BIOGNOSYS
NEXT GENERATION PROTEOMICS

Contract Research Services

TRUE DISCOVERY®

EXPLORE THE UNEXPECTED WITH THE POWER OF PROTEOMICS

Unbiased Biomarker Discovery: Deep Proteome Profiling for Translational and Clinical Research

DISCOVERY PROTEOMICS FOR ALL YOUR RESEARCH NEEDS

The Biognosys TrueDiscovery platform offers integrated proteomics solutions across the entire drug development pipeline, from disease biology profiling to mechanism of action studies and novel biomarker discovery. It is the only platform that searches the complete proteome to quantify thousands of the most relevant proteins, including an unlimited number of proteoforms. Our services offer unparalleled depth and sensitivity, with flexible workflow options optimized for depth and throughput. These solutions are applicable to a broad spectrum of sample types and species, ensuring exceptional performance across diverse applications.

PLASMA BIOMARKER DISCOVERY

Unbiased profiling of up to **9,000** proteins from plasma samples with Biognosys' proprietary P2 Enrichment System.

- Higher-throughput workflow optimized for large-scale population studies.
- Available as CRO service or for in-house use through a licensing agreement.

BIOFLUID BIOMARKER DISCOVERY

Comprehensive proteomic analysis with a depth of up to **5,000** proteins in cerebrospinal fluid (CSF) and up to **6,000** proteins from urine.

- Optimized for diverse biofluids, including CSF, urine, aqueous humor, lymphatic fluid, cell culture supernatant and others.
- Minimal sample requirement scalable for large-scale patient cohorts.

IMMUNO PEPTIDOME PROFILING

In-depth characterization of the immuno-peptidome, detecting up to **10,000** MHC Class I and **10,000** MHC Class II peptides.

- Optimized enrichment methods for human, mouse & rat tissues and cells.
- Automated pipeline enabling reproducible identification and quantification from minimal sample material.

TISSUE BIOMARKER DISCOVERY

Unmatched depth of proteome profiling reaching close to **14,000** proteins.

- Optimized for all types of solid biological samples, including fresh frozen, freeze-dried tissues, FFPE slices, and cell culture.
- Requires only a limited amount of material for robust quantification.

MECHANISM OF ACTION STUDIES

Hypothesis-free molecular profiling combined with tailored data analysis to identify potential drug targets and biological pathways.

- Optimized for all types of biological samples.
- High-throughput pipeline enabling reproducible identification and quantification from minimal sample material.

PHOSPHO PROTEOME PROFILING

Deep phosphoproteomics analysis with **thousands** of phosphoproteins identified.

- Optimized for all biological samples, with primary applications in cell lines and tissues.
- High-throughput technology, scalable for large-scale studies.

UNPRECEDENTED DEPTH FOR TRUE, UNBIASED DISCOVERY

The TrueDiscovery platform helps you decipher the complexity of biology and unlock true, unbiased discoveries for your research. Thanks to our hypothesis-free approach, we go beyond measuring a defined panel of known markers, with our 360° proteome visualization letting you explore protein biology from every angle. With our proteomics solutions, you gain a deeper understanding of the key pathways involved in your journey to discovery, providing data-driven insights that will propel your project to the next phase.

FEATURES	BENEFITS
Unbiased Analysis with Unprecedented Depth	We search the complete proteome to quantify thousands of the most relevant proteins, including an unlimited number of proteoforms such as isoforms and post-translational modifications.
Unparalleled Specificity and Quantitative Precision	Our analysis provides tens of thousands of peptide-level data points to assure high quantitative precision and unbeatable specificity.
High Throughput and Scalability	We provide flexible solutions that balance depth and throughput, ensuring rapid project completion while upholding consistent reproducibility across thousands of samples.
Tailored Data Visualization and Interpretation	We go far beyond simply measuring proteins. Our tailored data analysis provides you with actionable insights.
End-to-end Solutions and Support	Our tailored data analysis, supported by Proteoverse® visualization tool, transforms data into actionable biological insights.

