

## Biognosys announces Spectronaut™ 10 – the newest release of its software for discovery proteomics using Data Independent Acquisition (DIA)



### RELEASE NOTE

Spectronaut™ 10 includes new advanced features for improved protein quantification and spectral library generation. These new features were benchmarked utilizing the new software tool recently published in *Nature Biotechnology*<sup>1</sup>.

#### Key new features of Spectronaut™ 10:

- ❖ Improved quantification logics (Quant 2.0) with new protein quantification algorithm (Protein Quant 2.0)
- ❖ Advanced tuning of spectral library generation
- ❖ Seamless integration of Spectronaut™ spectral libraries to be used in SpectroDive™
- ❖ Advanced raw file loading module for faster loading of raw data
- ❖ Gene Ontology capabilities for the annotation of identified protein groups

In case you have any questions about this release note or Spectronaut™ 10 software please contact us at [support@biognosys.com](mailto:support@biognosys.com).



# Spectronaut™ Software

## THE FASTEST AND MOST PRECISE PROTEOMIC ANALYSIS TOOL

### Hyper Reaction Monitoring and Spectronaut™

Hyper Reaction Monitoring (HRM-MS™) is Biognosys' proprietary label-free discovery proteomics workflow based on the targeted analysis of data independent acquisition (DIA) similar to SWATH™. The HRM workflow allows an unmatched proteome coverage with reproducible and precise quantification of up to 9'000 proteins per sample and injection<sup>2,3</sup>. Using Spectronaut™, the HRM workflow is ideal for identifying differentially expressed proteins or highly multiplexed protein quantification on a proteome scale.

Recently, a multicenter study benchmarked software tools used for the analysis of DIA experiments<sup>1</sup>. In this publication two samples were used to assess different performance parameters such as number of peptides identified, number of proteins identified, median coefficient of variation (CV) on peptide and protein level and many more. Spectronaut™ 7 (the release used for the publication) showed outstanding performance, especially on the number of peptides and proteins identified and the median CVs on both peptide and protein level.

Biognosys has since continued to drive the development of Spectronaut™. Now, Biognosys is proud to announce that with our latest release of Spectronaut™ 10 on November 30<sup>th</sup> 2016 we are able to further demonstrate substantial improvements. We assessed these improvements in a similar fashion using the tool from the benchmark study published in Nature Biotechnology<sup>1</sup>.

**We can see a substantial improvement in the number of peptides identified and quantified with CVs below 20% when comparing Spectronaut™ 7 to Spectronaut™ 10.**

	Version	CVs below 20% in A	CVs below 20% in B	Data Completeness
Peptides	Spectronaut 10	33194	36007	88.5%
	Spectronaut 7	32011	34573	88.2%
Proteins	Spectronaut 10	5659	5892	94.0%
	Spectronaut 7	3985	4247	93.9%

