



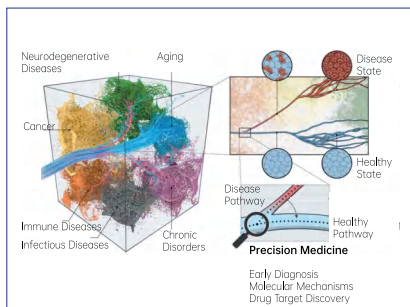
Spatial X Topographic Proteomics

**Centimeter-Scale
Spatial Coverage**

**Micrometer-Scale
Spatial Resolution**

**Integrated Spatial
PTM Profiling**

Technology Leadership — Advancing AI-Powered Spatial Proteomics

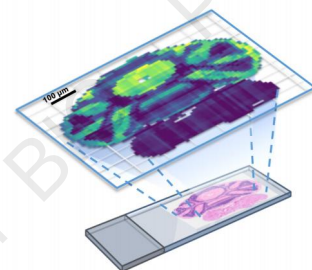


Spatial Proteomics: A Molecular Map of Life for Precision Medicine

Biological systems are inherently organized across space and time. Spatial heterogeneity provides the foundation for functional diversity within tissues. The spatial distribution and variation of proteins directly regulate biological processes ranging from cellular activities to organ-level functions. Moving beyond conventional bulk proteomics while preserving native tissue context is therefore essential for understanding tumor heterogeneity, immune microenvironment dynamics, development, and cell differentiation.

Spatial X Topographic Proteomics: Exploring the Next Frontier of Spatial Biology

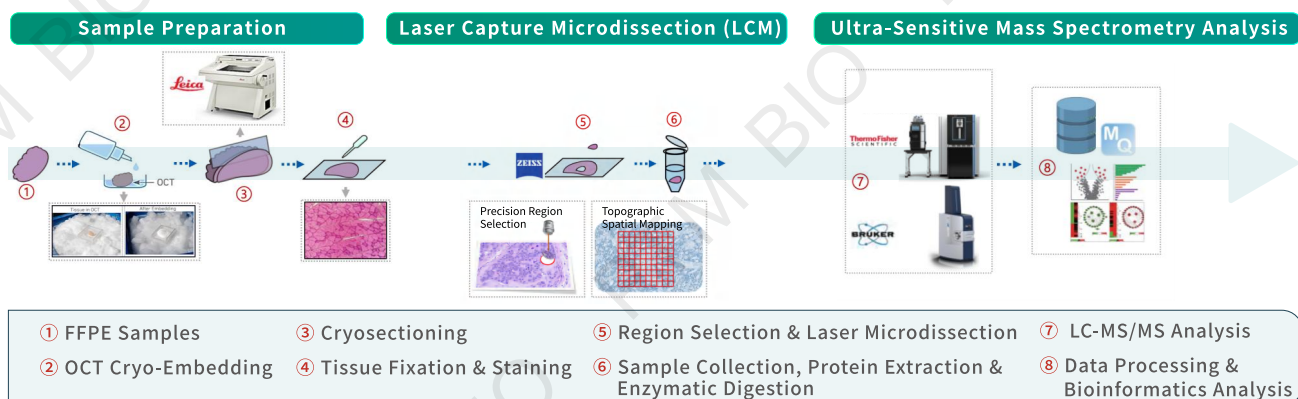
Powered by advanced AI-enabled image reconstruction, the Spatial X overcomes the conventional limitations of spatial coverage and proteomic depth. With centimeter-scale tissue imaging, micrometer-resolution spatial precision, and comprehensive post-translational modification (PTM) profiling, Spatial X delivers an integrated view of protein expression and regulation within intact tissues. The Spatial X generates high-resolution spatial maps of protein modifications, providing unprecedented insights into the molecular mechanisms underlying drug resistance, disease recurrence, and disease progression.



An End-to-End Spatial Proteomics Solution

Analysis Workflow	Proteome	Phosphorylome	Proteome × 100	Proteome Phosphorylome × M+N
Sample Compatibility	✓ FFPE samples ✓ Fresh-frozen samples ✓ Fixed-frozen tissue samples	✓ Fresh-frozen samples ✓ Fixed-frozen tissue samples	✓ FFPE samples ✓ Fresh-frozen samples ✓ Fixed-frozen tissue samples	✓ FFPE samples ✓ Fresh-frozen samples ✓ Fixed-frozen tissue samples
Data Scale	Single-site spatial proteomic dataset	Single-site spatial phosphoproteomic dataset	High-density spatial proteomic dataset (100 sampling sites per region)	High-dimensional spatial proteomic and phosphoproteomic datasets generated from an M × N sampling matrix