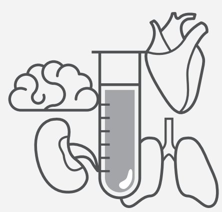
«Biognosys' biomarker discovery solutions are supported by a constantly improving platform and can be run in large-scale studies while maintaining high data quality.»

Kanna Palaniappan, PhD
Former Staff Scientist, Freenome

TRUE DISCOVERY®

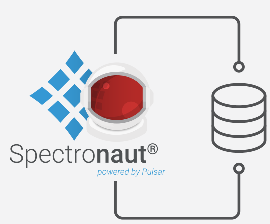
HRM™: THE LEADING DISCOVERY PROTEOMICS WORKFLOW

The TrueDiscovery platform utilizes our proprietary, patented Hyper Reaction Monitoring (HRM) technology to enable complete proteome quantification. HRM is a Data Independent Acquisition (DIA) mass spectrometry-based workflow developed by Biognosys that offers unmatched proteome coverage with precise and reproducible quantification of more than 13,000 proteins depending on the application.



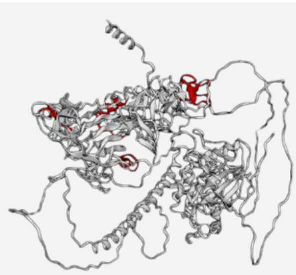
Robust Workflow

The high reproducibility of HRM enables proteomic profiling in large-scale, longitudinal studies with thousands of samples. The label-free analysis allows unbiased discovery through identification and quantification of complete proteomes and proteoforms, such as post-translational modifications.



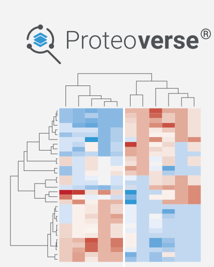
Advanced Data Processing

Data processing is performed by our Spectronaut® software, including our proprietary search algorithm, Pulsar. Artificial Intelligence and Machine Learning signal detection and data normalization is based on our patented Indexed Retention Time (iRT™) technology.



Peptide-level Resolution

HRM provides a comprehensive measurement of all detectable proteins in the sample by quantifying multiple peptides per protein. This peptide-level resolution ensures high reproducibility and specificity of the results and enables deeper understanding of biology.



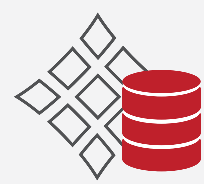
Tailored Data Interpretation

Our experts provide you with an in-depth study report and extensive data analytics package. We offer tailored data visualization and biological interpretation through our Proteoverse tool—available for free to help uncover biological insights from thousands of identified proteins. We also offer guidance on follow-up studies for validation.

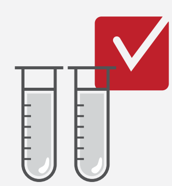
FROM EARLY DISCOVERY TO CLINICAL DIAGNOSTICS

Biognosys' end-to-end solutions and support help you upscale and translate your research across the entire drug development pipeline, from discovery through to clinical trials. The clinical transferability of our technologies enables you to move quickly from relative quantification in the discovery stage to absolute quantification of specific proteins of interest for clinical validation.

Proteome Database Insights Solutions
By analyzing tens of thousands of samples over the last years, we have developed an unparalleled knowledge of the human proteome. We acquired a unique, proprietary proteome database with reference data to contextualize and validate your study results.



Compliant with GCP Guidelines
For clinical studies requiring GCP compliance, our facility and processes comply with the ICH E6 and EMA guidelines. Studies under GCP are supported by our experienced Quality Operations and Quality Assurance team.



