FACT SHEET

SAPIENT

Scalable protein measures from discovery to single clinical assays

Sapient's high throughput proteomics services can be applied to **measure one or thousands of proteins at a time in diverse sample matrices** and with high specificity.

Leveraging state-of-the-art mass spectrometry, our **protein assays deliver high-confidence protein annotations while optimizing for coverage and throughput** to best suit your study requirements at each phase.

Mass spectrometry **measure of proteins and proteoforms.**

Our mass spectrometry approach annotates proteins and their isoforms, including post-translational modifications (PTMs), via direct peptide sequencing. **Peptide-level information** enables precise protein identification, and **capture of proteoforms and PTMs** allows for more in-depth analysis of protein function and regulation.

The additional value is that Sapient's proteomics methods are **scalable from nontargeted discovery to quantitative clinical protein assays,** and optimized across diverse sample matrices.

Our methods

	Plasma Proteomics	CSF Proteomics	Saliva Proteomics	Urine Proteomics	Tissue / Cell Proteomics
# PROTEIN GROUPS	5,400+	3,600+	6,000+	4,000+	12,000+
MEDIAN CV	~5%	~11%	~6%	~12%	~9%
TARGETS MEASURED*	>1,000	>10	>800	>500	>1,000

*Includes known and emerging drug targets

High-Throughput Profiling
with next-gen analytical technologies

Sapient's label-free, DIA proteomics methods use **nanoflow separation coupled to trapped ion mobility mass spectrometry and nanoparticle enrichment** to enable measure of thousands of proteins across diverse bioanalytical pathways.

Scalable breadth & depth of coverage
of proteins in biofluids, tissue, and cells, including proteoforms and PTMs, using specialized 'capture-and-hold' nanoparticle chemistry for high sensitivity

Applicable across species
including preclinical and clinical models

Measure of biologically important proteins
including exosomal and membrane-bound proteins

Biocomputational Analysis
with multi-omics data integration

Our data science team can provide **integrative analysis of proteomics data** with other omics, preclinical, and clinical data to elucidate protein biomarkers and their involvement in processes underlying disease and drug response.

Expert handling of large-scale datasets
using advanced statistical & machine learning models

Identification of drug targets & biomarkers
with mapping of phenotype & disease associations

The biomarkers we discover for sponsors can be applied to align:

Right Disease
- Target ID and validation
- Disease mechanisms
- Early disease detection
- Disease progression

Right Patient
- Patient stratification
- Safety profiling
- Companion diagnostics
- Clinical trial enrichment

Right Therapy
- Dosing strategies
- Timing of treatments
- Target engagement
- Toxicology

CAP ACCREDITED
COLLEGE of AMERICAN PATHOLOGISTS

Your partner to **discover more and develop faster.**

We are here to **extend multi-omics insights for your drug development programs beyond the genome,** to dynamic protein, metabolite, and lipid biomarkers that elucidate factors modulating health, disease, and drug response.

SAPIENT

Ready to discover more?
Schedule a time to discuss your programs with our scientists.

Visit: sapient.bio | Email: discover@sapient.bio | Call: 858.290.7010