



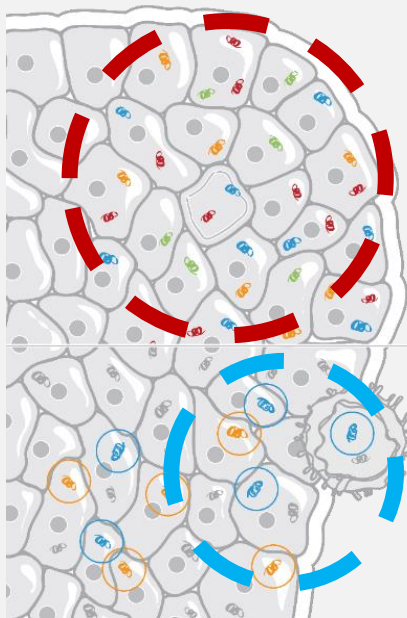
# ACCELERATING BIOPHARMA R&D WITH NEXT GENERATION PROTEOMICS

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Targeted Proteomics Platform

Contact us at  
[services@biognosys.com](mailto:services@biognosys.com)  
[www.biognosys.com](http://www.biognosys.com)

# Biognosys Provides Integrated Proteomics Solutions for Biomarker Discovery And Validation



## Biomarker Discovery

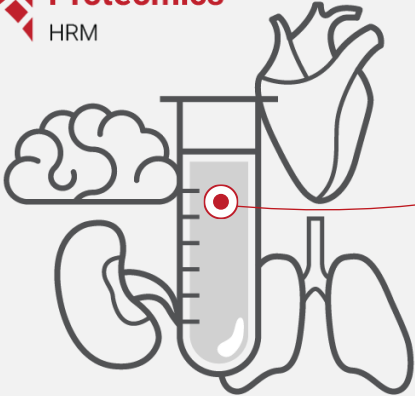
- Hypothesis-free approach
- Applicable in diverse biological matrices
- Relative quantification of thousands of proteins

## Functional Validation

- Customized protein panel development
- Applicable on high-throughput scale
- Absolute or relative quantification of 100+ proteins per panel

