

# Accelerate Insights with the Proteograph™ Analysis Suite



Fast, Efficient  
Workflows



Intuitive  
Interface



Robust  
Assessment



Powerful  
Insights



Explore PAS

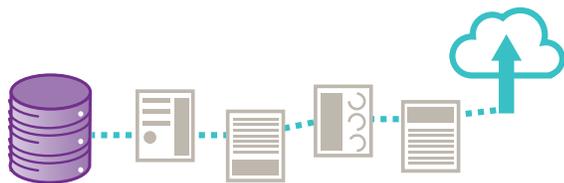




## Get a clearer view of the proteome

The Proteograph™ Product Suite enables unbiased, deep, and rapid proteomic analysis at scale. Survey thousands of human plasma proteins to discover new insights or quantify protein abundance to uncover biological meaning; Seer's Proteograph Product Suite delivers quantitative, accurate, precise, and reproducible data for proteome studies of any size.

The Proteograph Analysis Suite (PAS) is a dedicated cloud-based software solution for processing, analyzing, and visualizing proteomics data generated by liquid chromatography-mass spectrometry (LC-MS). The integrated search engines power rapid identification and annotation of LC-MS data and the variety of quality control tools ensure the highest confidence in your insights quickly and efficiently.



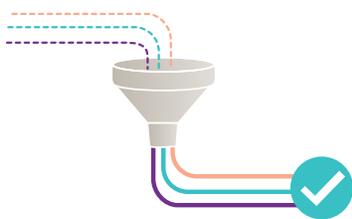
### Automated Data Upload

Upload data automatically from the LC-MS to PAS without manual intervention.



### State-of-the-Field Peptide Identification and Protein Quantification

Integrated database search engine and analysis wizard allows automated peptide identification and protein quantification for seamless generation of results. Seer's proprietary human spectral library files are a deep and extensive resource allowing users to identify and quantify proteins in their datasets.



### Pre-Configured Data Filtering Pipeline

Current best practices for peptide sequence annotation, statistical false discovery filtering, protein assignment, and protein quantification are pre-configured to enable routine analysis without the need for advanced bioinformatics expertise.



### Visualization Tools for Biological Insight

Results are automatically generated including data tables compatible with downstream analysis tools, and intuitive visualization options to evaluate assay results and performance.



### Analysis Summary and Metrics

Quickly and easily evaluate experimental results with automatically generated summary and metric plots showing plate map summaries, intensity and coefficient of variation (CV) plots, peptide and protein group counts, protein group overlaps between samples, and sample comparability.

**Plate Map Summaries:** Quickly assess the results of various experimental metrics across samples to for a high-level overview of experimental performance.

Protein Group Counts

A	1132	1179	1727	1237	780	1055	1243	1698	1222	740	1303	
B	1081	1349	1787	1150	686	1149	1531	1948	1383	833	561	
C	1251	1136	1602	1240	789	1257	1315	1888	1440	891	546	
D	1165	1420	1963	1413	909	1173	1485	1951	1371	900		
E	1098	1203	1756	1270	694	1281	1349	2091	1482	915		
F	1033	1218	1709	1220	801	1184	1628	1743	1270	1066		
G	1403	1727	2069	1421	1228	1151	1452	1861	1254	829		
H	967	1039	1617	1182	522	1621	1567	1914	1404	1838		534
	1	2	3	4	5	6	7	8	9	10	11	12

Figure 1: View results for protein groups (shown) and peptide counts, quant mass, miscleavage rate, oxidation ratio and ID rate in a simple and intuitive plate format.

**Protein Intensities:** Visualize similarity between samples by comparing the distributions of protein group intensities.

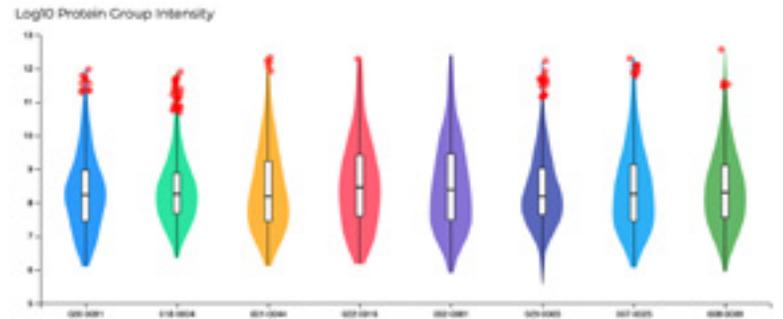


Figure 2: Distributions of protein group intensities and CVs across samples.

**Distribution of Detected Proteins in Plasma:** Visualize Proteograph’s compression of the plasma proteome’s dynamic range by comparing to a deeply covered reference plasma proteome dataset.