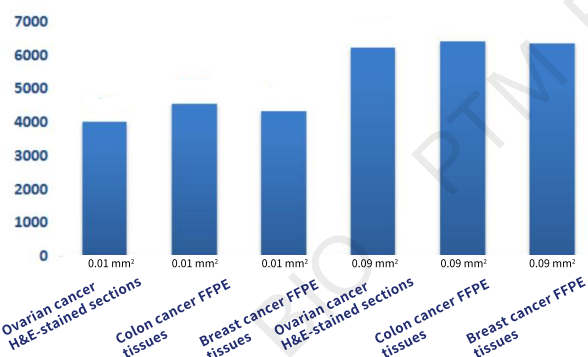
Integrated Infrastructure — End-to-End Spatial Proteomics Workflow



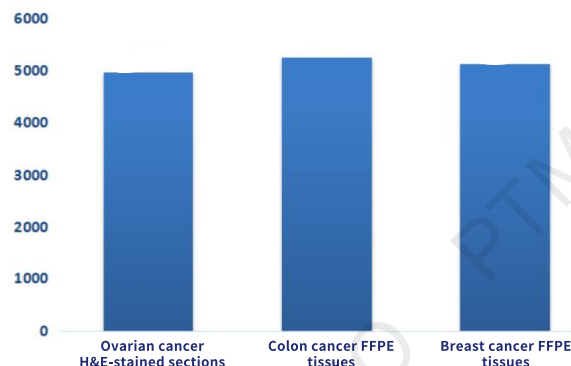
Quality Assurance — High-Quality Proteomics Data

Spatial Proteomics

Protein Identification Depth in Spatial Proteomics



Phosphoproteomics Identification Depth in Spatial Proteomics



Spatial X Topography Proteomics & PTM Proteomics

Centimeter-Scale Spatial Coverage

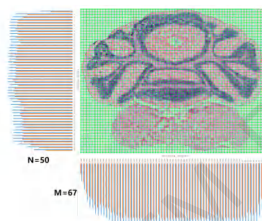
Comprehensive Spatial Coverage

- ✓ Comprehensive Spatial Coverage

Deep Proteome and Phosphoproteome Coverage

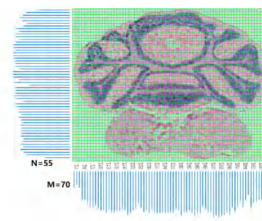
- ✓ >7,000 Proteins Identified
- ✓ >11,000 Phosphosites Identified

Spatial X Topographic Proteomics



Average protein identifications per sampling site: >5,200
Total protein identifications: >7,000

Spatial X Topographic Phosphoproteomics



Average phosphosite identifications per sampling site: >5,000
Total phosphosite identifications: >11,000

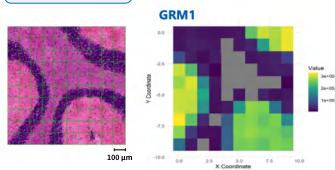
Micrometer-Scale Spatial Resolution

- ✓ Spatial Resolution Better Than 100 μ m

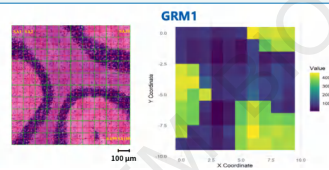
Accurate Spatial Quantification

- ✓ High Concordance Between AI-Based Quantification and Tissue Marker Expression

H&E Staining

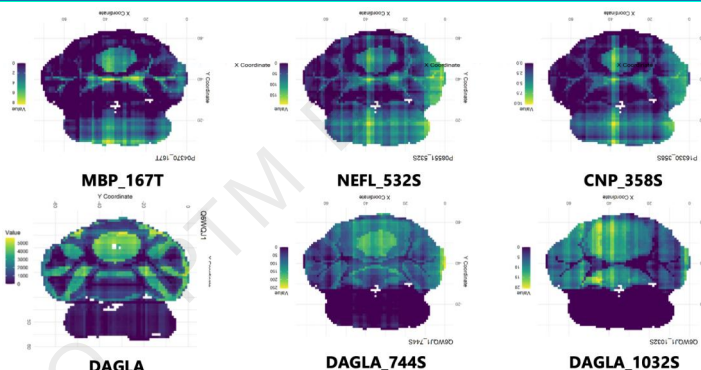


Marker Protein Spatial Distribution

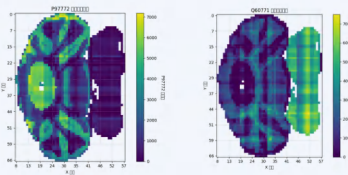


Comprehensive Spatial PTM Profiling

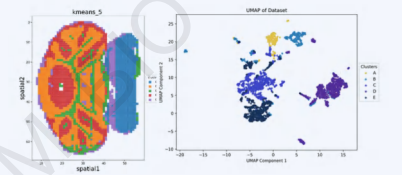
- ✓ Spatial Mapping of Protein Phosphorylation Sites
- ✓ Systematic Characterization of Protein Expression and PTM Landscapes



