

Press Release for immediate release.

## **New Spectronaut™ Pulsar from Biognosys enables spectral library free DIA**

**June 2nd, 2017 – Zurich-Schlieren (CH) – Biognosys AG, a leading proteomics company, announced today the release of its new toolbox for easy data-independent acquisition, DIA. The toolbox consists of the new directDIA™ workflow and Spectronaut™ Pulsar analysis software – enabling researchers with a DIA-performance workflow, without having to generate a spectral library.**

DIA is the most sophisticated discovery proteomics method available today. In a single measurement, all detectable peptides can be quantified with high sensitivity and reproducibility over a large sample size.

However, despite its benefits DIA has not been widely embraced by the global proteomics community, due to its perceived complexity. To perform targeted DIA analysis and achieve best performance, it is necessary to generate a spectral library through data dependent acquisition (DDA) measurements prior to commencing analysis. Until now, this has entailed long instrument runtime and significant overhead costs, especially in small experimental setups.

With directDIA™, available in Spectronaut™ Pulsar, proteomics researchers now have access to a workflow with the quantitative precision and reproducibility of DIA, and the operational simplicity of DDA.

Spectronaut™ Pulsar is a DIA analysis software with an integrated database search engine called Pulsar. It supports the spectral-library free workflow (directDIA™) as well as targeted analysis of DIA data using spectral libraries (Hyper Reaction Monitoring - HRM™).

"The development of the Pulsar search engine was the logical next step for Biognosys. It enabled us to seamlessly realize the directDIA™ workflow in Spectronaut™ Pulsar. We aimed for a user friendly and simple workflow and I think we have achieved that," said Lukas Reiter, Chief Technology Officer at Biognosys.

DirectDIA™ workflow is supported for Thermo Scientific™ Orbitrap™ platform while the HRM™ workflow supports data from high-resolution mass spectrometers from Bruker, SCIEX, Thermo Scientific™ and Waters.

With its diverse workflow capabilities and broad instrument vendor support Spectronaut™ Pulsar has the potential to cover the needs of a large number of proteomics researchers around the world.

### **About Biognosys**

Biognosys is the leading proteomics company offering innovative services and products for highly multiplexed protein quantification. We are dedicated to transforming the life sciences with superior proteomics solutions. Biognosys' next generation technology quantifies proteins with unbeatable precision and depth. Our solution relies on mass spectrometry, which allows simultaneous quantification of thousands of proteins in a single experiment. This new generation protein quantification technology is available to researchers worldwide through our contract research services or our portfolio of innovative reagent and software products. For more information, please visit [www.biognosys.com](http://www.biognosys.com).

### **About directDIA™**

DirectDIA™ is a data independent acquisition (DIA) based workflow implemented in Spectronaut™ Pulsar analysis software that enables reproducible and precise quantification of thousands of proteins in a single measurement without the need for DDA-based spectral libraries. For more information, please visit [www.directDIA.com](http://www.directDIA.com).

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