Next generation LC-MS based proteomics

A new era of speed, scale and robustness

Highlights

- Evosep Eno sets a new standard for high-performance separation
- Industry-leading robustness and throughput up to 500 samples per day
- Outstanding sensitivity and quantitative performance

A giant leap toward applied proteomics

Liquid chromatography-mass spectrometry (LC-MS) is a cornerstone of modern proteomics research, revealing the intricate interactions of proteins driving cellular function and disease. For decades, exploratory efforts pushed the boundaries of protein identification and quantification, with landmark studies mapping the human proteome, and generating deep protein profiles of single cell lines[1,2]. However, these achievements required extensive measurement times, laborious sample fractionation, and substantial starting material. Gaining proteomic depth meant sacrificing throughput, and labs developed specialized setups, which limited adoption by other research groups, hindered comparability, and precluded routine large-scale studies. Today, proteomics is undergoing a profound transformation. New technologies are overcoming these limitations, merging high proteome depth and throughput into standardized workflows. Among those advances is the Evosep Eno.

Three early adopters share how this instrument prepares them for next-generation proteomics – the paradigm shift that will launch scalable and robust sample interrogation in application areas like systems biology and precision medicine.

> *“We are very excited about the new Evosep Eno. When it was introduced, it was clear to me that it was the future.”*

Matthias Mann
Director of Proteomics and
Signal Transduction at the
Max Planck Institute

The Evosep Eno allows for:

- **Industry-leading robustness with 500 samples per day**
- **Boosts reproducibility across users**
- **Sets up and runs in a few hours**
- **Excellent peak definition and symmetry**

Evosep Eno: Charting a new course

Evosep is committed to improve the efficiency of LC-MS. We recognize that doing so with sights on next-generation proteomics hinges not on isolated technological advances but on integration across the complete workflow. True progress toward scalable analytics demands speed and sensitivity from sample to detector. Thus, workflow standardization is the core of our efforts. Consistent and robust workflows enhance the reproducibility of results, which is key to the widespread utility of an analytical tool. Second, standardized and easy-to-run methods promise to extend the benefits of proteomics to a wider user base.

The Evosep Eno is part of our contribution to next-generation proteomics: a robust high-throughput system for precise sample separation via, standardized workflows and enhanced integration with mass spectrometers. Evosep Eno is a bold step towards eliminating tradeoffs in proteomics. It massively accelerates sample throughput without compromising depth of coverage or reproducibility. Our early adopters agree.

> *“The Evosep Eno will make a big impact on the next generation of LC-MS based proteomics. We are very excited about the new 500 samples per day method that allows us to identify close to 7,000 proteins and quantify 70,000 precursors in every run. That is absolutely amazing.”*

Dr. Jesper V. Olsen,
Executive Director of the
Novo Nordisk Foundation
Center for Protein
Research

Throughput to fuel large-scale studies

Dr. Jesper V. Olsen is Executive Director at the Novo Nordisk Foundation Center for Protein Research, where he examines post-translational protein modifications involved in cell signaling.

From his perspective, next-generation proteomics “*will play a role in global health efforts and precision medicine.*” The scale of analytics needed to address clinical and public health questions is large, making throughput a decisive factor in the adoption of proteomics.

In Olsen’s lab, the Evosep Eno enabled unprecedented sample throughput and identifications. He shares that “*the main advantages of the new Evosep instrument are higher throughput and more identifications, even with the same gradients. The chromatographic performance is exceptional.*”

Precisely this throughput, says Olsen, opens a vast frontier of application areas, including systems biology research, drug development, and large-scale clinical studies. These complex, multifactorial research projects systematically analyze thousands of samples, various drug concentrations, multiple time points, and different cell lines. With a daily LC-MS throughput of 500 samples, work that previously took weeks or months to complete can now be done in days.

That higher throughput also translates to more efficient use of a mass spectrometer. Running samples at a pace that minimizes idling of the detector offsets the purchase, installation, and operation costs of these powerful instruments, making proteomics increasingly affordable.

Reproducibility to foster collaboration

For a technology to achieve widespread adoption, particularly in applied fields like clinical proteomics, consistent and reproducible results are paramount, regardless of the user’s technical proficiency. As Dr. Ulises Guzman from Olsen’s lab emphasizes, “*one of the big challenges is robustness and reproducibility across laboratories*”. This consistency underpins rigorous hypothesis testing and enables researchers to confidently exchange, compare, and build upon each other’s data.