# Integrated Biomarker Discovery and Validation Workflows

## Identification of Biomarker Candidates



## Targeted Assay Development

Assay development based on deep expertise in targeted proteomics

Use of experimental data or proprietary Biognosys assay repository

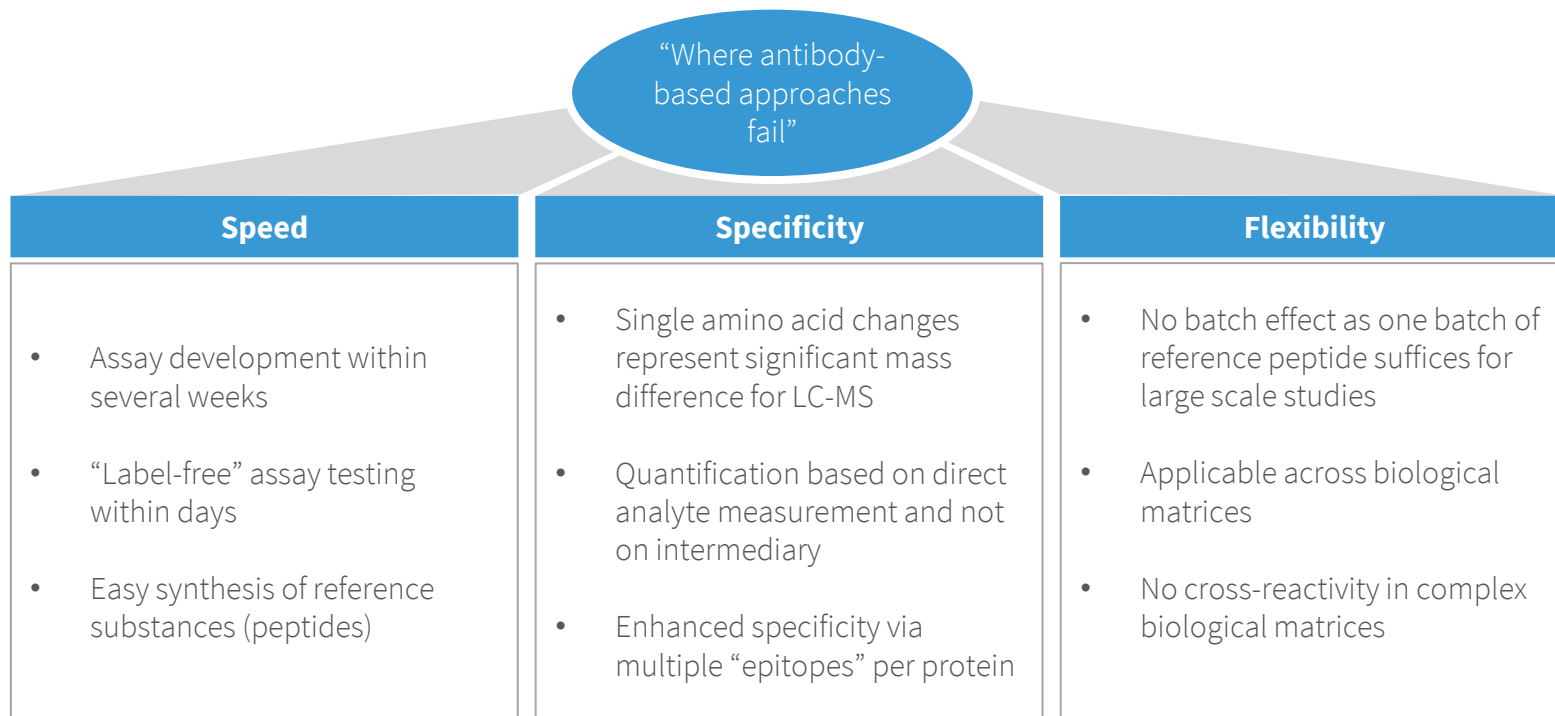
Proprietary PQ500 Plasma Panel



## Absolute Quantification

- Expertise in developing multiplexed panels for simultaneous analyte quantification
- Assay optimization to ensure high-throughput and cost efficiency
- Accurate differentiation between protein variants: e.g. mutations, truncations, PTMs, isoforms

# Speed, Specificity and Flexibility as Key Hallmarks of Targeted Proteomics



# Biognosys Offers Deep Expertise in Assay Development



## Peptide Selection

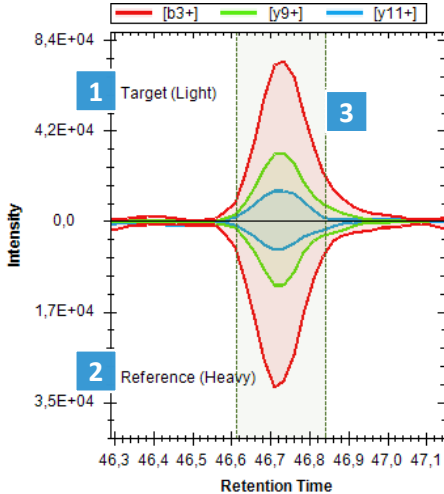
- Unique/proteotypic in the biological matrix of interest
- High response factor for enhanced sensitivity
- Low probability of modifications (both biological and during sample processing)



## Assay Characterization

- Selectivity in a given biological matrix
- Linearity range of quantification (calibration curve)
- Limit of quantification (LOQ and LLOQ)
- Stability
- Precision & accuracy (Intra- and inter-assay)
- Carry-over
- Recovery
- Robustness

# Absolute Quantification Based on Reference Peptides



## 1 Target signal

- Signal representing peptide in sample (“endogenous”)

## 2 Reference signal

- Signal representing reference (internal standard) peptide
- Peak shape, retention time, and fragment ions are equal to target
- Absolute quantification (known quantity of reference)

## 3 Peak

- Target to reference ratio provides peptide quantity in sample
- Peak boundaries are automatically detected by software (SpectroDive)
- Peak scoring via multiple scores
  - Omics approaches: FDR concept, multiple fragment ions
  - Classical analytical chemistry: LLOQ concept (yes/no detection), single or few fragment ions



# Working with Us: How We Deliver Value