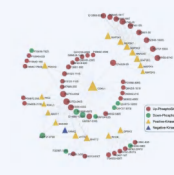
Bioinformatics Analysis — Reconstructing Spatial Proteomic Landscapes



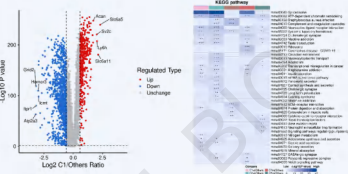
Spatial Visualization of Protein and Phosphoprotein Expression



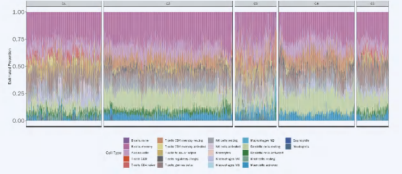
Unsupervised Clustering and Dimensionality Reduction of Spatial Data



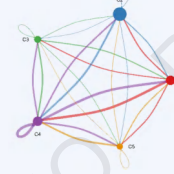
Kinase Activity Prediction



Differential Expression Analysis and Functional Annotation



Cell-Type Deconvolution and Proportion Estimation



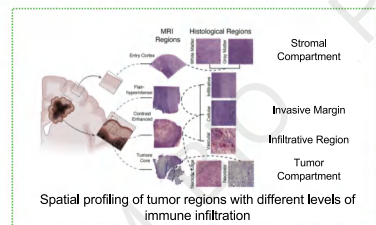
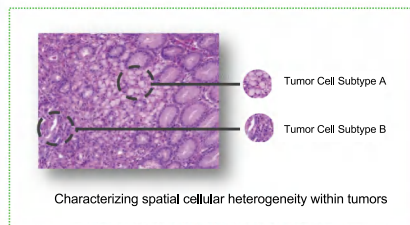
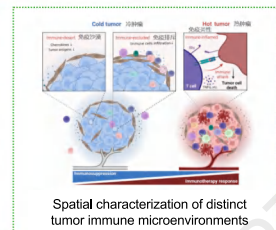
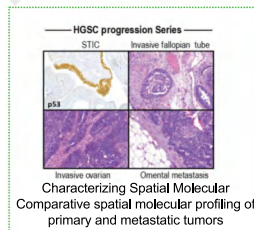
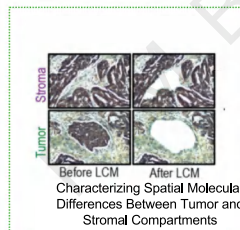
CellChat-Based Cell-Cell Communication Network Analysis

Generate high-resolution, whole-slide spatial molecular atlases of proteins and PTMs through an integrated bioinformatics workflow.

Applications — Driving Biological Discovery and Mechanistic Insights

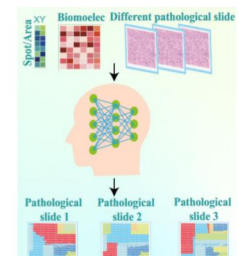
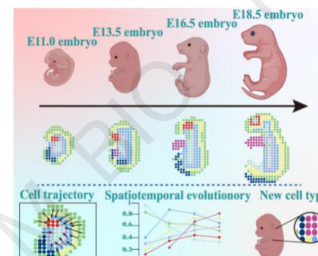
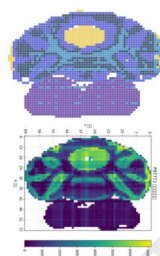
Oncology Applications

- ☐ **Spatial Molecular Profiling**
(Protein expression maps, PTM maps, protein interaction networks, etc.)
- ☐ **Spatially Informed Molecular Subtyping**
(Tumor vs. stromal compartments, tumor cell subtypes, etc.)
- ☐ **Discovery of Spatial Biomarkers**
(Diagnostic, prognostic, and predictive biomarkers)
- ☐ **Mechanistic Insights into Disease Biology**
(Tumor initiation, progression, metastasis, drug resistance, etc.)



