



FFPE Multi-Omics for Discovery Oncology

From **target discovery to functional validation**, in weeks.



Discovery oncology scientists are **under pressure** to identify and validate novel drug targets, but three recurring barriers challenge progress:

Genomics alone misses protein-level function. DNA-seq or RNA-seq fails to reveal key target expression, pathway activation, post-translational signaling, and drug response.

Fresh-frozen tumor tissue is limited. These samples are expensive to obtain and store, and often lack associated clinical and outcomes data.

Direct measure of proteins in FFPE tissue is traditionally challenging. Antibody-based proteomic approaches are typically low-plex and can be compromised by formalin-induced cross-linking.

Sapient's FFPE Multi-Omics Platform transforms archival tissue into a **discovery-ready molecular resource**.

Sapient's next-generation mass spectrometry-based FFPE proteomics method delivers **deep, quantitative proteomic data via the direct measure of >10,000 proteins and their isoforms in FFPE tissue**.

Through **Sapient's DynamiQ™ virtual biobank**, we can offer discovery teams **streamlined access to thousands of annotated FFPE samples**, including those linked with clinical outcomes.

The result? Programs advance targets with **incomplete functional validation**, leading to **high failure rates** in translation.

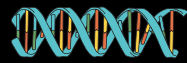
- ✓ **10,000+ protein groups measured**, including phospho- and glyco-proteins, across tissue & tumor types
- ✓ Measure of **200+ oncogenes**, **500+ approved drug targets**, and **100+ pathways**
- ✓ **Streamlined access to actionable FFPE tissue and tumor samples** via Sapient's DynamiQ virtual biobank

Multi-omic molecular mapping

Our FFPE proteomics **seamlessly integrates** with other omics offerings available through Sapient, including:



FFPE proteomics
for protein
expression and
pathway activity



**FFPE DNA
sequencing**
for mutation and
CNV mapping



**Single-cell
sequencing**
for cell-type
specific expression



**Spatial
profiling**
for tissue
contextualization

Designed to **accelerate discovery oncology**, Sapient's FFPE Multi-Omics Platform builds a unified molecular map of each tumor, enabling discovery teams to **move from gene nomination to functionally validated, human-relevant oncology targets in weeks**.

Typical Bottleneck	Sapient Solution	Program Impact
Limited fresh tumor access	Use existing FFPE tumor archives	Immediate human tumor data
DNA-seq / RNA-seq poorly reflect pathway activation	Deep proteomics + PTM mapping	Functional target validation
Fragmented CRO ecosystem	Integrated multi-omic workflow	Single provider and dataset for faster target ranking
Long timelines for target validation	Ready-to-query tumor biobank	Months saved per program

For **actionable insights** that
drive **meaningful discovery**.

Results are delivered as:

- Normalized **quantitative proteomic matrices**
- **Annotated pathway** and **PTM activity reports**
- **Drug-target engagement** overlays
- **Optional access via Sapient PrismatiQ™ data analytics package** for visualization of differentially expressed proteins and pathway activation

Accelerate your path **from target nomination to functional validation in weeks, not months**, with Sapient's FFPE Multi-Omics Platform.

For prioritized access opportunities, contact discover@sapient.bio.