

The background of the slide is a complex, artistic representation of protein structures. It features numerous white and light blue ribbon models of proteins, some of which are highlighted with translucent, flowing surfaces in shades of blue, yellow, and orange. The overall effect is a sense of dynamic biological activity and molecular complexity.

TRUE  **DISCOVERY™**

EXPLORE THE UNEXPECTED
WITH THE POWER OF
PROTEOMICS

Deeper Biological Insights for True, Unbiased Discovery

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 mechanisms 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 are optimized for various sample types across different species.

BIOFLUID BIOMARKER DISCOVERY

- Depth of 4,200 proteins in plasma or serum and over 11,000 proteins in other biofluids
- Optimized for a wide variety of other biofluids, e.g., cerebrospinal fluid (CSF), urine, or aqueous humor
- Can be combined with our PQ500 panel for absolute quantification of target proteins

IMMUNO PEPTIDOME PROFILING

- Depth of 10,000 MHC Class I and Class II peptides
- Optimized for human tissues and cells
- High-throughput pipeline offering reproducible identification and quantification from minimal sample material

MECHANISM OF ACTION STUDIES

- Identification of molecular targets and characterization of biological pathways
- Optimized for all types of biological samples
- High-throughput pipeline offering reproducible identification and quantification from minimal sample material

TISSUE BIOMARKER DISCOVERY

- Depth of over 13,800 proteins
- Optimized for all types of solid biological samples, including fresh frozen tissue, freeze-dried tissue, formalin-fixed paraffin-embedded (FFPE) slices, or cell cultures
- Only a limited amount of material is required

PHOSPHO PROTEOME PROFILING

- Depth of thousands of phospo-proteins
- Optimized for all biological samples most applied on cell lines or tissue
- Applicable on large scale studies thanks to the technology's high-throughput

UNPRECEDENTED DEPTH FOR TRUE, UNBIASED DISCOVERY

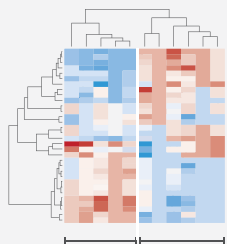
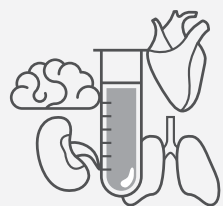
The TrueDiscovery™ platform helps you decipher the complexity of biology and unlock true, unbiased discoveries for your research. Thanks to our hypothesis-free approach, we go beyond measuring a defined panel of known markers, with our 360° proteome visualization letting you explore protein biology from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

Benefits	Features
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 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 a fast project turnaround time while maintaining high 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 solutions drive your research from early-stage discovery to clinical biomarkers and diagnostics
«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
Staff Scientist, Freenome

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 based on more than a decade of experience. We also provide guidance on follow-on studies to validate your findings.

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 GLP and GCP Guidelines

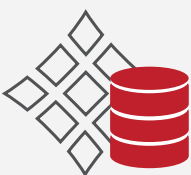
For pre-clinical studies requiring GLP compliance, our facility and processes comply with the OECD principles on GLP. For clinical studies requiring GCP compliance, we conform with all the applicable regulations for processing human samples. Studies under GLP or GCP are supported by our experienced Quality Operations and Quality Assurance team.

Clinical Diagnostics Development

Through our partnership with Siemens Healthineers, we support your diagnostics projects from assay development to commercialization. We ensure that any biomarker you discover can be applied in clinical settings.

