



Targeted protein assays via high throughput mass spectrometry

Do you have a specific protein of interest or target to modulate? Sapiient 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.

The differentiators of mass spectrometry for targeted protein measures

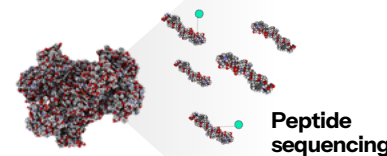
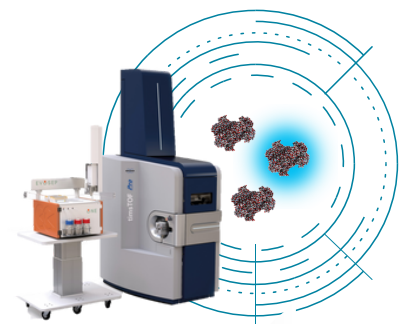
Rapid exploration of the expanding druggable space

Innovative new drug modalities are now able to target disease-modifying proteins once considered too challenging to reach. Sapiient'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 >6,000 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.



Identified	Not identified	Assigned to other Protein Group(s)
000101 - 100% coverage 77%		
1	MTFDQIDLGGDFWFLVGGDFEGFLAISRVTGPKKAALNLCIGDVTAIQENTDMHLEA	
47	QRLEGCTORLLEVALEENYKSPFLYEEGFRFTENMLAREPQVLEIGSANNJANGPTAIPA	
133	QSTTARYITNGVNRALYKSEKISKFNWALEKRTAAAGVYANRPLMAGQFSLYDRSEVYK	
199	RLQKQKLENEFQKTFELVQLLEKEREKGGKDFGFRVKAFTKVAALIQAGLQKRCQK	
245	TVIVGFFVYELASRRKFKCYKCTCOTRLRQGRFFVQDTCEFRAREVTFKQELVYVTFK	

Enables high confidence protein identification & measure of PTMs

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 mass spectrometry-based proteomics 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.**

High-**accuracy**
protein measures.

High **throughput**
for scale.

High **confidence** to
advance your study.



EXPLORE OUR FULL TARGETED PROTEIN ASSAY MENU