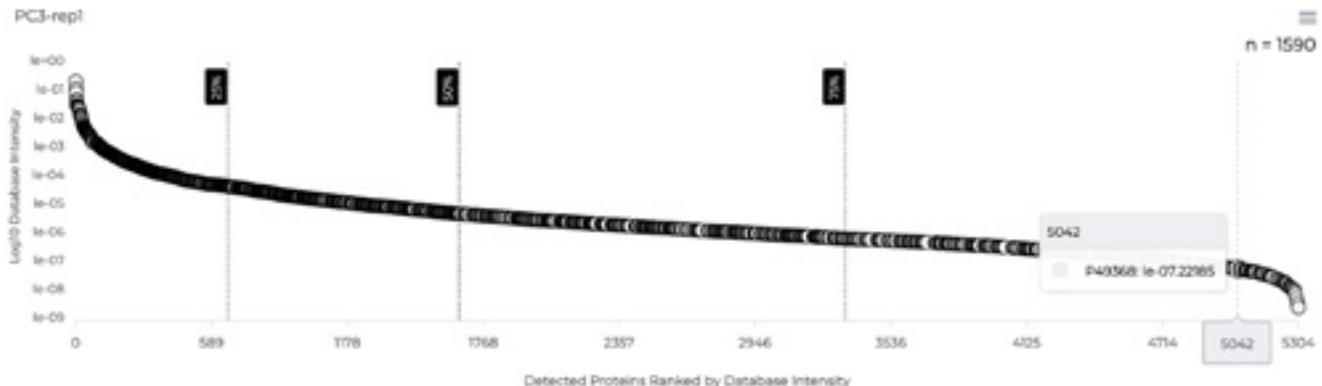
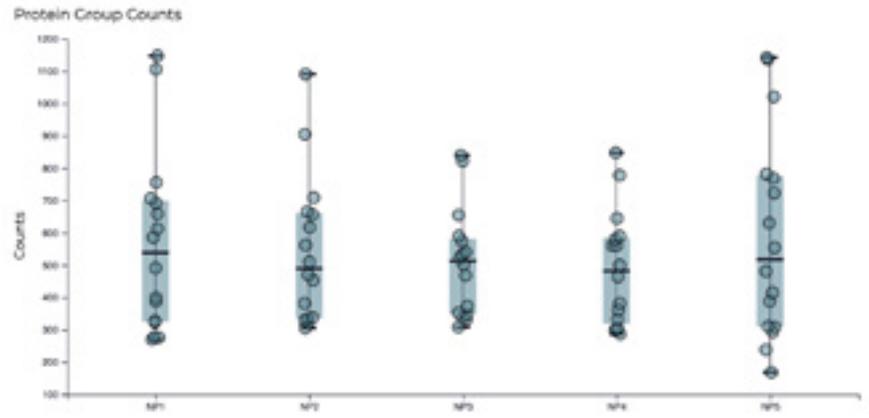


Figure 3: Plots show the dynamic range of identified proteins compared to the deepest reported human plasma proteome index.

**Peptide/Protein Group Counts:** Gain insight to differences in protein groups captured across nanoparticles by examining the number of protein groups identified across NPs.



**Figure 4:** Box plots showing the number of protein groups identified across NPs. Hovering over a dot reveals the peptide or protein count, file, and sample name. Hovering over a box shows the quantile for the NP.

**Protein Group Overlap:** The Protein Group Overlap Sets section is divided into two bar graphs and a matrix that together show protein group intersections.



**Figure 5:** (A) Graphs and a matrix show protein group overlaps; Intersection Size bar graph (B) Protein group count bar graph (C) Matrix.

**Sample Comparability:** Displays the degree of statistical correlation between samples based on the Pearson correlation coefficient (PCC), which measures the linear correlation of data.



**Figure 6:** A color-coded matrix displays sample comparability data using PCC (left) or the Jaccard index (right). Samples on the green end of the spectrum have high correlation, while samples on the red end of the spectrum have low correlation.



## Quality Control Metrics

Visualize quality control data in an intuitive, color-coded dashboard. Each chart plots one metric for one process control category. QC charts are organized with the same metric across each row and the control type in each column. The x-axis is labeled with the date of analysis and the y-axis depends on the metric.

