

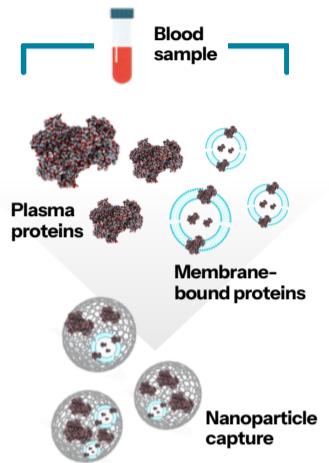
A revolutionary approach to discovery proteomics

Sapient's **high throughput, mass spectrometry-based method for discovery proteomics** is transforming the depth and efficiency at which we can measure the blood and tissue proteome to extract greater biological insight. **Here's how.**

1

Measure of >5,400 proteins in plasma and >12,000 proteins in cells and tissue.

Our nontargeted approach using nanoparticle and affinity enrichment provides a broad view of the proteome and functional pathways to **greatly amplify discovery potential.**



2

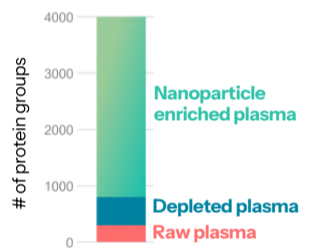
Measure of PTMs and protein variants.

Mass spectrometry **captures these biologically important structural changes**, unlike affinity-based binding which can only measure whole proteins.

3

High confidence protein identification.

Mass spectrometry **negates issues of imperfect binding fidelity** via direct peptide sequencing.



4

Lower cost.

Mass spectrometry **eliminates need for costly binding agents.**

5

Bioinformatics for deep biological insight.

We can perform pathway and tissue enrichment analysis across **9** key biological processes, **40+** tissue signaling pathways, and **28** tissues of origin in plasma.

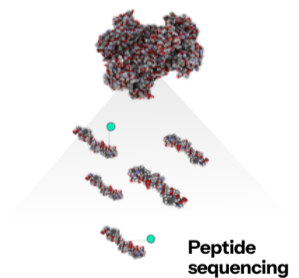


Bruker timsTOFHT mass spectrometry for label-free DIA discovery proteomics

6

Applicable to liquid & tissue matrices.

Our method can be **used in preclinical and clinical systems**, including plasma, tissue, urine, CSF, and more.



7

Scalable throughput.

We have capacity to **handle tens to tens of thousands of biosamples** with rapid turnaround.



Enables high confidence protein identification & measure of PTMs

8

Efficient clinical translation.

Sapient can **develop targeted, quantitative CLIA assays** for proteins of interest.



Speak to our scientists today.

Visit sapient.bio/proteomics to request a project or email discover@sapient.bio to set a meeting.