

# PROTEOVERSE®

## DIGITAL PROTEOME FOR DRUG DISCOVERY AND BIOMARKER RESEARCH

An Ultra-Deep, Qualitative Map of Tissue-Specific Protein Expression Across Species

Biognosys' mass spectrometry-based Digital Proteome is one of the most comprehensive resources available for tissue-specific protein expression, covering over 20 healthy and diseased tissue types from both human and preclinical species (Figures 1 & 2). Continuously expanded with new tissues and species, the dataset serves as a robust reference for biomarker discovery, translational research, and tissue-targeted drug development.

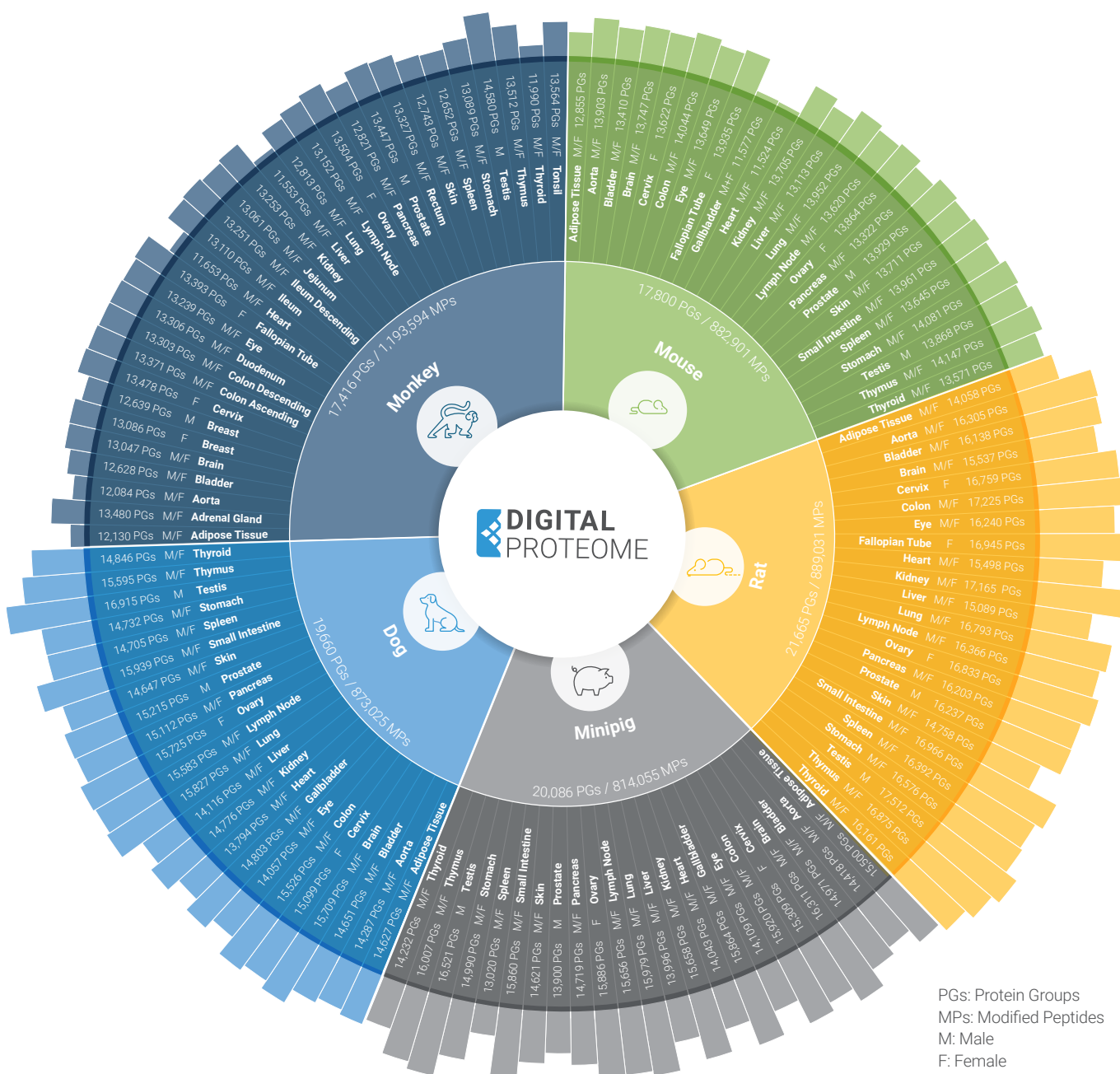


Figure 1. **Overview of Biognosys' Digital Proteome.** It offers high-resolution, peptide-level insights into protein expression across a broad range of healthy tissues from preclinical species (human: see next page).

