

EVOS EP LAUNCHES END-TO-END PROTEOMICS WORKFLOW, SETTING A NEW STANDARD FOR AUTOMATED SAMPLE PREPARATION

Making clinical proteomics 100x more robust and 10x faster

[Houston, June 5th 2023] - Evosep, a leading provider of innovative solutions for proteomics research, proudly announces the release of End-to-End Proteomics Workflow. By combining advanced technologies with streamlined processes, Evosep has revolutionized the field of proteomics research, empowering scientists with enhanced throughput and automation capabilities.

Proteomics research plays a pivotal role in understanding complex biological systems and discovering novel biomarkers and therapeutic targets. However, the lack of standardized workflows and the labor-intensive nature of proteomics experiments have hindered progress in the field. Evosep's End-to-End Proteomics Workflow addresses these challenges head-on, offering researchers a comprehensive solution that accelerates discovery while maintaining high data quality and reproducibility.

Key features of Evosep's End-to-End Proteomics Workflow include:

- **Advanced Standardization:** Evosep has developed a novel approach to standardization, ensuring consistent and reliable results across experiments and laboratories. By implementing rigorous quality control measures and calibration protocols, researchers can confidently compare data and collaborate with colleagues, fostering advancements in proteomics research.
- **Enhanced Automation:** Leveraging state-of-the-art automation technologies, Evosep's workflow significantly reduces manual labor and improves reproducibility, allowing researchers to focus on data analysis and interpretation. From sample preparation to data acquisition, the entire process is seamlessly integrated, providing researchers with more time for critical decision-making and accelerating research timelines.
- **Scalability and Flexibility:** Evosep's workflow is designed to accommodate a wide range of sample types, including complex biological matrices with starting material containing 1 μ g of protein, i.e. 10 to 100 times less than most other automated workflows, while it also works highly efficiently and can be recommended over manual processing down to 1 ng of starting protein material.

- Cost of sample processing: Costs of enzymes, reagents, and buffers for processing proteomics samples is now on the order of 30 cents per single sample. With the high capacity of our workflow and its low running costs, the overall costs of large scale proteomics is thus greatly reduced and proteomics is now very affordable compared to every other large scale omics technique.

"We are thrilled to introduce our End-to-End Proteomics Workflow, which addresses long-standing challenges in the field of proteomics research," said Ole Vorm, Founder and Chairman of Evosep. "By combining standardization and automation, we aim to empower researchers with an efficient and reliable solution that propels the discovery of novel biomarkers, therapeutic targets, and personalized medicine. Eventually the cost of proteomics will be dominated by the cost of the depreciation of the mass spectrometer, but this new reliable and highly productive workflow is an important step for the field in terms of cutting expenses and assuring productivity!"

The system's modular design and customizable protocols enable researchers to adapt the workflow to their specific experimental needs, opening doors to diverse proteomics applications and expanding the boundaries of scientific discovery.

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For more information, please call +45 2633 2021, e-mail info@evosep.com, or visit www.evosep.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 today's alternatives. Information about Evosep is available at www.evosep.com.

The Evosep One instrument is for Research Use Only (RUO).

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