BIOGNOSYS
NEXT GENERATION PROTEOMICS

TrueDiscovery

TISSUE PROTEOMICS FOR BIOMARKER DISCOVERY AND TARGET VALIDATION

High-Resolution Protein Expression Profiling of Tissue Samples to Uncover Disease Biology and Therapeutic Targets.

Traditional tissue analysis methods, such as those based on affinity-based probes, often suffer from limited specificity and poor quantitative accuracy. While RNA sequencing provides valuable gene expression data, it often correlates poorly with actual protein abundance due to factors such as translational regulation, protein degradation, and post-translational modifications.[1]

Biognosys' mass spectrometry-based TrueDiscovery tissue proteomics platform provides deep, unbiased, and label-free protein profiling with peptide-level resolution, capturing the full complexity of the proteome. From just 1 mg of fresh-frozen tissue or a single FFPE slide, up to 12,000 protein groups are quantified, covering intracellular, secreted, and surface proteins. This flexible and high-throughput approach supports a range of applications from biomarker discovery and mechanism of action studies to the identification of therapeutic targets for precision therapies (Figure 1).

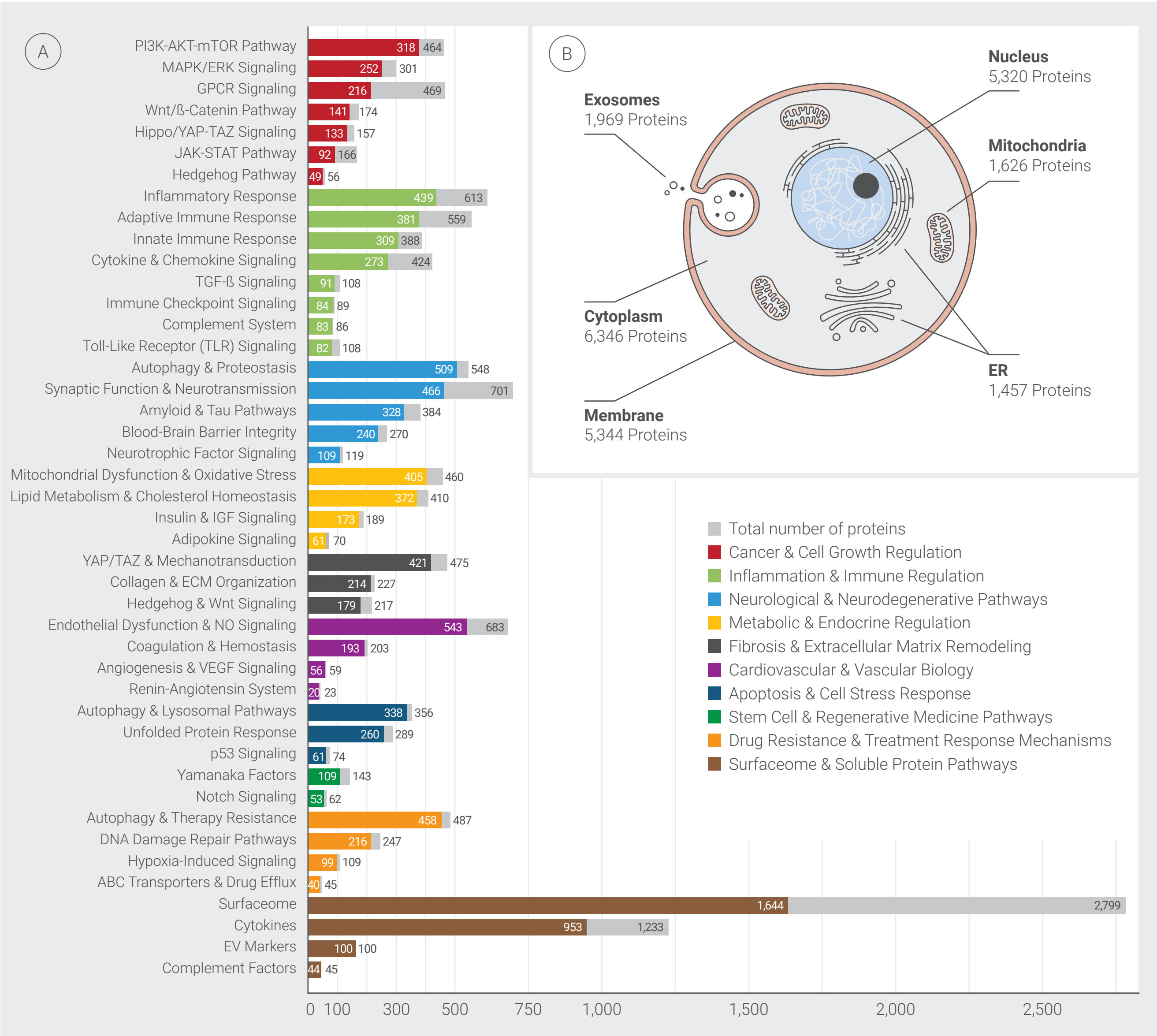

Figure 1. **Examples of proteins quantified using Biognosys' discovery proteomics platform across 19 healthy human tissue samples.**
A Coverage by subcellular localization. Colored bars indicate proteins detected by our platform; gray bars represent the total number of known proteins in each category.[2,3,4,5,6,7,8]
B Coverage across selected biological processes and signaling pathways.

HIGHLIGHTS

UltraDeep Proteome Coverage
Detect up to 12,000 proteins per sample, with >50% consistently observed across a range of different tissue types, ensuring robust proteome coverage.

Accurate Protein Quantification
Directly measure peptides for precise protein quantification, overcoming the limitations of RNA-based methods or antibody specificity variability.