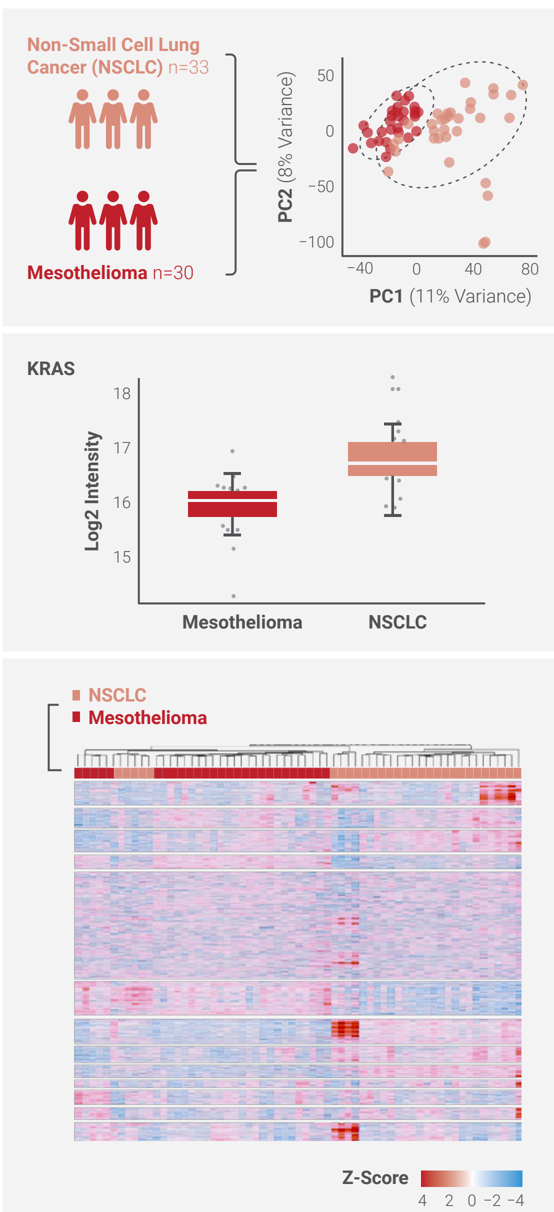
Explore Your Data with Ease
Our study reporting platform, Proteoverse®, offers you numerous possibilities to intuitively and dynamically visualize and explore your data, access the details of each analyzed protein, and gain even richer biological insights to advance your research.

Future-proof Data
Thanks to our unbiased data acquisition approach, your data can always be reaccessed and reanalyzed, considering new scientific insights. Our team of experts is always ready to look deeper for you.

Case Study

UNLEASHING NEW DISCOVERIES IN PLASMA PROTEOMICS

Biognosys' P2 Enrichment System sets a new standard in proteomics, enabling researchers to uncover low-abundance proteins in human plasma and other biofluids. Built on proprietary particles and optimized reagents, the system combines the highest achievable plasma depth with superior reproducibility and throughput. In this study, we profiled over 9,000 proteins in a clinical trial cohort to uncovering novel disease-specific proteomic signatures.



Study Design

To gain deeper insights into the circulating proteome of NSCLC and Mesothelioma patients, we analyzed plasma samples from two clinical cohorts using the proprietary P2 Enrichment System and the TrueDiscovery™ UltraDeep platform.

Novel Proteomics Signature

P2 Enrichment resulted in an unprecedented depth of over 9,151 protein groups across all 63 samples. Of these, 6,057 proteins were confidently quantified in all samples with no missing values. This extensive coverage allowed us to quantify approximately 50% of the Therapeutic Target Database proteins, including KRAS, a well-known oncogene and a critical target in lung cancer therapy.

Uncovering Key Biological Insights

Unsupervised clustering revealed distinct biological process associated with each cancer type:

- Mesothelioma patients exhibited upregulation of pathways related to Antigen Processing and Ubiquitin-Proteasome Degradation, highlighting immune response and protein turnover mechanisms.
- NSCLC patients showed significant upregulation of the Neutrophil Degranulation pathway, suggesting a key role of innate immune activation in the disease pathology.

These findings demonstrate the power of P2 Enrichment in uncovering critical disease mechanisms and identifying potential therapeutic targets in oncology.

Reference: Viodé A., Bruderer R. et. al. Human Proteome Organization (HUPO) World Congress 2024, (OP-76).