Non-Oncology Applications

- ☐ **Tissue Atlas Construction**
(Physiological and pathological tissues, including liver, stomach, uterus, ovary, etc.)
- ☐ **Developmental Biology**
(Embryonic development and organogenesis)
- ☐ **Neuroscience**
(Brain tissues and multiple brain regions)
- ☐ **Cardiovascular and Chronic Inflammatory Diseases**
(Heart, vasculature, atherosclerotic plaques, etc.)



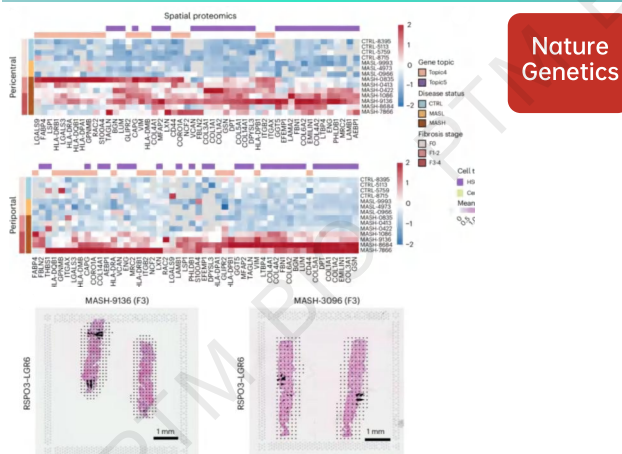
Comprehensive Spatial Proteome and PTM Atlas of a Tissue or Organ

Comparative Spatial Molecular Profiling Across Developmental Stages

Comparative Spatial Molecular Profiling of Healthy and Diseased Tissues

Research Excellence — High-Impact Collaborative Publications

Spatially resolved multi-omics of human metabolic dysfunction-associated steatotic liver disease



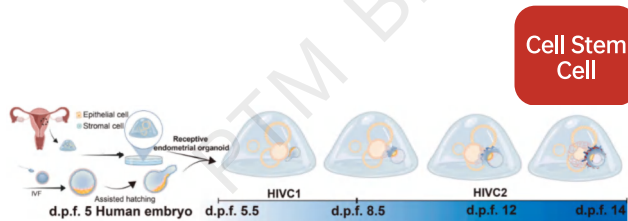
Nature Genetics

Research Focus: Spatial cellular and molecular mechanisms underlying inflammation and fibrosis progression in metabolic dysfunction-associated steatotic liver disease (MASLD).

Sample Cohort: Control, MASL, and MASH human liver samples, including pericentral and periportal regions of interest for spatial proteomic profiling.

Key Findings: Integrated spatial multi-omics generated a spatial atlas of human MASLD and revealed disease-associated cellular states, metabolic programs, and fibrosis-related signaling networks, including interactions between hepatic stellate cells and central vein endothelial cells.

3D post-implantation co-culture of human embryo and endometrium



Cell Stem Cell

Research Focus: Cellular communication between the human embryo and the endometrium during implantation.

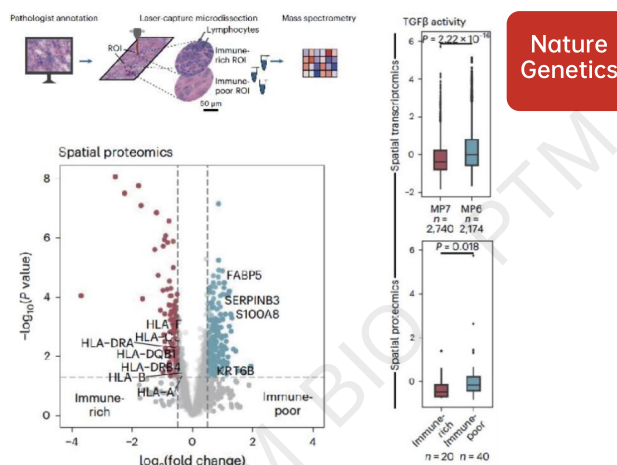
Sample Cohort: Human embryos, isolated endometrial tissue, and endometrial organoids.

Key Findings:

Established the first 3D co-culture model supporting post-implantation human embryos and endometrial organoids. Demonstrated that endometrial microenvironment promotes extravillous trophoblast (EVT) development and functional maturation in vitro.

Applied spatial proteomics to characterize the molecular communication network at the embryo–endometrium interface, identifying hCG–LHCGR signaling as a key regulatory pathway during implantation and early embryonic development.