Future-proof Data

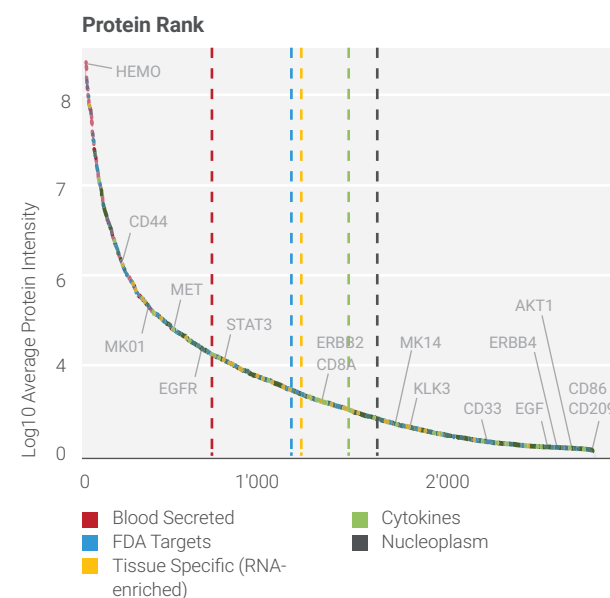
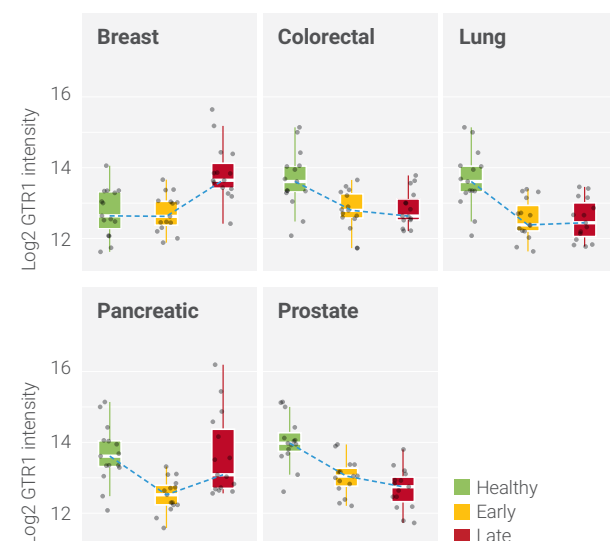
Thanks to our unbiased data acquisition approach, your data can always be reaccessed and reanalyzed, considering new scientific insights. Our team of experts is always ready to look deeper for you.



Case Study

UNBIASED PROTEOMIC PROFILING FOR PLASMA BIOMARKER DISCOVERY

Measuring circulating biomarkers in cancer supports early detection, differential diagnosis, and predicting response to therapy. In this study, we deployed an optimized discovery workflow to access the unexplored part of the proteome and identify novel biomarkers associated with different cancer indications.



Study Design

To develop a greater understanding of the circulating proteome, we developed a deep proteomics workflow and profiled 180 samples across five different cancer types.

Identification of Biomarker Candidates

We reached eight orders of magnitude of dynamic range, covering the tissue leakage proteome, interleukins, and signaling proteins such as EGF. Using classification algorithms, we were able to identify a protein panel with a significant positive predictive value associated with individual cancer stages.

Deeper Insights

The biomarker candidate proteins separated healthy from early and late-stage cancer patients, with increasing or decreasing trends that were cancer-agnostic. There were an average of 129 candidates, making biological interpretation and follow up more feasible.

Reference: Biomarker Candidates for Tumors Identified from Deep-Profiled Plasma Stem Predominantly from the Low Abundant Area; Marco Tognetti, Kamil Skłodowski, Sebastian Müller, Dominique Kamber, Jan Muntel, Roland Bruderer, Lukas Reiter bioRxiv 2021.10.05.463153; doi: <https://doi.org/10.1101/2021.10.05.463153>

Case Study

UNBIASED DISCOVERY OF TISSUE-BASED BIOMARKERS

With the approval of immune checkpoint inhibitors, cancer management has improved significantly. However, predicting the likelihood of response to these drugs remains an unmet medical need. We analyzed the proteome of melanoma tumors biopsies to uncover biomarkers for treatment responsiveness. A set of 25 protein candidates were identified as a proteomic signature associated with response to PD-1 immunotherapy.

Study Design

To understand responsiveness to treatment in melanoma patients, we analyzed the proteomes of 23 FFPE specimens prior to PD-1 treatment and correlated the results with responses to therapy.

