



Targeted protein assays via high throughput mass spectrometry

Do you have a specific protein of interest or target to modulate? Sapient can provide **targeted, quantitative measures of key proteins and PTMs** in plasma, cells, and tissue with rapid turnaround.

Our mass spectrometry-based proteomics method provides **high-accuracy protein annotations** with throughput for large-scale studies, making the same measure across tens to thousands of samples at a time.

With **>12,000 proteins and PTMs in our current list of measurable proteins**, we can most often provide an off-the-shelf assay for your protein of interest in your sample matrix of choice, and rapidly optimize it to your specific study requirements. We can also provide custom assay development for difficult-to-measure proteins of interest.

Search key proteins which may represent therapeutic targets or biomarkers of disease processes and drug response.

SEARCH BY

[Clear search](#)

FILTER BY

[Clear filters](#)

1433B

14-3-3 protein beta/alpha;14-3-3 protein beta/alpha;
Isoform Short of 14-3-3 protein beta/alpha

Matrix Type

Plasma
Tissue/Cells

1433E

14-3-3 protein epsilon

Matrix Type

Plasma
Tissue/Cells

1433F

14-3-3 protein eta

Matrix Type

Plasma
Tissue/Cells

1433G

Matrix Type

Plasma
Tissue/Cells

Filter proteins by biological and phenotypic associations to identify assays that could inform your study.

1433T

14-3-3 protein theta

Matrix Type

Plasma
Tissue/Cells

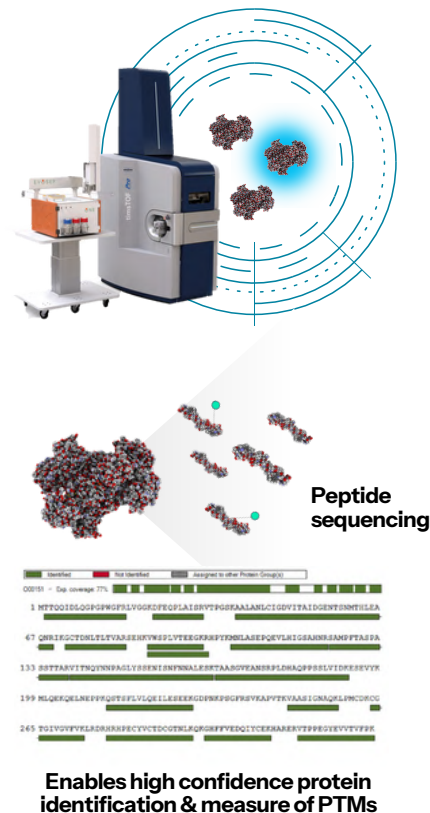
Visit sapient.bio/protein-menu to search our list of available protein assays.

The differentiators of mass spectrometry for targeted protein measures

Rapid exploration of the expanding druggable space

Innovative new drug modalities are now able to target disease-modifying proteins once considered too challenging to reach. Sapient's expansive protein assay menu allows you to **go beyond the well-characterized targets for novel discovery of druggable proteins.**

We can target analyses among >5,400 proteins and PTMs in plasma and >12,000 in cells and tissue, including **thousands of biologically important exosomal and membrane-bound proteins.**



High confidence protein identification

Our mass spectrometry approach annotates proteins and PTMs via direct peptide sequencing. This provides not one, but **multiple peptide-level measurements per protein to improve the specificity of identification** over affinity-based binding methods. It also negates issues of imperfect binding seen with affinity proteomics.

Capture of PTMs and protein variants

Mass spectrometry uniquely captures PTMs and protein variants to allow for more in-depth analysis of protein function and regulation.

While affinity-based binding can only measure whole proteins, Sapient's proteomics method captures these **important structural changes that can be biomarkers of disease processes and drug response or that may represent targets for therapeutic intervention.**

Measures in liquid and tissue matrices

Many proteomics methods are optimized for a single sample type, but Sapient's approach is **amenable to multiple matrices including plasma, serum, CSF, urine, cells, media, tumors, and tissue.**

Efficient clinical translation

The high analytical specificity with which mass spectrometry can identify proteins makes translation much more efficient. Sapient can **leverage our CLIA-certified, CAP-accredited laboratory to develop key proteins of interest into clinical assays.**



©2025 Sapient Bioanalytics, LLC. All rights reserved.

High-accuracy protein measures. **High throughput** for scale. **High confidence** to advance your study. **Get started today.**

Visit sapient.bio/protein-menu to request your targeted assay.