



Tumor Protein Mapping Platform

A unified system for **measuring functional biology across 12,000+ proteins in human tumors**

As ADCs, T-cell engagers, radioligand therapies, and immunotherapies have reached technical maturity, success in modern oncology drug development is no longer limited by the availability of therapeutic modalities but rather **increasingly depends on accurately characterizing tumor biology across multiple functional dimensions of the tumor proteome**, including druggable surface targets, signaling pathway activation, immune engagement, and mechanisms of resistance.

Sapient's Tumor Protein Mapping Platform **directly measures** the functional tumor proteome by integrating complementary mass spectrometry workflows into a single platform that **enables end-to-end measurement of tumor biology at scale across the proteome**.

In combination, these workflows create a closed-loop system that captures tumor biology across 12,000+ protein groups, providing a **unified, system-level understanding of tumor biology** to guide oncology drug development from target selection through clinical proof of concept.

DiscoverySeek™

What proteins and pathways exist in the tumor

SurfaceSeek™

What is druggable and accessible on the tumor cell surface

SignalingSeek™

What pathways are functionally active

ImmuneSeek™

How the immune system is engaged or suppressed

ResistanceSeek™

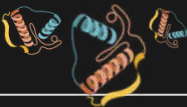
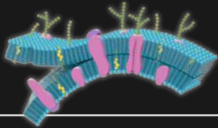
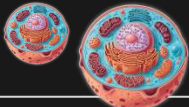
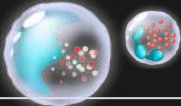
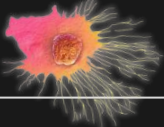
What mechanisms will drive therapeutic escape

Targeted Assays

Measurement of key identified proteins with quantitative accuracy

A Closed-Loop System for Tumor Biology

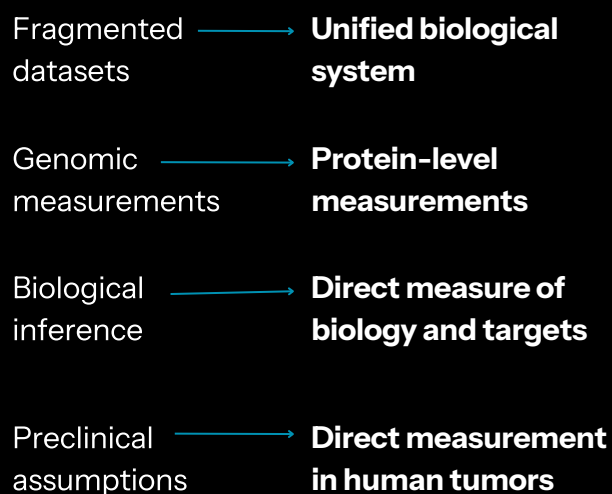
The Sapient Tumor Protein Mapping Platform **generates and integrates direct protein measurements** that inform critical decisions across oncology programs. All workflows are performed using the same analytical framework, allowing direct comparison across biological dimensions within a study.

Sapient Workflow	Biological Dimension	Depth and Insight
DiscoverySeek™ 	Global protein expression, including protein isoforms	Comprehensive measure of over 12,000 proteins across tissues
SurfaceSeek™ 	Cell surface protein expression	Surface protein density and druggable target accessibility for ADC, T-cell engager, and radioligand therapies
SignalingSeek™ 	Phosphorylation-driven pathway activity	Functional pathway activation, mechanism of action, and adaptive response
ImmuneSeek™ 	Immune cell composition and activation states	Tumor immune microenvironment characterization
ResistanceSeek™ 	Resistance-associated protein networks	Resistance pathway activity and therapeutic vulnerability
Targeted Protein Assays 	Precise quantitative measurement of specific proteins of interest	Target quantitation, drug distribution, MOA, target engagement, and pharmacodynamics

This transforms tumor profiling from a collection of disconnected assays into a coherent biological system of record. Each workflow informs the others, enabling teams to **build a complete picture of the tumor proteome within a single experimental framework.**

Seek Insights to De-Risk Drug Development

Historically, drug development has relied on incomplete and indirect measurements of tumor biology. **Sapient shifts oncology development from:**



SAMPLE COMPATIBILITY

All workflows are compatible with:

- **Fresh-frozen tissue**
- **FFPE tissue**
- **Preclinical tumor models**
- **Cellular samples including cell lines**
- **Conditioned media**
- **Organoids**