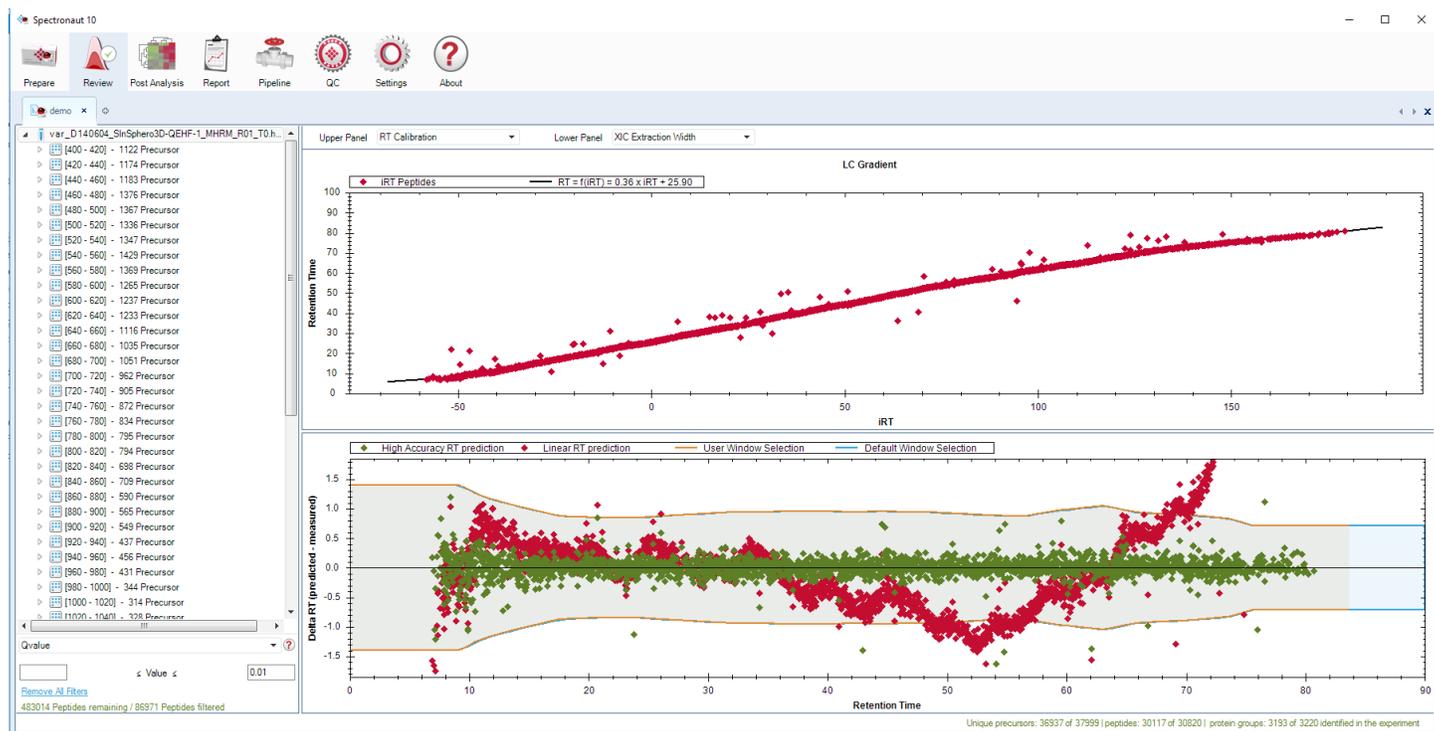
**Table 1:** Using the benchmark tool we evaluated Spectronaut™ 7 and Spectronaut™ 10. Spectronaut™ 10 features significantly more peptides and proteins quantified with CVs below 20%. Due to an improved algorithm to determine protein quantities the improvement is particularly large on the protein level. The coverage improvement is achieved without a decrease in data completeness (i.e. without increasing number of missing values).

On the protein level the same trend is observed. Remarkably, the novel quantification algorithm (Protein Quant 2.0) implemented in **Spectronaut™ 10 leads to 40% more protein quantities with CVs below 20%** as compared to Spectronaut™ 7 which was the version used in the publication. Importantly, these improvements are accomplished without a decrease in data completeness. As usual with Spectronaut™, the default analysis settings can be used for optimal performance. Tedious, manual optimization of multiple parameters is not necessary.

The main features in all perspectives of Spectronaut™ 10 have been revisited and extended. In the Prepare Perspective we have added more options for spectral library generation which allows the user to build spectral libraries that can be easily exported and used as panels for PRM and MRM



measurements in the SpectroDive™ software. For the DIA data analysis we have programmed a new data loading algorithm. Tested on Sciex data we could see a roughly four fold speed up in analysis time (41 as compared to 150 min for the analysis of six wiff files).



**Figure 1:** Review Perspective of Spectronaut™ 10 with the RT calibration using the high precision iRT concept showing in the upper panel and the dynamic, gradient dependent XIC extraction width in the lower panel.

We are continuing to drive the quality of quantification, robustness and scalability of the Spectronaut™ software to provide a professional solution for large scale experiments.

Spectronaut™ 10 – the newest and best release of Biognosys' proprietary software Spectronaut™ for LC-MS based discovery proteomics using data independent acquisition (or DIA) is now available. Request your license <https://biognosys.com/shop/spectronaut> or simply update your current version of Spectronaut™.

Additionally, Biognosys is giving a webinar on the new release on **Wednesday, December 7<sup>th</sup> 2016 at 5.00PM CET**. To register for the webinar please go to: <https://attendee.gotowebinar.com/register/217425504670634498>.

## References

1. Navarro, P. et al. A multicenter study benchmarks software tools for label-free proteome quantification. *Nat. Biotechnol.* (2016). doi:10.1038/nbt.3685
2. Bruderer, R. et al. Extending the limits of quantitative proteome profiling with data-independent acquisition and application to acetaminophen-treated three-dimensional liver microtissues. *Mol. Cell. Proteomics* 14, 1400–10 (2015).
3. Bruderer, R., Bernhardt, O. M., Gandhi, T., Gomez-Varela, D. & Reiter, L. Single shot deep DIA methods with optimal coverage, reproducibility and quantification precision. *ASMS 2016, San Antonio*.