

First cell type-resolved MS-based proteomic map of the human body — integrated into the Human Protein Atlas

[Stockholm, May 28 2026] — The Human Protein Atlas (HPA) today announces the release of version 25.1, featuring the first mass spectrometry (MS)-based proteomic map of the human body at cell type resolution. In total, over 13,000 genes are detected across both RNA and protein modalities, enabling direct comparison at cell type resolution. The dataset was generated through a collaboration between the laboratories of Prof. Matthias Mann at the Max Planck Institute of Biochemistry and Prof. Mathias Uhlén, founder of the HPA.

This joint effort marks an important step toward integrating complementary proteomics technologies and data modalities, expanding the Atlas to provide deeper, more comprehensive insights into human biology. By combining large-scale MS with the Atlas' established multi-omics framework, the collaboration lays the groundwork for increasingly unified views of RNA and protein expression across tissues and cell types.

The v25.1 release introduces a newly generated Deep Visual Proteomics (DVP) dataset, bringing cell type-resolved protein profiling directly into tissue context through advanced MS. Generated in the Mann lab, the dataset spans 14 human tissue types and 27 distinct cell types from a healthy female donor, quantifying nearly 14,000 proteins, two thirds of all human protein-coding genes, with up to 8,500 in a single cell type, representing one of the most detailed MS-based maps of the human proteome at cellular resolution to date. Among the findings enabled by this resolution, the data show that the human proteome partitions into a universal core sustaining cellular life and tightly restricted programs that define cell type identity, and reveal cancer-testis antigens, proteins normally confined to immune-privileged tissues and frequently targeted by immunotherapies, in oocytes of the female germline, a finding largely invisible to bulk tissue profiling.

Explore RNA-protein relationship

The DVP data is now available in the Single Cell resource in the HPA, where users can explore protein expression in a gene-centric view alongside matched single-cell RNA sequencing (scRNA-seq) data. This side-by-side comparison enables researchers to directly investigate the relationship between RNA and protein levels across individual cell types.

While RNA levels are often used as proxies for protein abundance, it is well established that global correlations between RNA and protein data can vary depending on temporal and spatial context. The matched dataset reveals that the concordance is organized primarily by biological pathway rather than by cell type: metabolic pathways are

consistently better captured at the protein level, while signaling pathways are more strongly represented at the transcript level. This provides users with a practical guide for when transcriptomic data can serve as a proxy for protein expression. The integration of these datasets provides a valuable opportunity to study the complex and context-dependent relationship between transcripts and proteins.

All data is searchable, visualizable, and downloadable, allowing researchers worldwide to explore and reuse the resource for hypothesis generation and validation.

Complementing the DVP dataset, the release also includes bulk MS data from the same 14 tissues, extended with six additional tissue types and integrated into the Tissue resource of the Atlas. Together, these datasets provide both high-resolution cellular detail and broader tissue-level proteomic coverage.

State-of-the-art mass spectrometry at unprecedented depth

The integration highlights recent advances in MS-based proteomics, particularly the ability to measure relative protein abundance with increasing sensitivity and spatial resolution directly in intact tissue environments.

“Cell type-resolved proteomics is no longer a technical aspiration but a deployable strategy,” says Prof. Matthias Mann, senior author and director at the Max Planck Institute of Biochemistry. “Deep Visual Proteomics allows us to isolate defined cell populations directly from intact tissue and measure thousands of proteins in each, in days rather than years. By placing this layer alongside transcriptomic and antibody-based data in the HPA, we give the community a foundation for asking biological questions that bulk MS measurements simply cannot resolve.”

The dataset was developed with a strong emphasis on accessibility and community use, reflecting the broader goals shared by both research groups involved in the collaboration.

“Making this dataset publicly available has been a key priority,” says Caroline Weiss, first author of the study. “By integrating the data into the HPA, we make it accessible to a much wider community of researchers interested in protein biology. We are very happy to finally share this resource.”

For the HPA team, the integration represents an important expansion of the platform’s long-term mission to map human biology across multiple molecular dimensions.

“It is a privilege to integrate this type of high-resolution proteomics data into the HPA” says Dr. Evelina Sjöstedt, representing the HPA side of the collaboration. “Mapping the fundamental building blocks of life across tissues and cells is essential. By adding more protein data, we can now provide a richer comparative view of RNA and protein side by side.”

She adds: “Even though global RNA–protein correlations vary, there are many cases where we can now directly confirm protein presence and cell type specificity. For proteins that have been difficult to profile using antibodies, MS data provides a powerful way to validate both their distribution and specificity.”

The integration also reinforces a central principle in biology: while RNA provides critical information about gene expression, proteins remain the primary functional molecules in cells and tissues.

“RNA data gives us valuable insights into gene expression, but in most cases, it is the protein that carries out the biological function,” says Prof. Mathias Uhlén. “Proteins are what we detect in blood, measure in diagnostics, and target in therapeutic interventions. Expanding the high-quality protein data in the HPA is therefore essential for advancing both basic research and clinical applications.”

The HPA is an open-access resource used by hundreds of thousands of researchers worldwide. With the addition of DVP, version 25.1 significantly strengthens its role as a comprehensive, integrative platform for exploring human biology across multiple molecular layers.

The full dataset is now live and freely accessible through the HPA portal, www.proteinatlas.org