Multiomic analysis of cervical squamous cell carcinoma identifies cellular ecosystems with biological and clinical relevance



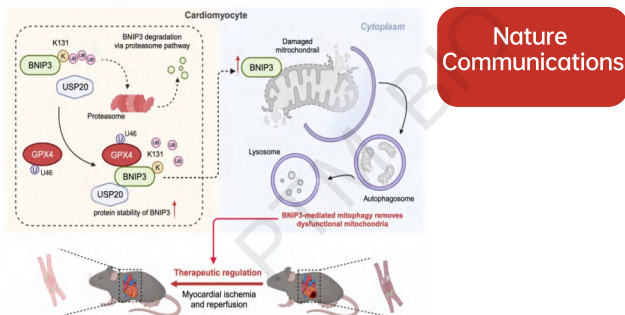
Nature Genetics

Research Focus: Spatial cellular states and the tumor immune microenvironment in cervical squamous cell carcinoma (CSCC).

Sample Cohort: Sixty ROIs representing different immune infiltration patterns, including 20 immune-rich and 40 immune-poor regions.

Key Findings: Using spatial proteomics together with multi-omics approaches, the study systematically characterized tumor heterogeneity in CSCC, identified interactions between tumor cells and the immune microenvironment, and provided new insights into the cellular ecosystem of cervical cancer.

Cardiomyocyte-derived GPX4 stabilizes BNIP3 to facilitate mitophagy and mitigate myocardial ischemia/reperfusion injury



Nature Communications

Research Focus: The role of glutathione peroxidase 4 (GPX4) in myocardial ischemia/reperfusion injury (MI/RI).

Sample Cohort: Human clinical samples and datasets, together with sham-operated and MI/RI mouse models.

Key Findings: By integrating spatial proteomics, spatial transcriptomics, and single-cell RNA sequencing, the study mapped the spatiotemporal dynamics of GPX4 during MI/RI and identified the GPX4–BNIP3–USP20 axis as a regulator of mitophagy and myocardial protection.

Spatial Excellence — Landmark Publications in Spatial Proteomics

Title	Journal
NEW Robust neurogenesis in chronic stroke monkeys following mesenchymal stem cell transplantation plus intermittent theta-burst stimulation	Signal Transduction and Targeted Therapy (IF=52.7)
Multimic analysis of cervical squamous cell carcinoma identifies cellular ecosystems with biological and clinical relevance	Nature Genetics (IF=29.0)
NEW Spatially resolved multi-omics of human metabolic dysfunction-associated steatotic liver disease	Nature Genetics (IF=29.0)
NEW Cardiomyocyte-derived GPX4 stabilizes BNIP3 to facilitate mitophagy and mitigate myocardial ischemia/reperfusion injury	Nature Communications (IF=15.7)
Spatiotemporal proteomic atlas of multiple brain regions across early fetal to neonatal stages in cynomolgus monkey	Nature Communications (IF=15.7)
Single-cell sequencing depicts tumor architecture and empowers clinical decision in metastatic conjunctival melanoma	Cell Discovery (IF=12.5)

Selected Publications Featuring PTM BIO Products and Services

Title	Journal
Metabolic regulation of gene expression by histone lactylation	Nature (IF=48.5)
NEW Alanyl-tRNA synthetase, AARS1, is a lactate sensor and lactyltransferase that lactylates p53 and contributes to tumorigenesis	Cell (IF=42.5)
NEW Metabolic regulation of homologous recombination repair by MRE11 lactylation	Cell (IF=42.5)
Increased glucose metabolism in TAMs fuels O-GlcNAcylation of lysosomal Cathepsin B to promote cancer metastasis and chemoresistance	Cancer Cell (IF=44.5)
Branched-chain amino acid catabolism promotes thrombosis risk by enhancing tropomodulin-3 propionylation in platelets	Circulation (IF=38.6)
NEW Sex-determining region Y gene promotes liver fibrosis and accounts for sexual dimorphism in its pathophysiology	Journal of Hepatology (IF=33.0)
NEW An integrated multi-omics analysis reveals osteokines involved in global regulation	Cell Metabolism (IF=30.9)
Senescent immune cells release grancalcin to promote skeletal aging	Cell Metabolism (IF=30.9)
NEW Proteogenomic insights into early-onset endometrioid endometrial carcinoma: predictors for fertility-sparing therapy response	Nature Genetics (IF=29.0)
NEW Multimic analysis of cervical squamous cell carcinoma identifies cellular ecosystems with biological and clinical relevance	Nature Genetics (IF=29.0)
Global profiling of crotonylation on non-histone proteins	Cell Research (IF=25.9)
Lysine 2-hydroxyisobutyrylation of NAT10 promotes cancer metastasis in an ac4C-dependent manner	Cell Research (IF=25.9)
NEW Targeting ube2t potentiates gemcitabine efficacy in pancreatic cancer by regulating pyrimidine metabolism and replication stress	Gastroenterology (IF=25.1)