

Spectronaut™

powered by Pulsar

TAKE YOUR DIA DATA
TO THE NEXT LEVEL

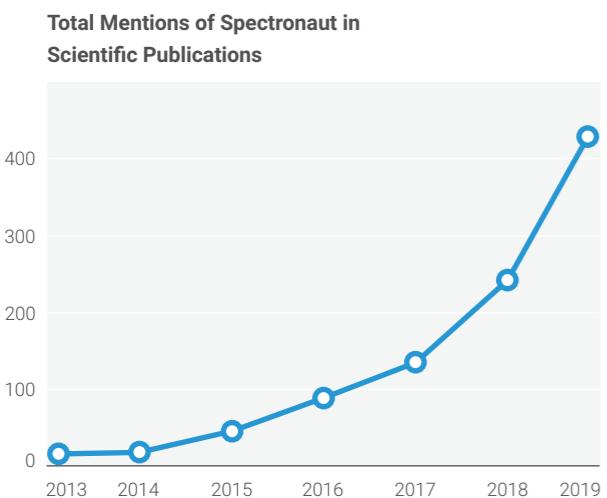
The Most Complete and Versatile Solution
for Quantitative Proteomics

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, we 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.



Supported Instrument Vendors

- Bruker
- SCIEX
- Thermo Fisher
- Waters

Recommended System

- For a typical experiment of 200 runs with a 100k precursor library
- Windows 10 x64
 - Intel or AMD CPU with 4 or more cores
 - 2 TB of hard drive space or more (2x data set size)
 - 16 GB of memory or more (1 precursor in 1 run amounts to ~0.5 KB of RAM)



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FEATURES

Performance

Unmatched accuracy and speed

Scalability

Analyze 10,000+ samples with large libraries and parallel batch processing

Versatility

Compatible with a wide variety of instruments and workflows including HRM™, WiSIM-DIA, SWATH™, SONAR™, BoxCar DIA, dia-PASEF®, FAIMS Pro, HDMS® 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

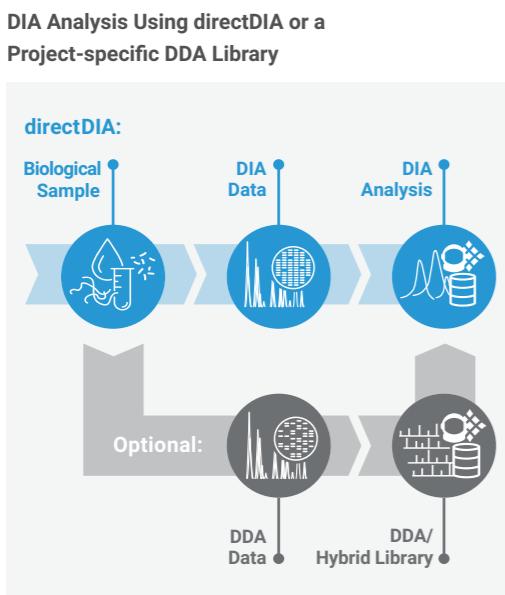
Effortless and robust analysis with automatic optimization of parameters

«We found Spectronaut to be the best match for our DIA projects. It provides the quantitative reliability we aim for, and the speed and scalability our workflows require.»

Prof. Jesper Velgaard Olsen,
CPR University of Copenhagen

LIBRARY GENERATION MADE EASY

Skip straight to peptide identification and quantification with Spectronaut's directDIA analysis, or create high-quality spectral libraries from DDA and DIA runs for your analysis workflow.



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 1). 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).

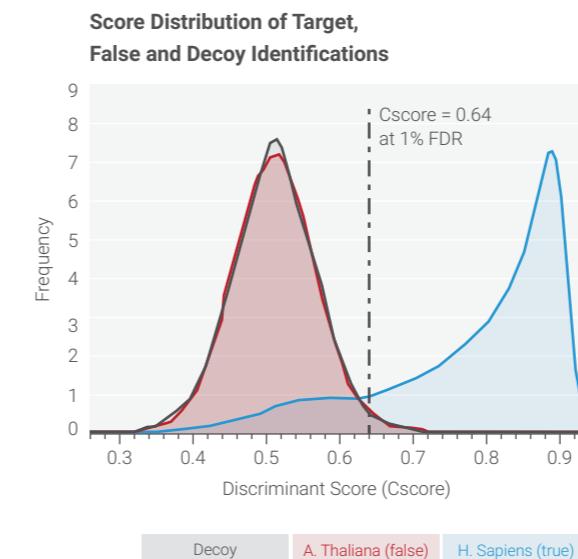
For cases where spectral library generation is still necessary, our powerful Pulsar search engine with deep learning augmentation is seamlessly integrated into Spectronaut, making it easy to generate state-of-the-art libraries from both DDA and DIA data. Different acquisition methods and search archives can also be combined to create hybrid libraries of increased depth while maintaining high precision indexed retention time (iRT) and full false discovery rate control. To help you jump-start your proteomics projects, Spectronaut comes pre-loaded with a selection of high-quality, species-specific search archives.

