Case study

EVOSEP

Evosep Eno accelerates high-throughput targeted proteomics at the University of Iceland

Highlights

- 192 samples in 2 days instead of 9
- Reduction in solvent cost and consumption of isotopically labeled peptides
- Seamless Evosep Eno™ and Evosep Pod™ integration with Waters™ MS simplifies control and daily operation

A national hub for proteomics

At the University of Iceland, Professor Margrét Thorsteinsdottir leads a highly versatile mass spectrometry (MS) laboratory in collaboration with Professor Óttar Rolfsson. Her group develops and applies quantitative MS methods for a wide range of applications - from natural product discovery and metabolomics to bioanalytical studies in clinical research - and diverse biological matrices. Working closely with Landspitali - University Hospital, Iceland, they search for biomarkers for disease diagnosis and progression and monitor therapeutic response in patients. As demand for large-scale quantitative proteomics grew, the existing LC-MS workflow became a limiting factor.

Because Iceland's research community is small, Margrét's lab is essentially a national resource for MS-based quantification, supporting projects that span pharmaceutical, clinical, and environmental sciences. In collaboration with Professor Christoph Borchers at Segal Cancer Proteomics Centre at Jewish General Hospital, Lady Davis Institute, McGill University and MRM Proteomics in Montreal, Canada, they have developed a targeted proteomics workflow for quantification of protein biomarkers in biofluids for different research projects.

Her team recently installed an Evosep Eno system and an Evosep Pod, integrated with a

> *"We're the only group in Iceland equipped for large-scale LC-MS quantification, and we collaborate with everyone from clinicians to chemists and develop methods that fit their research."*

Margrét Thorsteinsdottir
Professor of Pharmaceutical Sciences, University of Iceland

By integrating the Evosep Eno and Evosep Pod with the Waters MS system, the University of Iceland lab achieves:

- **Above 99% solvent reduction per run**
- **75% shorter LC-MS runtime (1 hour to 15 min)**
- **4.5x higher throughput (192 samples in 2 days instead of 9)**
- **Improved automated data analysis**
- **90% reduction in ^{13}C-labeled internal standard peptide use**

Waters Xevo TQ Absolute. The Evosep Eno is a low-flow LC system for high-throughput peptide separations, while the Evosep Pod provides seamless integration with stable column temperature control during analysis. This configuration expands the lab's capabilities into high-throughput, reproducible proteomics, bringing robust, large-scale LC-MS workflows to Iceland.

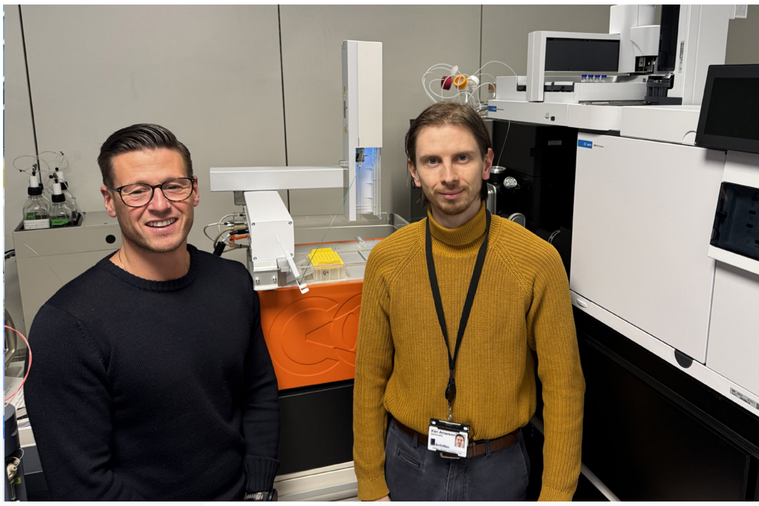
Seamless system setup and onboarding

When the Evosep Eno system was installed, Margrét's team became the first in Iceland to operate this configuration.

Before adopting the Evosep Eno, the lab relied on a conventional UPLC-MS (ultra-performance liquid chromatography MS) platform. Analyzing 192 samples on that system took about nine days, with each run lasting more than an hour. Sample preparation took roughly two full days and involved several labor-intensive steps, including lyophilization and solid-phase extraction.

