illumina®

CUSTOMER INTERVIEW

Beyond the Genome: How Proteomics Is Transforming Precision Medicine Research

Introduction

María Bueno Álvez
Postdoc at Mathias Uhlén Lab, KTH in Stockholm, Sweden

María Bueno Álvez earned her PhD from the Royal Institute of Technology (KTH) in Stockholm, Sweden, in May 2026. She conducted her doctoral research under the supervision of Professor Mathias Uhlén at SciLifeLab, where her work focused on plasma proteomics and the identification of circulating protein signatures associated with a broad spectrum of diseases, including cancer, cardiovascular, metabolic, autoimmune, infectious, and pediatric conditions. Her research contributed to the Human Disease Blood Atlas, a comprehensive resource aimed at mapping the circulating proteome across diseases and throughout the human lifespan to support biomarker discovery and precision medicine research. María holds a BSc in Genetics from the Autonomous University of Barcelona and an MSc in Molecular Techniques in Life Science from KTH, Karolinska Institutet, and Stockholm University.

"The most exciting insight is that we can learn so much from such a simple blood sample."

Proteomics is rapidly becoming a critical layer in multiomics research, offering a dynamic readout of biology that can connect molecular changes to disease mechanisms, population-scale studies, and precision medicine research. In this interview, María Bueno Álvez discusses what plasma proteomics can reveal from a simple blood sample, how affinity-based approaches and mass spectrometry complement one another, and what breakthroughs could shape the field over the next five years.

Interview

What were the most surprising biological insights that emerged from mapping the human blood proteome at this scale?

The most exciting insight from this project was how dynamic the proteome is across the lifespan. In healthy adults, the proteome is remarkably stable: many proteins remain consistent, and individuals resemble themselves across the years. In contrast, during development, when the body is undergoing major physiological changes, the proteome reflects those changes in a very elegant way.

The same is true in disease. We are able to capture proteins in the blood that originate from specific tissues, for example. This means it is possible to begin disentangling what is happening across the whole body, and across different organs, using just a drop of blood. For me, the most exciting insight is that we can learn so much from such a simple blood sample.

Where does proteomics add unique value in multiomics studies that cannot be captured by genomics or transcriptomics alone?

Compared with genomics, proteomics offers a dynamic readout of biology, changing across a lifetime and even within a day. Longitudinal sampling can capture these shifts and reveal how the body changes over time.

Transcriptomics is also dynamic, but proteomics sits closer to the biological pathways that shape disease. Although more complex, it brings us nearer to the molecular mechanisms driving disease.

This makes plasma proteomics especially valuable: circulating proteins offer an accessible path toward precision medicine, from new screening tools to understanding drug effects.

How would you describe the current state of proteomics in terms of scale, reproducibility, and biological insight compared with other omics layers?

Proteomics is rapidly catching up with genomics and transcriptomics. It is already being applied at scale, measuring thousands of proteins across thousands of samples, while both mass spectrometry and affinity proteomics continue to expand measurable targets.

Reproducibility is also improving, with strong coefficients of variation across platforms as technologies mature.

Where proteomics really shines is biological insight and actionability. Although protein complexity made it slower to scale, its potential is enormous.

What are the most important technical or analytical bottlenecks still limiting broader adoption of proteomics in research?

In plasma proteomics, many challenges come from the sample matrix. Plasma has an extremely wide dynamic range, where a few abundant proteins can mask lower-abundance ones.

This is where affinity proteomics shines, with broad targeted platforms that measure thousands of proteins. Key barriers to broader clinical research adoption remain absolute quantification, isoform resolution, and interpreting the biological meaning of detected proteoforms.

Coverage is also still incomplete. Current platforms capture thousands of proteins, but the measurable plasma proteome remains only a fraction of the potential human proteome.

As more data is generated, interpretation will become the major challenge: understanding what appears in the plasma proteome, which tissues and processes contribute to it, and how computational analysis can keep pace with platform development.

Affinity-based proteomics and mass spectrometry are often seen as complementary. How do you define their respective roles today?

