An Evosep White Paper

# Evosep Proteomics: A standardized ecosystem from sample to separation

## Introduction

Proteomics is entering a phase where scale, reproducibility, and data insights define its value. The field is shifting from maximizing depth in individual analyses to establishing consistent, comparable measurements across large cohorts, laboratories, and time. This transition is not incremental, it represents a structural change in how proteomics generates impact in research, drug development, and clinical applications[1].

At the center of this shift is the need for standardized, scalable workflows that produce data that can be trusted beyond a single instrument or study. Without this, increasing throughput only amplifies inconsistency, and incremental sensitivity gains do not translate into real-world utility.

A critical gap remains: the inability to generate reproducible proteomics data across sites and workflows at scale. This limitation continues to constrain confidence in results, slow down translational research, and limit the adoption of proteomics in regulated and clinical environments. Standardization is therefore not an optimization—it is the prerequisite for the field to scale.

At the same time, proteomics is becoming inseparable from AI-driven analytics. These approaches depend fundamentally on structured, high-quality, and comparable datasets. Fragmented workflows and variable outputs force models to learn noise rather than biology, undermining their predictive value. In contrast, standardized data enables models to generalize across cohorts, uncover subtle biological signals, and support decision-making in drug discovery and clinical research.

Evosep Proteomics is designed to address this convergence. It represents a transition from isolated tools to an integrated ecosystem that standardizes the entire proteomics workflow—from sample input to LC–MS separation. By combining Evokit™ sample preparation, the Evosep Lupo™ Sample Preparation System, and Evosep Eno™ separation platform, Evosep Proteomics establishes a unified, sample to separation solution built for reproducibility,

scalability, and AI-ready data.
In this framework, standardization is not limited to harmonizing protocols. It is implemented as a fully integrated system, where consumables, instrumentation, and workflows are co-designed to deliver consistent performance across operators, studies, and laboratories. The result is a shift from proteomics as an expert-driven practice to proteomics as a reliable, operational capability.

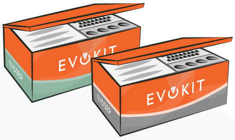
The path forward is clear: proteomics must evolve into a standardized, scalable measurement system capable of supporting large-scale biology, AI-driven discovery, and clinical translation. Evosep Proteomics defines this new operating model.

## Robust sample preparation is the key to scalable proteomics

Sample preparation remains the largest source of variability in proteomics workflows and therefore the primary barrier to reproducibility at scale. Manual handling, protocol variability, and differences in reagents and execution introduce inconsistencies that propagate through LC–MS analysis. As study sizes increase into hundreds or thousands of samples, these inconsistencies obscure biological signals and reduce confidence in downstream conclusions.

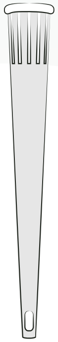
Addressing this challenge requires a fundamental shift: variability must be controlled at the sample input level, not only downstream. This demands standardized, automated, and traceable workflows that minimize operator dependency and ensure consistent sample quality across all runs.

Evosep Proteomics extends standardization upstream by integrating sample preparation into the same controlled ecosystem as LC separation. The combination of Evokits, Evosep Lupo, and the Evosep Eno creates a unified workflow with Evotip Pure as the crucial link between sample preparation and LC-MS analysis, ensuring each stage delivers consistent, optimized outputs.

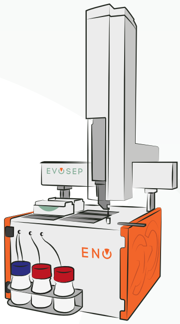


**Evokits**
– standardized kits combining all required reagents, consumables and Evotips with predefined, standardized workflows.

**Evosep Lupo**
– a dedicated platform to execute Evokits with minimal hands-on time and built-in traceability.



**Evotip Pure**
– the critical link between sample preparation and LC-MS analysis, ensuring clean, consistent sample transfer and enabling decoupling of the workflow.



**Evosep Eno**
– robust, high-throughput, LC separation, maintaining reproducibility at scale.

Together, these components form an integrated ecosystem where processes, and outputs are controlled as a single system rather than independent steps.

This ecosystem approach eliminates the need for method development and optimization, accelerates adoption, and ensures that proteomics workflows scale without introducing additional variability. The initial Evokit portfolio – including digestion and quality control kits – establishes the foundation, with a clear path toward application-specific kits tailored to different sample types and research needs.

## Built-in controls, traceability, and automation

For proteomics to operate reliably in large-scale and regulated environments, reproducibility must be continuously verified – not assumed. This requires integrated quality control, full traceability, and automation that reduces risk at every step.

Evosep Proteomics embeds these capabilities directly into the workflow.

> Each Evokit incorporates built-in quality controls, including:
>
> - Process control samples that monitor the full sample preparation workflow
> - System suitability controls that verify LC–MS performance over time

These controls are executed as part of the routine workflow, enabling continuous performance monitoring without adding operational complexity.

At the same time, end-to-end traceability ensures that every parameter – from sample identity to reagent usage and execution steps – is digitally recorded and linked to the dataset. This structured approach enables complete auditability, supports long-term studies, and meets the requirements of regulated environments.
Automation through the Evosep Lupo platform further reduces variability and operational risk. The system incorporates intelligent checks for consumables, plate positioning, and workflow execution, minimizing human error. Combined with a simplified interface and predefined workflows, this allows true walk-away operation, enabling users to generate reproducible, high-quality data without specialized expertise.

Importantly, this level of control does not add complexity – it removes it. By embedding standardization into the system itself, Evosep Proteomics makes reproducibility inherent rather than dependent on operator skill. Furthermore, the entire ecosystem is fully supported, providing the additional trust and security needed in the experimental execution.

## Standardization as the enabler of AI-driven proteomics

A standardized ecosystem fundamentally changes the role of proteomics data. When variability is controlled across sample preparation, separation, and analysis, datasets become directly comparable across runs, sites, and time. This increases statistical power, reduces bias, and enables new classes of analysis that are not possible with fragmented workflows.

This is particularly critical for AI-driven applications. Machine learning models require large volumes of structured, consistent data to deliver reliable outputs. Evosep Proteomics provides the foundation for this by ensuring that data is generated in a uniform, analysis-ready format.

As a result, proteomics can:

- Detect subtle biomarker patterns across large and diverse patient cohorts
- Enable robust predictive models for disease classification and treatment response
- Support AI-driven decision-making in drug discovery and development

By delivering low-variance, comparable datasets at scale, Evosep Proteomics transforms proteomics into a viable data layer for AI – bridging the gap between biological measurement and computational insight.

## Conclusion

Proteomics is moving from a fragmented, expert-driven discipline toward a standardized, scalable infrastructure for biology, medicine and industry. The limiting factor is no longer instrumentation capability, but the ability to produce consistent, comparable data across workflows and environments.

Incremental optimization of individual workflow steps is no longer sufficient. The next phase of the field requires fully integrated systems that deliver reproducibility, scalability, and simplicity as a baseline.

**Evosep Proteomics** defines this transition. By standardizing sample preparation, automation, consumables, and LC separation into a unified ecosystem, it removes variability at the source and enables proteomics to operate as a reliable, high-throughput measurement platform.

This ecosystem approach allows proteomics to scale across research, drug development, and clinical applications while providing the data foundation required for AI-driven discovery. It transforms proteomics from a specialized analytical technique into a standardized, operational capability that can be deployed across laboratories and organizations.

The direction is clear: Proteomics must become consistent, scalable, and accessible to deliver its full impact.

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[1] *Evosep white paper, WP 001 The Era of Industrial Proteomics.*