> *"Everything connected immediately – the LC, the MS, and the software – and we could start analyzing samples soon after."*

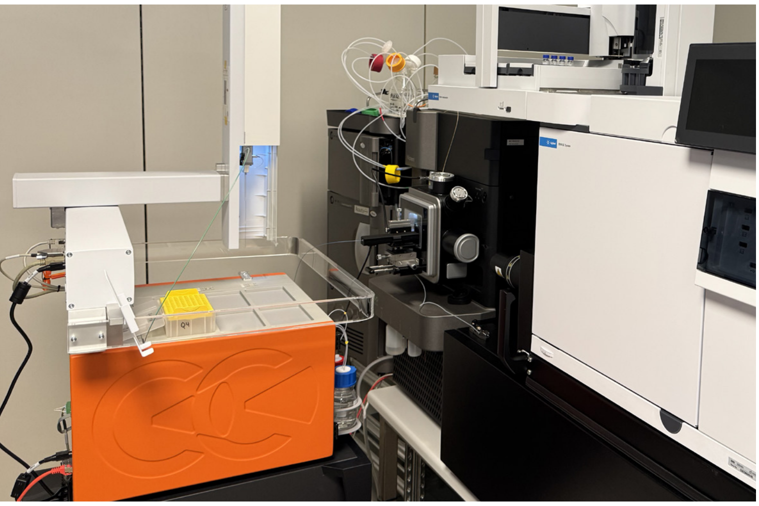
Margrét Thorsteinsdottir
Professor of Pharmaceutical Sciences, University of Iceland



The installation of the Evosep Eno, followed by integration of the Evosep Pod, replaced that workflow entirely. The new configuration is fully integrated and controlled through Waters MS control software, eliminating the need for manual temperature controllers and external connections.

Setting up the new system was straightforward. Evosep's field engineer, already experienced with Waters instruments, completed the installation and software configuration in less than a day, and the team could start collecting data right away. "*Everything connected immediately – the LC, the MS, and the software – and we could start analyzing samples soon after*," Margrét recalls.

The new workflow allows a small team to manage a demanding number of samples efficiently. One LC-MS technician oversees instrument operation, while a PhD student prepares and runs samples for their ongoing study. The system is easy to operate and is ideal for demanding quantitative workflows.



Streamlined control and clean results

Once the Evosep Eno was running routinely, Margrét's group began to see how its engineering refinements translated into everyday efficiency.

The Evosep Eno–Evosep Pod–Waters integration replaced the lab's improvised setup that had required external controllers and additional attention. With everything now managed from a single interface, the team no longer needs to monitor separate heaters, valves, or switches. "*Now we control everything directly through MassLynx,*" Margrét says. "*It's stable, predictable, and a lot simpler to run.*"

The new setup also simplified sample handling. Using Evotip Pure™ eliminates lengthy wash steps and minimizes the risk of carryover, making batch preparation faster and more consistent. Now, the same number of samples can be prepared in about ten hours, including a four-hour digestion step. For future projects, the team expects to shorten digestion to just two hours, further reducing total preparation time to around eight hours.

"*Loading is quick and reproducible,"* she explains. *"We still run calibration curves and QC samples in every batch, using isotopically labeled peptides for absolute quantification, but the system runs smoothly.*"

This reliability has increased the lab's overall mass spectrometer utilization; previously idle hours are now filled with consistent data acquisition, while QC metrics remain stable across multi-day sequences.

Reduced runtime by 75%

The performance gains with the new setup were immediately clear. With the Evosep Eno, the average sample runtime dropped by 75%, reducing the time to process 192 samples from about nine days to two.

"*If we'd tried to run our current study on the old system,*" says Margrét, "*we'd still be collecting data this time next year.*"

The team also reports stronger signal intensity and better peak symmetry, especially for early-eluting peptides. "*Before, we sometimes lost signal on those front-end peptides,*" Margrét notes. "*Now the peaks are symmetrical and clean enough that Skyline's automatic quantification can handle them without manual adjustment.*"

These cleaner peaks have made data analysis faster and more consistent, reducing the need for hands-on review while maintaining quantitative precision.

Across multi-day batches, the system has shown consistent performance with no significant drift or carryover.

Orders of magnitude reduction in solvent consumption to 99% relative to conventional LC methods - a meaningful difference when running thousands of samples.

For Margrét's team, the impact is clear: faster analysis, improved signal quality, and less hands-on review, all without sacrificing precision.

Scaling up with confidence

For Margrét and her team, the real measure of success will be whether the workflow can hold up when the sample count moves from

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hundreds to thousands. Her group is now applying the Evosep Eno-Evosep Pod-Waters MS configuration to a collaboration with the Icelandic Heart Association, analyzing 4000 clinical serum samples from well-characterized patient cohorts. The goal is to identify protein biomarkers that can flag individuals at risk for myocardial infarction.

"*These samples represent years of clinical data,*" she says. "*With our new setup, we can analyze them efficiently and hopefully make a real impact.*"

So far, they have processed about 1400 of the samples. The stability of the LC-MS pairing has been critical: retention times remain consistent and peak shapes reproducible across multi-day sequences, supporting direct comparison over long study timelines.

To further increase throughput and reduce hands-on time, the team is working to integrate a liquid-handling robot for automated sample preparation and Evotip loading. The workflow is still being adapted for automation as they refine timings and conditions for robotic operation.

For now, the focus is on completing the 4000-sample study, but the momentum is clear. Several new projects are already waiting in line for instrument time - a sign of how valuable high-throughput proteomics has become within Iceland's research community. With a reliable workflow in place, the team is well positioned to expand collaborative studies and continue pushing the boundaries of clinical proteomics.

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