tests, to ensure that strict FDR control is maintained.

Spectronaut's unique advanced parallel processing functionality makes the best use of time and computing power. The software makes it easy to batch large datasets from thousands of samples for simultaneous processing across multiple nodes in the cloud or to start analysis while additional data is still being acquired (Figure 5).

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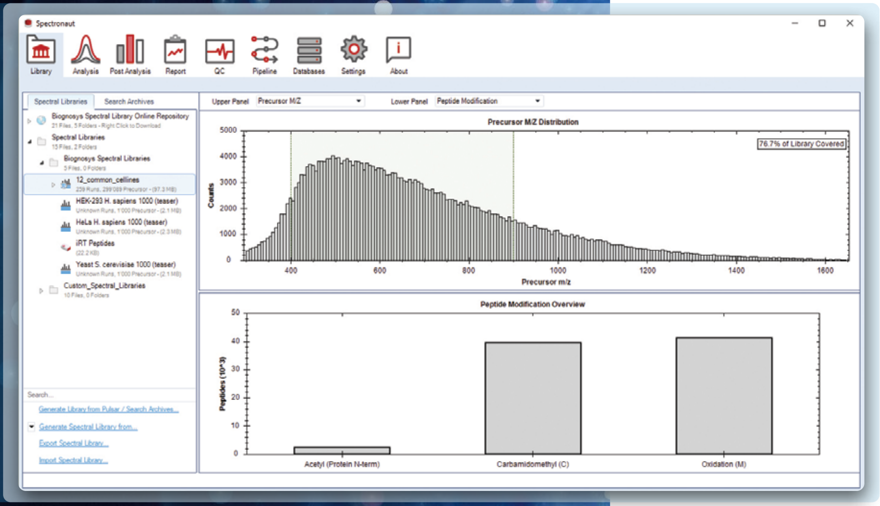
2 Rosenberger et al., Nat. Methods 2017,14, 921-927

PLUG-AND-PLAY DIA

Spectronaut® is the leading all-in-one solution for DIA, from library generation to biological interpretation of your results, with easy set-up and an intuitive user interface. Just add your data and start exploring.

Build and Import Spectral Libraries

Featuring Pulsar, Biognosys' search engine for DIA and DDA data, and Hybrid Library generation, Spectronaut also supports search results from MaxQuant, Mascot, Proteome Discoverer, ProteinPilot, and a text file format.



Upper Panel: Precursor M/Z

Lower Panel: Peptide Modification

Run and Review Your Analyses

Spectronaut's wizards make DIA analysis set-up simple and fast. Raw data can be reviewed during or after analysis with various visualization options including XICs, ion mobility plots, cross-run intensity alignments, protein coverage and more.

Upper Panel: XIC Graph

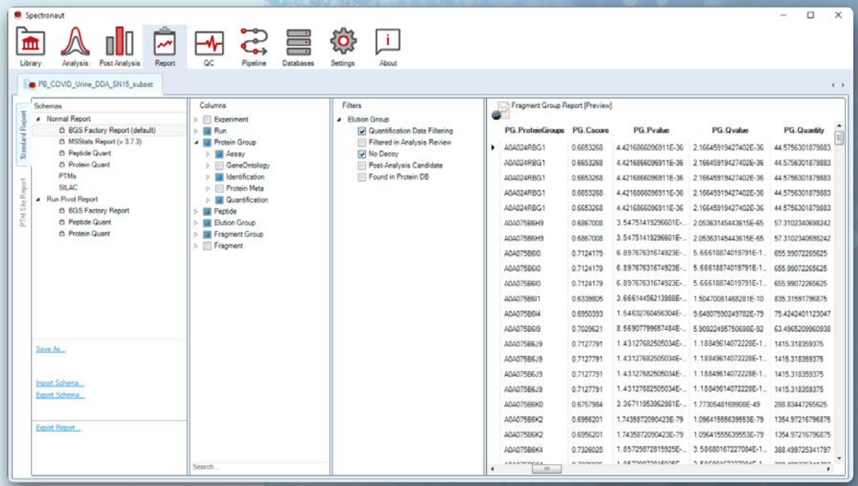
Lower Panel: MS2 Spectrum at Apex

380'976 Peptides remaining / 772'734 Peptides filtered

Unique precursors: 54'912 of 76'914 | modified peptides: 48'068 of 67'203 | peptides: 43'467 of 59'882 | protein groups: 5'112 in the experiment (Qvalue <= 0.01)

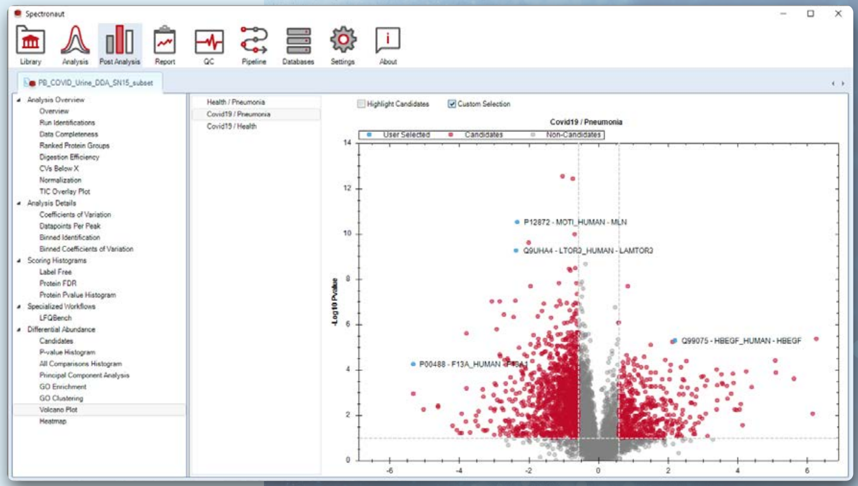
Explore Your Results with Ease

Take advantage of the interactive browser to quickly check for protein coverage. Use a range of plotting options to check data quality and relative abundance for proteins of interest.



Generate Custom Reports

Exporting your results is fully customizable. Obtain information about your analysis down to the fragment ion level and build detailed PTM localization reports. Our pre-built report schema make it easy to connect with external software.



Draw Experiment-level Conclusions

Explore results with intuitive visual plots. Spectronaut® routinely performs statistical analyses of all conditions, and exporting differential abundance candidates takes one click. Specialized plots provide insights into PTM profiles with no need for additional software.

HOW TO GET SPECTRONAUT®

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 Spectronaut 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 in order 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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