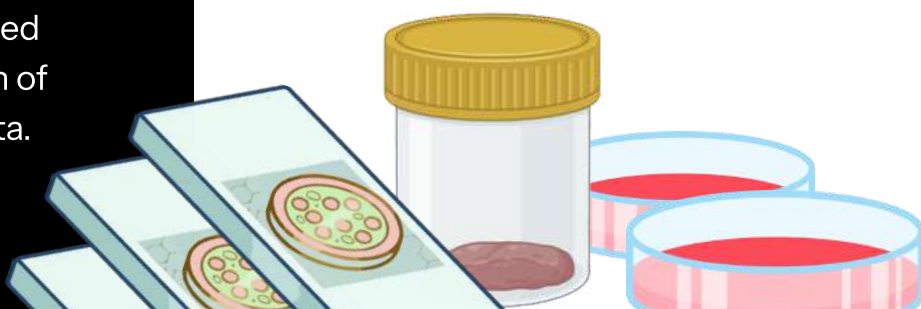
This enables prospective studies, retrospective analysis of archived clinical cohorts, and integration of preclinical and translational data.

Why Tumor Biology Has Been Fragmented

The functional dimensions of tumor biology are typically measured in isolation using fragmented technologies that fail to capture tumor dynamics as an integrated system.

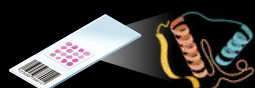
Approach	Key Limitation
DNA sequencing	Identifies mutations but does not measure protein function or expression
RNA expression profiling	Does not reflect protein abundance, surface accessibility, or post-translational regulation
Targeted protein panels (IHC, MRM)	Limited to predefined hypotheses and small numbers of analytes
Preclinical models	Often fail to recapitulate the proteomic complexity of human tumors

*As a result, target selection lacks functional validation, pathway activity is inferred rather than measured, immune biology is incompletely understood, and resistance mechanisms are identified only after clinical failure. **There is no system of record for tumor biology at the protein level.***



Integrated Multi-Omics Molecular Mapping

In addition to proteomics, Sapien enables integrated multi-omics analysis in FFPE tumor samples. This allows **comprehensive characterization of tumor biology within the same tissue context**. Integrated capabilities include:



Functional tumor proteome mapping in FFPE tumors and tissue



FFPE DNA sequencing for mutation and CNV mapping



Single-cell sequencing for cell-type specific expression



Spatial profiling for tissue contextualization

This integrated approach enables **alignment of genomic alterations with functional protein output, cell-type-specific interpretation of tumor biology, and spatial understanding** of tumor-immune interactions.

How the Tumor Protein Mapping Platform Guides Development Decisions

Programs that integrate functional proteomic evidence earlier in development **reduce the risk of late-stage failure** by validating biological hypotheses directly in human tumors.

Development Question	Platform Insight
What defines tumor biology or drug mechanism of action in this indication?	DiscoverySeek proteome-wide mapping
Which cell surface targets are accessible and druggable?	SurfaceSeek direct surface proteomics
What signaling pathways are functionally active?	SignalingSeek phosphoproteomics
How is the immune system engaged?	ImmuneSeek immune cell and checkpoint profiling
Why are patients failing therapy?	ResistanceSeek resistance pathway measurement
Is the therapeutic working as intended?	Quantitative target engagement assay

Characterize critical dimensions of functional biology directly in human tumors.

By directly measuring proteins – the molecules that define cellular function – Sapient provides an **integrated and actionable view of tumor biology across discovery, translational research, and clinical development.**

Our Tumor Protein Mapping workflows can be delivered singularly or in the combination that best informs your studies, and are available through **flexible engagement models** including project-based proteomics services, data licensing, and integrated discovery partnerships.

From Genomic Inference to Direct Protein Measurement

Sapient enables mechanism-driven development strategies grounded in human tumor biology rather than genomic inference. Our platform is particularly valuable in programs where teams are asking:

- What is the true biological state of tumors in our indication?
- Which targets are both biologically relevant and druggable?
- Are signaling pathways functionally active in patient tumors?
- What resistance mechanisms should we anticipate before they emerge in the clinic?
- How can we design more effective combination strategies?

**To request a study
using the Tumor
Protein Mapping
Platform, contact
discover@sapient.bio.**



Discover more today.

+ sapient.bio
+ discover@sapient.bio
+ 858.290.7010