Focused on developing methods to improve proteomics, Guzman underscores the importance of reproducible gradients to bring reliability to applied proteomics. “*Evosep is working to provide the same gradient that can be easily reproduced between labs globally. This is essential for putting proteomics at the center of clinical applications.*” And the coupling of reproducibility with high throughput and resolution is what stands out in the performance of Evosep Eno. “*I think the throughput is fantastic*,” Guzman continues. “*We can get very deep proteome coverage at high throughput, which is a powerful combination, especially for plasma proteomics or clinical proteomics in general.*”

Crucially, achieving these reproducible and reliable results at scale is intrinsically linked to robust usability – analytical systems that are straightforward to implement and minimize operator-dependent variability. LC-MS based proteomics was initially developed within expert communities, but the transformative potential of next-generation proteomics lies in its accessibility and ease of use for non-experts. The Evosep Eno excels on this front as well.

With robust engineering, intuitive handling, and ease-of-use, Olsen’s lab had the instrument installed and running in two hours.

Standardization to disrupt the status quo

Asked what it will take to introduce proteomics into clinics, Dr. Matthias Mann has one word: *Standardization*. As Director of Proteomics and Signal Transduction at the Max Planck Institute, Mann has worked tirelessly to make

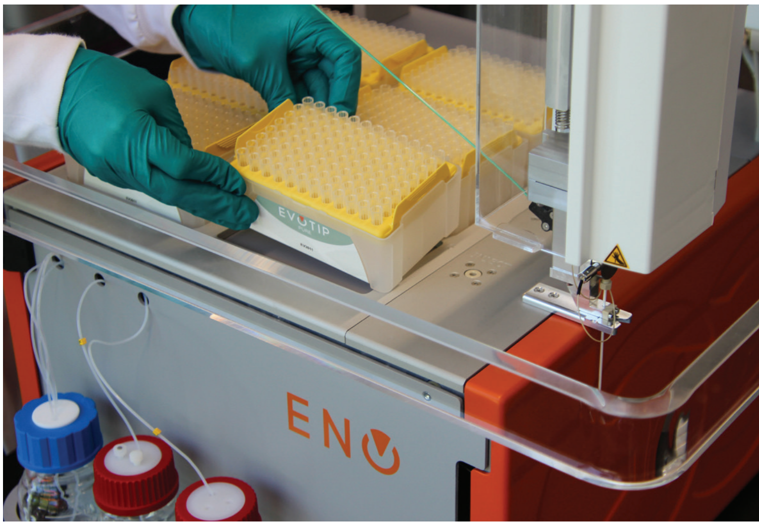
> *“I was very surprised by how easy it was to work with the Evosep Eno. We had it up and running within 2 hours of receiving it. Optimizing MS methods was so fast that it was challenging for our QC system to keep up with the data generation!”*

Dr. Ulises Guzman,
Postdoctoral Researcher in
the Olsen Group

proteomics ready for the clinic. His group has made significant contributions to enabling next-generation proteomics, like tackling the challenges of adequate depth in the proteomic analysis of plasma. In fact, Dr. Mann highlights a liver test by plasma proteomics that you can order today at the University Hospital. "*This is a first in the world,*" he explains, "*but it needs to be spread globally, which will take some time.*"

A significant hurdle until now has been reliance on expertise. "*Historically, proteomics has been very cumbersome,*" Mann explains. "*People had their own columns and setups, which weren't comparable. That has now changed.*" For Mann and his team, the Evosep Eno delivers high performance and long-awaited throughput while maintaining the routine setup needed for clinical applications. "*This is the highest performance instrument in terms of peak shapes, resolution, and sensitivity. The retention time accuracy between runs is within a few seconds, which I never thought possible for an LC system. I'm excited that we can now do everything needed for the clinic without sacrificing performance.*"

Looking into the future, all three scientists recognize the importance of establishing a norm within the proteomics community that democratizes the use of LC-MS. "*It will be important to standardize the full workflow, from sample prep to LC-MS and the downstream computational analysis of datasets,*" says Olsen. "*But it has been hard to come to an agreement in the community on how to do this.*" Mann agrees and urgently calls for a change in mindset. "*We need to move away from lab- and person-specific protocols and focus more on standardization and simplified workflows. That may restrict choices a bit, but it's necessary to make proteomics accessible and robust for non-specialists.*"



Unleashing next-generation proteomics hinges on that evolution in thinking, with platforms like Evosep Eno leading the way in facilitating accessible and robust analytics. In Olsen's words: "*Innovative, carefully engineered platforms like the Evosep Eno contribute to standardization, robustness, and the implementation of automated workflows. This is definitely where we need to go as a community to enable the next stage of proteomics.*"

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1 Aebersold, R. et al. 2016. Mass-spectrometric exploration of proteome structure and function. Nature.

2 Bekker-Jensen, D. et al. 2017. An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. Cell Systems.

The Evosep Eno is for General Laboratory Use