



Discovery Proteomics: directly measure the key effectors of health & disease

Elucidate **functional biology**, **novel targets**, and the influence of **protein variants**.

Proteins are the mediators of cellular processes, and **measuring the proteome directly, at scale, is necessary to understanding the dynamic functional events** that drive disease processes and therapeutic response.

While RNA levels can infer potential protein activity, they cannot capture the breadth of changes that may occur post-translation, including PTMs, protein-protein interactions, or pathway activation. In fact, studies consistently show that mRNA levels correlate poorly with protein abundance, particularly in disease or treated states.

High-specificity profiling for **protein- and pathway-level insights**.

Sapient's **mass spectrometry-based** discovery proteomics method combines label-free, DIA workflows with advanced protein extraction and enrichment techniques to maximize proteome coverage across diverse sample matrices.

This approach enables direct quantitation with **peptide-level readouts for precise identification of proteins and their proteoforms, scalable across the breadth of the proteome** including protein variants contributing to functional biology.

Protein Groups Measured

12,000+

Tissue / Cells

including cell surface & intracellular proteins

10,000+

FFPE Tissue

including glyco- and phospho-proteins

5,400+

Plasma

with high reproducibility (CV ~5%)

6,000+

Saliva

including both host & microbiome proteins

3,600+

CSF

including those released by nervous tissue

Other matrices (dried blood spots, urine, stool, etc.) can also be analyzed. Please inquire about your specific sample type.

Unparalleled depth, speed,
and precision enabled by
**next-generation mass
spectrometry innovation.**



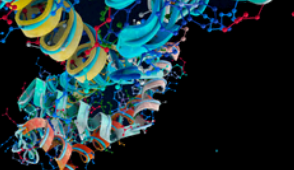
Category	Sapient Discovery Proteomics
Proteome Coverage	Advanced extraction and enrichment processes, including specialized ‘capture-and-hold’ nanoparticle chemistry in plasma, enable high-sensitivity measures across thousands of proteins – including the low-abundance proteome.
Reproducibility	Direct, peptide-level sequencing of proteins negates the need for antibodies and the risk of non-specific binding. Single fraction-single injection processing yields exceptional reproducibility (median CV <12% across matrices).
PTMs & Isoforms	Workflows detect splice, truncation, indel, missense, and other non-canonical variants as well as PTMs including phospho-proteins and glyco-proteins.
Throughput	Amenable to high throughput analyses across hundreds of samples per day.
Multi-Omic Integration	Integration with other Sapient omics offerings, including metabolomics, lipidomics, and cytokine profiling, and with DNA/RNA sequencing data to improve mechanistic understanding from upstream regulation to downstream outcomes.

By quantifying proteins and their modified forms, we help researchers gain a **much more accurate and actionable view of signaling events, cellular interactions, and mechanistic drivers** – bridging the gap from inferred to actual biology.

Minimum Sample Requirements

- **Fresh-Frozen Tissue:** 10 – 20 mg
- **FFPE Tissue:** 5 µm section per workflow
- **Cells:** 1,000,000 per sample
- **Plasma:** 150 µL
- **Saliva:** 150 µL
- **CSF:** confer with Sapient

Please inquire about low-input samples or other sample types.



Contextualize and extend findings with DynamiQ™ insights.

As the only multi-omics partner with a population-scale molecular-clinical database, we can **both analyze your samples and validate the findings in independent real-world cohorts** – as well as **uncover novel biology** that can differentiate your programs.



- **>67,000 pre-characterized plasma samples** linked with rich metabolomics, multi-omics, and clinical data
- **Diverse tumor samples** across grades and stages and **normal human tissues** for global differential analyses

Ready-to-access samples

If you are looking to generate discovery proteomics data without the hurdles of new sample collection, Sapien offers our **DynamiQ Tumor-Tissue virtual biobank for streamlined access to archived samples**, including FFPE tumors and normal tissue for differential analysis.

DynamiQ Applications

Biological Contextualization

We use this large-scale reference dataset to **confirm and contextualize** disease and clinical links of proteins observed in your study.



Confirm Preclinical Findings

Accelerate translation of identified targets and biomarkers with **cross-validation in a real-world cohort** to confirm observed signals are human-relevant.



Target Identification

Our Tumor-Tissue virtual biobank enables rapid discovery and validation of **tractable, disease-modifying targets** (proteins and PTMs).



Bridging discovery and clinical with **real-world validation & targeted assays.**

We can rapidly move biomarkers and targets identified through our discovery screenings – and validated as human-relevant in DynamiQ – to quantitative **targeted assays with analytical validation based on appropriate context of use (COU)** statements. This ensures that your study findings are not only clinically meaningful, but clinically actionable.

What **actionable insights** will Sapient's discovery proteomics **deliver for you?**

Functional insights to complement and extend DNA and RNA datasets.

Proteins and their proteoforms are the active mediators of biology. Directly quantifying them provides a more accurate readout of dynamic disease processes and drug effects.

Deep and precise proteome coverage across matrices.

We deliver high-specificity, reproducible measures across thousands of proteins simultaneously to maximize discovery potential and confidence in findings.

Seamless multi-omic integration & rapid translation.

As a comprehensive multi-omics partner, Sapient can generate additional omics datasets in your same samples, integrate and interpret them, and use the results to guide targeted assay development.

Faster breakthroughs with DynamiQ.

Whether using our reference dataset to contextualize disease and clinical links of proteins observed in your study, or tapping our virtual biobank for efficient sample access, DynamiQ provides a unique solution to rapidly build evidence for advancing the right targets and markers.

Key Use Cases

Biomarker Discovery and Validation

Target Identification and Prioritization

Mechanistic Insight and MoA Studies

Preclinical-to-Clinical Translation

Patient Stratification and Precision Medicine

To request a discovery proteomics study, contact **discover@sapient.bio**.



SAPIENT

Discover more today.

+ [sapient.bio](https://www.sapient.bio)

+ discover@sapient.bio

+ 858.290.7010