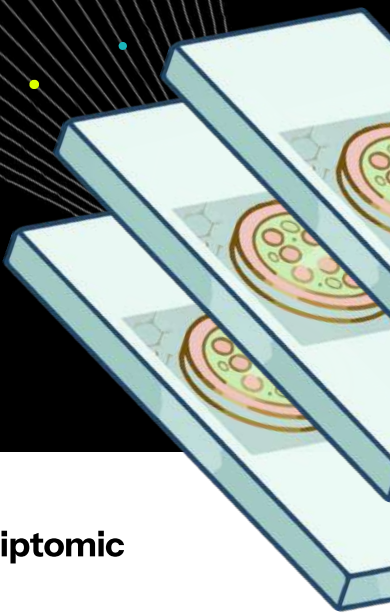
PRECISION ONCOLOGY

SAPIENT

FFPE Multi-Omics for Precision Oncology Platforms

Extending molecular insights with FFPE proteomics.



Precision-oncology leaders have **revolutionized genomic and transcriptomic profiling of FFPE tumors**, yet they face the same strategic limitations:

Lack of direct measures of target expression, pathway activity, or drug-target engagement. DNA/RNA data do not provide *functional* measures for understanding tumor biology and drug response.

Missed opportunity for therapy-response prediction. Many tumors still respond due to downstream protein signaling or post-translational modifications (PTMs) that are invisible to genomics.

Under-leveraged archives. Millions of FFPE tumors already profiled via genomics lack the proteomic dimension needed for full functional interpretation.

The result?
Incomplete molecular insight for pharma partners and clinicians, and **unrealized value** from existing datasets and biobanks.

Sapient's **FFPE proteomics** adds the **functional layer** to existing genomics data.

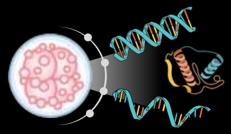
Sapient's FFPE proteomics **directly quantifies >10,000 proteins, including phospho- and glyco-proteins, 200+ oncogenes, and 500+ approved drug targets** in low input FFPE samples. This includes demonstrated detection across **100+ pathways including for EGFR, KRAS, p53, JAK3, and immune-checkpoint signaling.**

By unlocking previously inaccessible protein insights from FFPE tissue, Sapient **allows precision oncology platforms to enhance their partner offerings and expand monetization of their existing tumor datasets.**

- ✓ **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**
- ✓ **High reproducibility with >97% overlap** across serial FFPE sections & inter-section **CV < 8%**

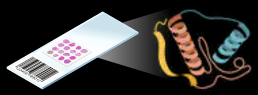
Multi-omic integration opportunities

Sapient's FFPE proteomics **seamlessly integrates** with existing genomics, RNAseq, and spatial datasets – including those generated by Sapient's multi-omics workflows – supporting diverse uses cases such as:



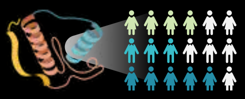
Combining mutation and pathway activation in oncology reports

Add proteomic data feed to NGS / RNA reports



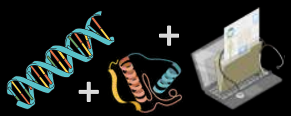
Retrospective validation of key targets

Re-analyze archived FFPE tissue samples for new insights



Identification of **predictive responders beyond genomics**

Enable proteomic enrichment of existing comprehensive genomic profiling panels



Integrated multi-omic datasets for **pharma RWE programs**

Add protein-level functional data to real-world cohorts

Platform Challenge	Sapient Solution	Strategic Impact
Genomics provides only one view of biology	Add functional proteomics layer	**Deliver actionable pathway & PD insights**
Pharma engagement	Joint proteogenomic datasets	**Expansion of pharma engagements with new biomarker & target opportunities**
Limited differentiation vs. competitors	Unique multi-omic offering	**Distinct market positioning**
Under-used legacy FFPE archives	Retrospective proteomic re-analysis	**New RWE & data licensing revenue**

Enhance **oncology insights** and your **pharma co-development opportunities.**

- **True FFPE-native proteomics** – no fresh tissue required
- **Quantitative functional biology** – insight into pathway activity, PTMs, and isoforms
- **Complementary** to existing genomics for additive value
- **Optimized for scale** with capacity to analyze thousands of samples per project

Sapient's FFPE proteomics workflows are **optimized for discovery and clinical programs with hundreds to thousands of FFPE samples,** ensuring capacity and rapid turnaround of results.

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