I think these two platforms are indeed complementary, and they have very different analytical strengths, which is a good thing. Today, both are heavily used in discovery studies. Mass spectrometry excels at unbiased discovery and peptide-level characterization of proteins, including resolution at the level of proteoforms and post-translational modifications.

When we want to carry out large-scale proteomic discovery in the very low-abundance proteome, affinity-based methods really shine. We have seen impressive libraries that can now measure thousands of proteins very reproducibly.

It is an exciting time for proteomics because these two platforms can increasingly be combined. They are becoming cheaper and more accessible to the community. By using them together, we can obtain isoform resolution and deep characterization of the most abundant to medium-abundance proteins, while also gaining very sensitive detection of thousands of low-abundance proteins. I really think we are at a point where we should be running these two approaches in parallel as much as resources allow.

How do affinity-based proteomics and mass spectrometry methods compare in the information they provide per sample?

Overall, mass spectrometry offers a broader, unbiased overview of the sample, while affinity-based approaches provide more comprehensive characterization of the proteins included in their panels. Again, I see them as complementary: they provide different angles on the same biology.

The information that is really unique to mass spectrometry is the ability to look at isoform resolution and changes occurring within a single protein species. With affinity-based proteomics, the exact information depends on the platform, but we can also obtain different readouts for the same protein. What is unique here is that we get a robust signal for every protein, with the ability to measure thousands of relevant proteins in very large cohorts.

What are the key trade-offs between these approaches, particularly around depth versus scale and specificity versus throughput?

Both approaches have advanced tremendously and are now capable of generating very large-scale proteomics datasets, but they have evolved with slightly different strengths. Mass spectrometry offers a more unbiased view of the proteome with peptide-level information, while affinity-based methods use predefined panels.

Depth often comes at the expense of throughput, and processing very large cohorts is still more challenging with mass spectrometry. Affinity-based methods sacrifice some flexibility in exchange for higher throughput.

As I mentioned earlier, affinity-based platforms excel at sensitive and reproducible measurements across very large cohorts. Mass spectrometry, on the other hand, provides greater resolution for detecting protein proteoforms and different post-translational modifications.

How do you see high-throughput proteomics advancing translational research, particularly in large-scale population or longitudinal studies?

I believe we are seeing a revolution in population and longitudinal studies. I recently returned from a community meeting on the human proteome and health, and it was clear this is where the future is heading.

We are now using these technologies to profile thousands of biobank samples. From plasma, we can stratify individuals by disease risk, monitor changes over time, identify potential therapeutic targets and better understand differences in the circulating proteome across ancestries.

Many biobank samples already exist, and as technologies catch up, we can apply proteomics to deeply characterized samples with genomic, transcriptomic, and rich phenotypic data. Proteomics adds a key layer of biological insight, and I am excited to see how it will push translational research and precision medicine research forward. Although advances have been made in several diseases, there is still much more to uncover.

Looking ahead five years, what technological or computational breakthroughs will most shape the future of proteomics?

I am excited to see how the field develops over the next five years. Technologically, both mass spectrometry and affinity-based proteomics will continue improving at what they already do well. We will see better coverage and learn more about what each approach is still missing.

For example, affinity-based methods may cover more proteoforms and expand protein coverage. I also expect us to profile more sample types. I work a lot with plasma, and the growth of dried blood spots makes me optimistic about their potential for precision medicine research.

As technologies improve and costs decrease, we will be able to profile more biobank samples. This will help us compare findings across ancestries and across diverse or rare diseases that smaller studies may miss. I am also looking forward to deeper integration of proteomics with other omics.

Even more exciting is how plasma proteomics will connect with single-cell proteomics, spatial proteomics, and other emerging fields. As we generate more data, computational integration will become essential.

In large-scale biobanks, shared reference samples can help bridge datasets and connect results directly, increasing study power. I am very excited about the future. I think it is bright.

Learn more

Illumina SomaSeq Discovery

Explore the proteome with NGS

Protein Analysis on Illumina Connected Multiomics

Illumina Multiomics