Spectronaut also supports analysis of labeling experiments, such as (pulsed) SILAC and spike-in workflows, with the ability to create completely labeled spectral libraries.

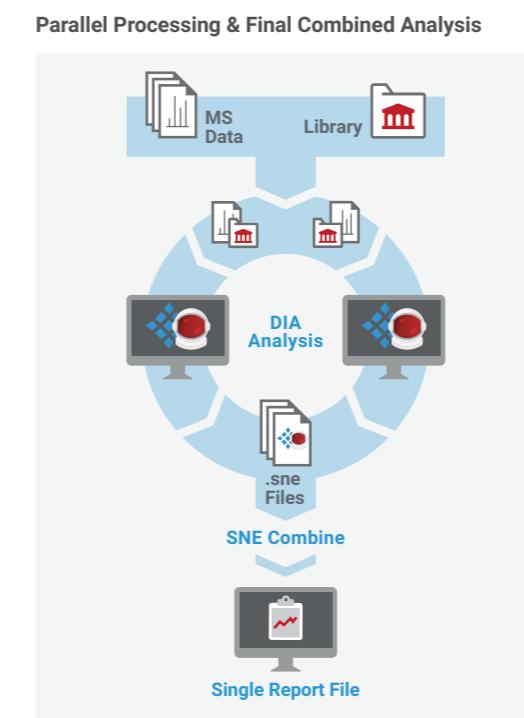


HIGH PERFORMANCE AND RELIABILITY AT SCALE

Spectronaut is the comprehensive solution for robust and reliable data analysis in DIA proteomics². Innovative data handling and false discovery rate control solutions allow efficient processing of large proteomics data sets with confidence.



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 1). 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 workstations or to start analysis while additional data is still being acquired. Outputs can then be merged to create the final report for statistical analysis (Figure 2).

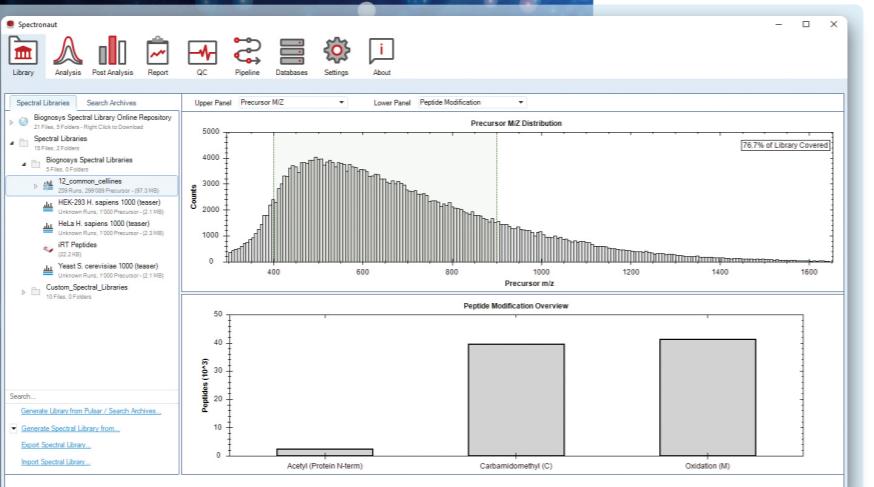
²) Rosenberger et al., Nat. Methods 2017, 14, 921-927

DIA MADE EASY

Spectronaut is the leading all-in-one solution for DIA, from library generation to biological interpretation of your results, with foolproof set-up and an intuitive user interface. The only thing you need to add is your data.

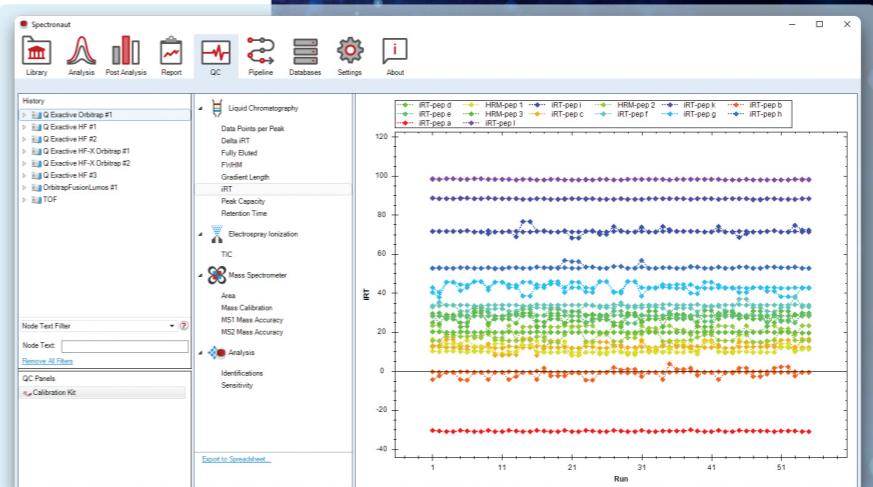
Library Perspective

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.