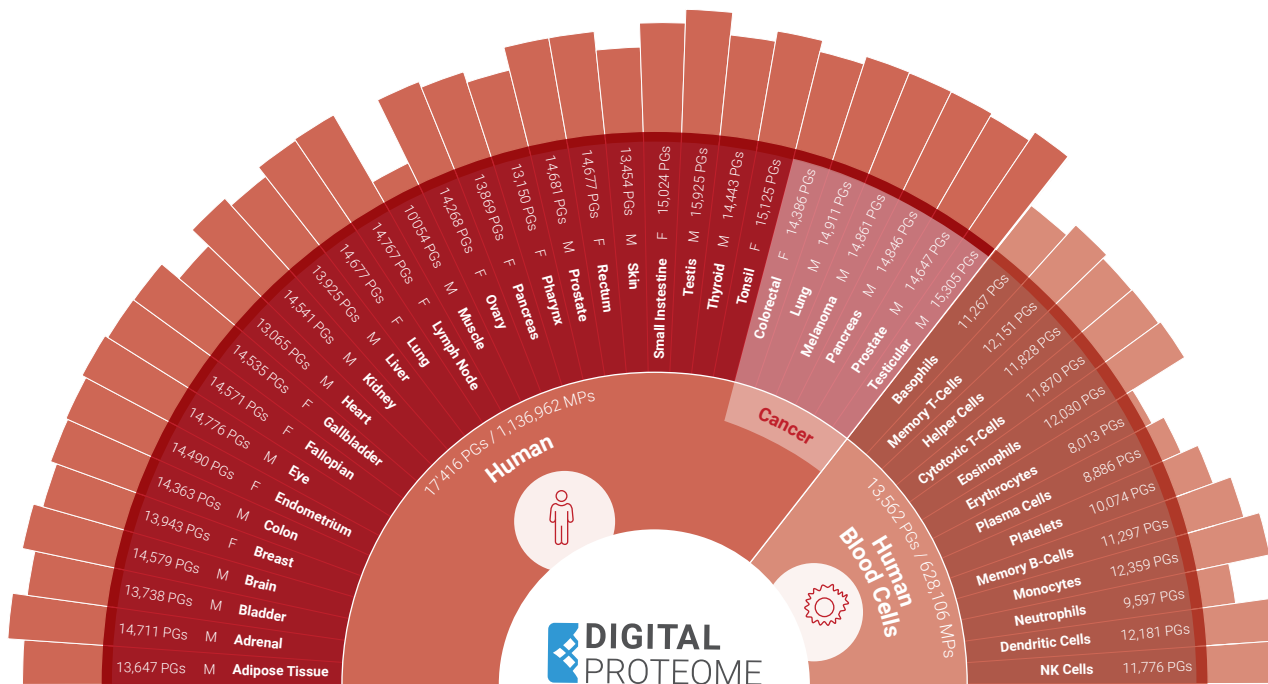


Figure 2. **Overview of Biognosys' Digital Proteome.** It offers high-resolution, peptide-level insights into protein expression across a broad range of healthy and diseased human tissues (preclinical species: see previous page).

PGs: Protein Groups  
MPs: Modified Peptides  
M: Male  
F: Female

## HIGHLIGHTS

### Comprehensive, High-Resolution Library

Deep fractionation DDA-MS profiling identified over 5 million modified peptides, mapping to 17,944 (human tissues), 13,562 (human blood cells), 17,800 (mouse), 21,665 (rat), 20,086 (minipig), 19,660 (dog) and 17,416 (monkey) protein groups, including protein-level evidence for previously unconfirmed or predicted sequences.

### Quantitative Multi-Species Expression Map

Using single-shot DIA-MS over 1 million peptides were quantified, covering 11,042 (human tissues), 6,366 (human blood cells), 12,822 (mouse), 14,099 (rat), 14,494 (minipig), 13,420 (dog) and 14,170 (monkey) protein groups.

### Biological Relevance

Broad coverage of biological pathways, drug targets, and tissue-specific isoforms supporting diverse applications from mechanism-of-action studies to therapeutic target validation.

### Ready-to-Use Data Modules

One-time delivery of raw files and curated protein tables (DDA and DIA) for each species and tissue module, ready for immediate integration into your research workflow.

## APPLICATIONS

- Survey tissue-wide target and off-target protein expression profiles to inform safety and toxicological risk assessment.
- Identify tissue-specific proteoforms, including isoforms, post-translational modifications, mutations, and non-canonical proteins.
- Support translational research with consistent and comparable proteomic data across human and preclinical species.
- Identify peptides suitable for absolute quantification in customizable targeted protein panels.
- Estimate baseline expression levels of therapeutic targets across tissues and species.
- Use dataset as robust input for machine learning and predictive modeling.

### Abbreviations

MS: Mass Spectrometry  
DDA: Data-Dependent Acquisition  
DIA: Data-Independent Acquisition



Ready to explore the depths of the Digital Proteome?  
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