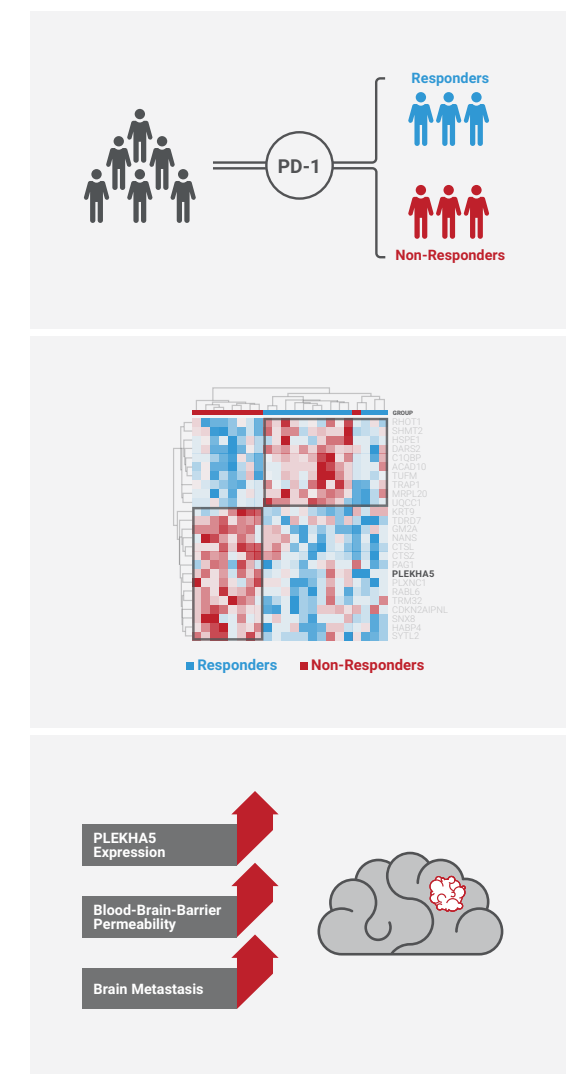
Proteomic Signature

The global proteomic analysis provided deep and unbiased quantification of tumor proteomes. Starting from the complete proteome, we identified a signature of 25 protein candidates that were differentially expressed in responders and non-responders, which clustered into distinct subgroups.

Biological Relevance

These proteomic profiles correlated significantly with clinical outcomes of PD-1 therapy. Several biologically significant insights were identified. For example, CNS metastasis was significantly associated with non-response, while PLEKHA5 was strongly correlated with non-response and brain metastasis.

Reference: Response and Skin Toxicity Related Protein Signature in Late Stage Melanoma Patients after Anti-PD-1 Treatment. E-poster presented at AACR 2021 in collaboration with Instituto Nazionale Tumori IRCCS Fondazione Pascale, Napoli, Italy; NanoString Technologies, Seattle, WA



BIOGNOSYS: A LEADING INNOVATOR IN PROTEOMICS

As the leading inventor and innovator of mass spectrometry-based proteomics solutions, we offer industry-leading technology and actionable insights that you can trust to accelerate your research.



> 14

years of
innovation in
Proteomics



> 50%

PhD scientists
on staff



> 55

granted
international
patents



> 2,400

publications
on Biognosys'
technology



10,000

sqft lab and
LC-MS facilities



> 800

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 at services@biognosys.com to discuss your specific study needs with one of our scientific or technical consultants.

At Biognosys, we believe that deep proteome insights hold the key to breakthrough discoveries that can dramatically improve human health. We enable life science researchers and drug hunters to look at the proteome from every angle with our versatile portfolio of proprietary proteomics services, software, and kits. These solutions provide a multi-dimensional view of protein expression, function, and structure in all biological species and sample types. Through advanced data analytics, Biognosys translates data into actionable insights for R&D and clinical research.

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NEXT GENERATION PROTEOMICS