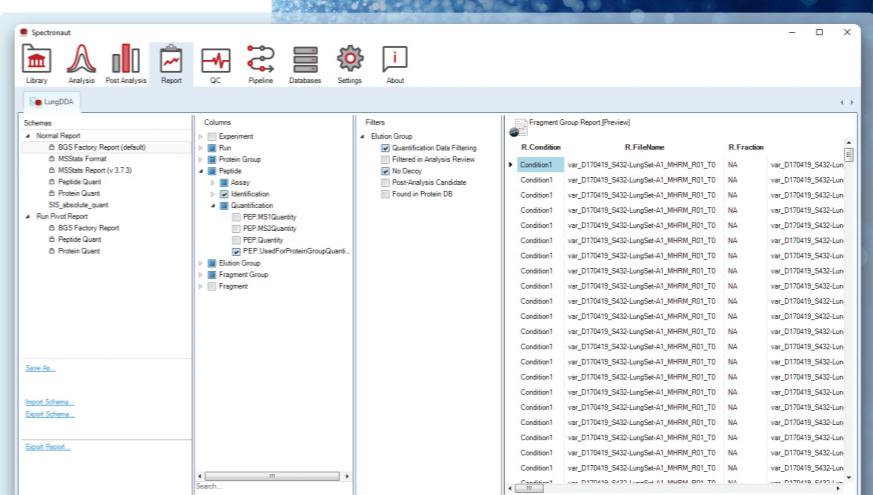
Analysis Perspective

The Spectronaut wizard makes DIA analysis set-up simple and fast. Raw data can be reviewed during or after the data analysis with various visualization options such as XICs, cross-run intensity alignments, protein coverage and more.



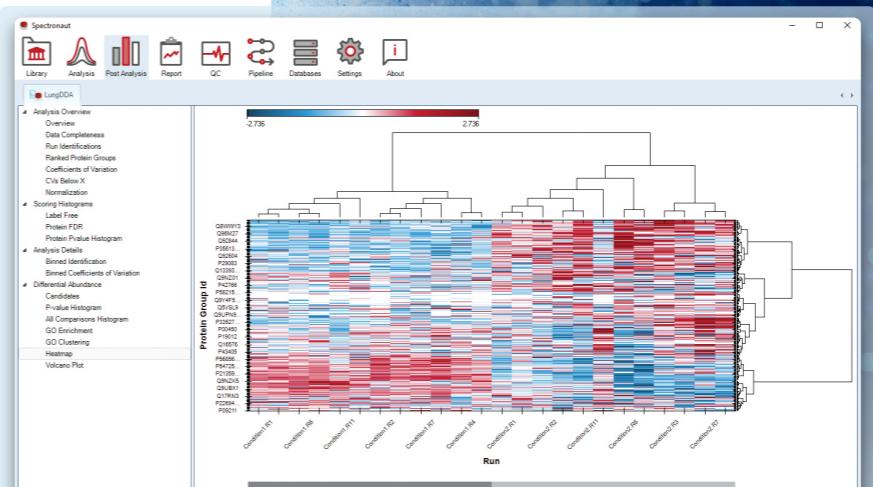
QC Perspective

Integrated quality control is achieved through the iRT Kit. Chromatography behavior and data analysis are monitored over time using several performance indicators including MS1 and MS2 accuracy, number of identifications, sensitivity, and more.



Report Perspective

Exporting your results is fully customizable. Obtain information about your analysis down to the fragment ion level and build custom report templates to automate future exports. Our pre-built report schemas are compatible with other pipelines.



Post Analysis Perspective

Explore experimental results with intuitive visual plots. Spectronaut routinely performs pairwise t-test comparisons of all conditions, and exporting your candidates takes one click. Enriched GO terms for further biological insights into your experiment are calculated by default.

HOW TO GET SPECTRONAUT

If you are interested in learning more about Spectronaut or would like to receive a free trial license, contact us at **order@biognosys.com**. For in-depth discussions or to arrange personal meetings to support you in implementing next-generation proteomics in your research facility, please reach out to **support@biognosys.com**. The Biognosys Team is looking forward to learning more about your specific research questions.

Biognosys is a leader in next-generation proteomics, dedicated to transforming life sciences by providing researchers with the most advanced proteomics tools. Biognosys offers a comprehensive suite of products and services to allow researchers unprecedented insights into the proteome through protein profiling and quantification in a variety of biological systems.

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NEXT GENERATION PROTEOMICS