News

FOR IMMEDIATE RELEASE
Mass Spectrometry

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Biognosys and Evosep promote joined robust, high-throughput workflows for clinical plasma proteomics

Making clinical proteomics 100x more robust and 10x faster

Orlando, Florida – HUPO 2018 – (October 1, 2018) Today, at the 17th Human Proteome Organization World Congress, Biognosys and Evosep jointly promote a robust, high-throughput workflow for clinical research proteomics.

Mass spectrometry (MS)-based proteomics has become a powerful technology in biological research, and it is now poised to allow the characterization of the plasma proteome in great depth for clinical research applications. Together with recent advances in speed and increases in robustness in sample preparation, chromatography and data analysis, accurate proteome quantitation in high-throughput mode for thousands of samples is now possible.

Dr. Oliver Rinner, CEO Biognosys explains: "*Our PQ500™ multiplexed assay panel is suitable to quantify more than 500 proteins in a single measurement, and the resulting titration curve can be used for absolute label-free quantification of additional proteins not included in PQ500. With its ease of use and possibility for integration into several workflows, the panel is particularly well suited for large-scale experiments requiring high-throughput*."

Dr. Nicolai Bache, Head of Application, Evosep elaborates: "*The Evosep One separation solution fits perfectly with the multiplexing kits and DIA analysis software from Biognosys, offering robust, high-throughput sample separation for MS analysis with ease of mind for the customer*".

Dr. Petra Oliva from Genzyme (Sanofi) summarizes: "*The combination of PQ500 and Evosep One has streamlined some of our critical R&D workflows freeing up time and resources to take on new tasks*". Dr Oliva will be presenting her recent findings at HUPO in the joint seminar hosted by Biognosys and Evosep.

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For more information about the new Evosep One solution, please refer to a recently accepted paper in molecular cellular proteomics (1) and visit our booth #503 at HUPO 2018. Alternatively, please call +45 2633 2021, e-mail info@evosep.com, or visit www.evosep.com.

For access to all Evosep news and product photos related to HUPO 2018, please visit the online media room at www.evosep.com

About Biognosys

Biognosys is the leading proteomics company offering innovative services and products for highly multiplexed protein quantification. Biognosys is dedicated to transforming the life sciences with superior proteomics solutions. Biognosys' next generation technology quantifies proteins with unbeatable precision and depth. The 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 contract research services or the portfolio of innovative reagent and software products. For more information, please visit www.biognosys.com.

About Evosep

Evosep aims to improve quality of life and patient care by radically innovating protein based clinical diagnostics, initially through collaborations with world-leading scientists about developing new technologies and solutions to make sample separation 100 times more robust and 10 times faster than todays' alternatives. Proteomics is about the study of proteins in a biological mechanism, both their individual function and their combined interactions. For clinical proteomics the goal is to be able to quickly and efficiently compare a biological sample against a profile panel of selected proteins in order to deliver a diagnose / verdict of healthy or diseased (within given statistical margins). Such a profile is typically called a biomarker and for official approval, it must be demonstrated successfully on a large population. This calls for fast sample processing and because such clinical samples, in the form of blood or biopsies, are much more crude that the relatively clean cell cultures used in basic research, very robust protocols and consumables are also required.

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(1) "A novel LC system embeds analytes in pre-formed gradients for rapid, ultra-robust proteomics", *Nicolai Bache et al.,* Molecular & Cellular Proteomics August 13, 2018: http://www.mcponline.org/content/early/2018/08/13/mcp.TIR118.000853