Case Study

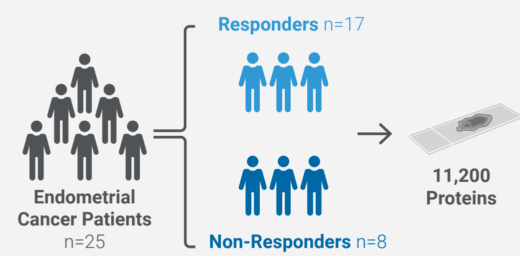
IDENTIFYING PREDICTIVE BIOMARKERS FROM FFPE TUMOR SAMPLES

Clinical scientists at Institut Gustave Roussy in France used Biognosys' TrueDiscovery platform to identify biomarkers for immunotherapy response in endometrial cancer. Proteomics analysis of FFPE samples revealed increased collagen expression, validated by spatial imaging. These findings suggest that, alongside mismatch repair deficiency, collagen expression could serve as an additional predictive biomarker for response in metastatic endometrial cancer.

TISSUE BIOMARKER DISCOVERY

Study Design

FFPE tumor samples from 25 patients with endometrial cancer, taken prior to immunotherapy, were analyzed using the TrueDiscovery UltraDeep Tissue Biomarker Discovery platform. The study aimed to identify differentially regulated proteins between responders (n=17) and non-responders (n=8) with the goal of uncovering potential predictive biomarkers for treatment response.



Collagen as Predictive Biomarker Candidate

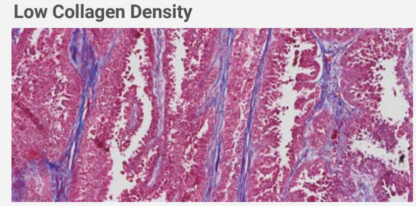
Close to 11,200 proteins were quantified across all samples with an average of 10,000 proteins quantified per sample. Unbiased differential analysis identified collagen alpha-2 (V) chain (CO5A2), and collagen alpha-1 (XXII) chain (COMA1) as significantly upregulated in the non-responder group, emerging as potential biomarkers of immunotherapy resistance.

Protein Candidates	CO5A2	COMA1
Description	Collagen alpha-2 (V) chain	Collagen alpha-1 (XXII) chain
AVG Log Ratio	2.9	1.1
% Change	86.9%	54.8%
p-Value	0.008	0.006
Responders(R) vs Non-responders (NR)	↑NRs	↑NRs

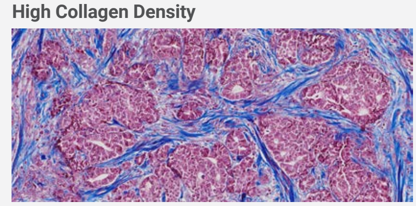
Validation with Spatial Imaging

To validate these findings spatial imaging was used to revealed significantly higher collagen density in intra-tumoral areas of the non-responders. Alternative microscopy method confirmed that fibrillar collagen content was greater in non-responders, while a linear collagen pattern correlated with treatment response.

Low Collagen Density



High Collagen Density



Taken together mass spectrometry and imaging identified collagen expression as a potential predictive biomarker for immunotherapy response in mismatch repair deficiency endometrial cancer, opening new opportunities for patient stratification and therapeutic interventions.

Reference: Grau-Béjar J., Lachaud A.A., Leary A. et. al. American Association of Cancer Research (AACR) Annual Meeting 2024, (5149).

BIOGNOSYS: A LEADING INNOVATOR IN PROTEOMICS

As the inventor and leading innovator of mass spectrometry-based proteomics solutions, we offer trusted state-of-the-art contract research services and software solutions that deliver actionable insights to accelerate your research.

> 15	> 50%	> 4,000	> 1,000
years of innovation in Proteomics	PhD scientists on staff	publications on Biognosys' technology	global customers

YOUR PARTNER THROUGHOUT THE RESEARCH JOURNEY

Biognosys is your trusted partner throughout the discovery and development journey with attentive pre-study consultation, high quality and timely data delivery, and insightful reporting.

Contact us to discuss your key research objectives and discover how our expertise can support your success.
biognosys.com/contact

At Biognosys, we believe that deep proteome insights hold the key to breakthrough discoveries that transform science for better lives. We make the proteome actionable to empower research, drug development, and clinical decision-making with our versatile portfolio of mass spectrometry-based proteomics research services, software, and kits. These solutions provide a multi-dimensional view of protein expression, function, and structure in all biological species and sample types.

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