High Specificity
Capture peptide-level information with multiple peptides per protein, and explore diverse proteoforms, including splice variants, truncations, and PTMs.

Species-Independent Platform
Analyze human or preclinical disease model samples, including PDX, PDO, and PDOX.

High-Throughput Workflow
Analyze Phase I trials in real-time or process large tissue biobanks, including pre-processed samples.

INPUT MATERIAL

Fresh-Frozen (FF)
≥1 mg of FF tissue, or 50 µg of total protein.

Formalin-Fixed Paraffin-Embedded (FFPE)
Single slide (5 µm, 50 mm^2) or curl, including recycled slides such as unstained, H&E-stained, stripped, or acid-decalcified. Compatible with both macro- and microdissected samples.

APPLICATIONS

Biomarker Discovery
Identify differentially expressed proteins and pathways, including intracellular (e. g. mitochondrial proteins and transcription factors), membrane-bound and extracellular proteins.

Medical oncologists at the Institut Gustave Roussy identified increased collagen expression as a biomarker of immunotherapy resistance in metastatic endometrial cancer using unbiased proteomics, further validated by orthogonal methods. A targeted assay is in development for improved patient stratification.

Mechanism of Action Studies
Assess treatment effects across diseases by measuring changes in protein abundance and therapeutic pathway modulation, including phosphorylation status and other PTMs.

Deep phosphoproteomics and global proteomics revealed autophagy pathway activation by a small molecule drug in development by a leading biotechnology company, identifying reticulophagy (ER-phagy) as a key mechanism, later validated by orthogonal assays.

Therapeutic Target Detection
Support clinical trial applications and decision-making by enabling the detection of key therapeutic targets, including those for ADCs, monoclonal, and bispecific antibodies. Consolidate testing for multiple targets into a single experiment, replacing serial IHC and maximizing the use of limited tissue biopsies.

Collaborators at Genmab conducted a study using single FFPE slides to profile and screen for 24 approved or clinical-stage ADC targets across hematological and solid tumors. Deep proteome profiling successfully quantified all 24 therapeutic targets, highlighting the platform's exceptional robustness and sensitivity[9] (Figure 2).

Global Surfaceome Profiling
Cell surface proteins are key therapeutic targets, yet many are inaccessible to antibody-based detection and cannot be accurately predicted by transcriptomics. Our platform covers over 1,600 surface proteins, or roughly 60% of the human surfaceome[2], enabling therapeutic target monitoring and identification of new targets.

Extracellular Protein Profiling
Analyze ECM components, EVs and soluble proteins such as complement factors (e. g. C1QA, C3 and C9) and other immune-related pathways to better map the extracellular environment and tumor-immune interactions.

Transferability to Clinical Panels
Seamlessly transition biomarkers into a fully customizable targeted protein assay (GCP-compliant if needed) for ultra-sensitive absolute quantification of up to 50 proteins.

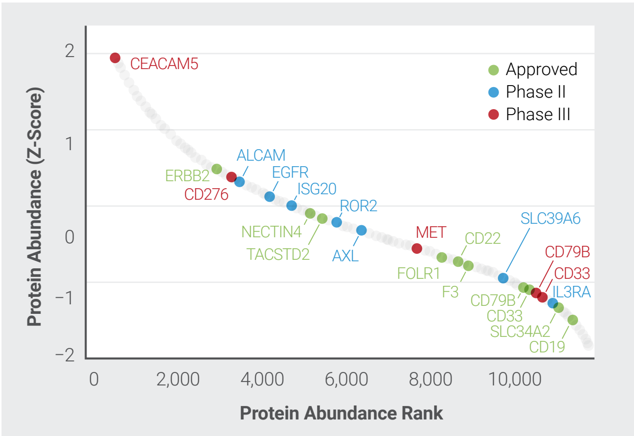

Figure 2. **Therapeutic targets for solid tumors identified by Biognosys' discovery proteomics platform using a single FFPE slide.**

Ready to dig deeper into the tissue proteome?
Contact our experts today for further information at **biognosys.com/contact.**

Abbreviations
MS: Mass Spectrometry / FFPE: Formalin-Fixed Paraffin-Embedded / PTMs: Post Translational Modifications / PDX: Patient-Derived Xenograft / PDO: Patient-Derived Organoids / PDOX: PDO Xenografts / H&E: Hematoxylin and eosin / ER: Endoplasmic Reticulum / ADC: Antibody Drug Conjugates / IHC: Immunohistochemistry / ECM: Extracellular Matrix / EVs: Extracellular Vesicles

References
1 Liu Y. et al., Cell, 165(3), 2016, 535–550, doi:10.1016/j.cell.2016.03.014
2 Bausch-Fluck D. et al., PNAS, 115(46), 2018, E10988–E10997, doi:10.1073/pnas.1808793115
3 Keerthikumar S. et al., J Mol Biol, 428(4), 2016, 688–692, doi:10.1016/j.jmb.2015.09.019
4 Milacic M. et al., Nucleic Acids Res, 52(D1), 2024, D672–D678, doi:10.1093/nar/gkad1025
5 Uhlén M. et al., Science, 347(6220), 2015, 1260419, doi:10.1126/science.1260419
6 Thul P.J. et al., Science, 356(6340), 2017, eaal3321, doi:10.1126/science.aal3321
7 Ashburner M. et al., Nat Genet, 25(1), 2000, 25–29, doi:10.1038/75556
8 The Gene Ontology Consortium, Genetics, 224(1), 2023, iyad031, doi:10.1093/genetics/iyad031
9 Dumontet C. et al., Nat Rev Drug Discov, 22(8), 2023, 641–661, doi:10.1038/s41573-023-00709-2