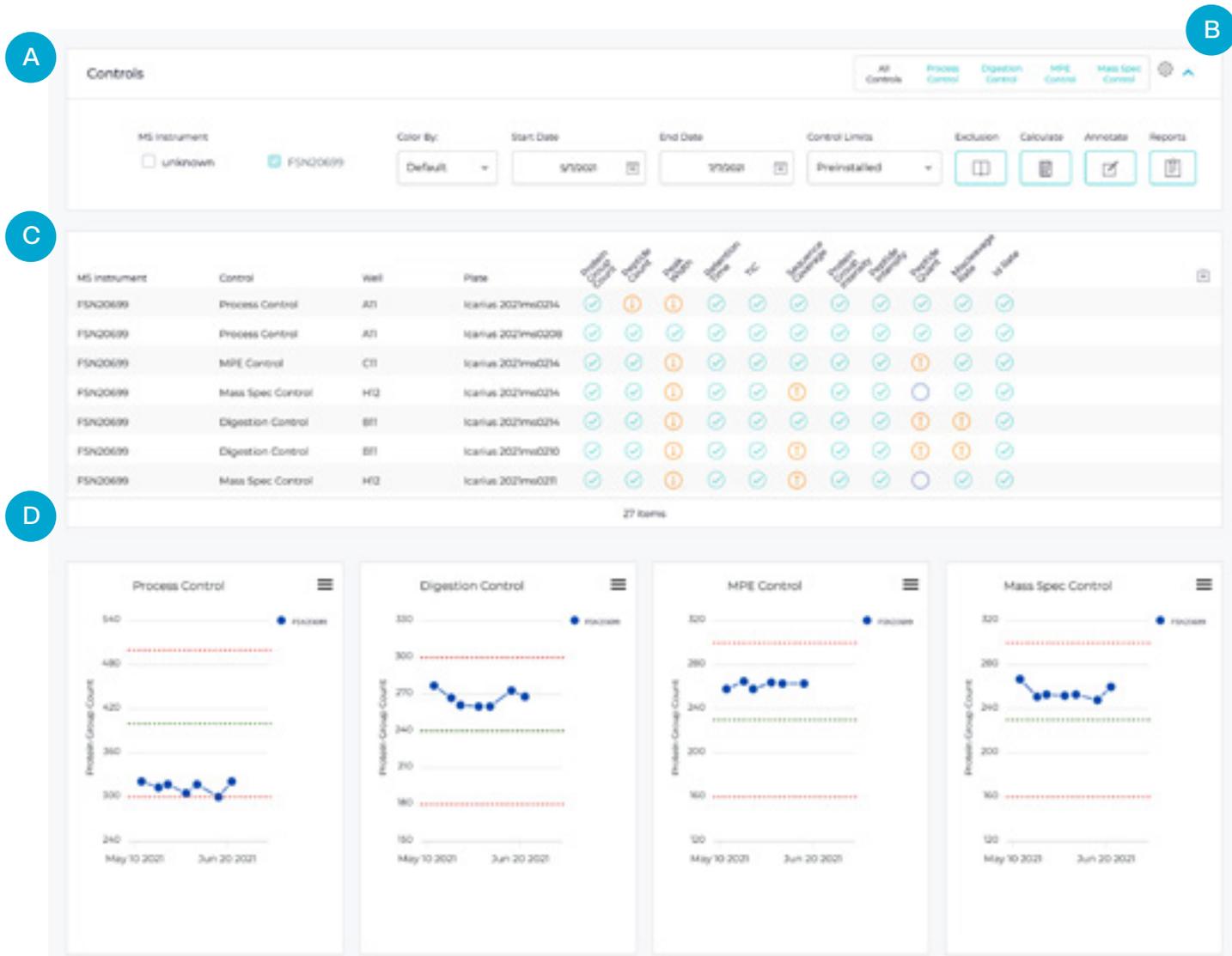


Figure 7: Control Results: (A) Filters for viewing charts for all controls or a selected control type. (B) Toolbar with additional filters and functions. (C) Summary of control data for the selected analysis time frame. (D) QC charts with metrics for each control.



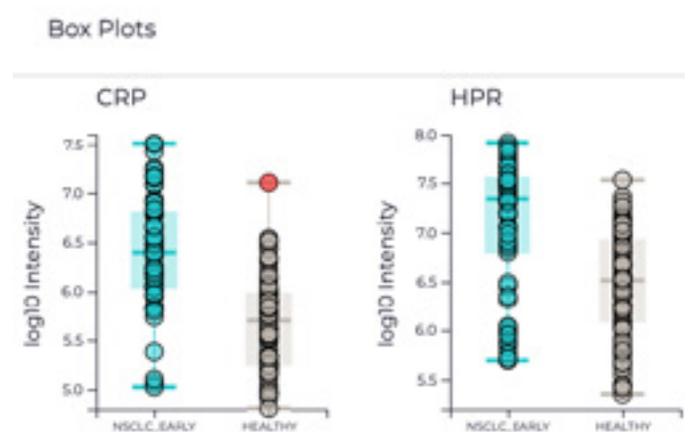
## Differential Expression Analysis

Interactive plots enable functional and biological interpretation of results. Seamlessly evaluate expression differences between study samples using Group Analysis or output raw and processed protein expression tables for custom analyses. To support Group Analysis, PAS provides a variety of MS database search engines including MaxQuant<sup>1</sup> for DDA-based analyses, and either EncyclopeDIA<sup>2</sup> or DIA-NN<sup>3</sup> for DIA-based analyses.

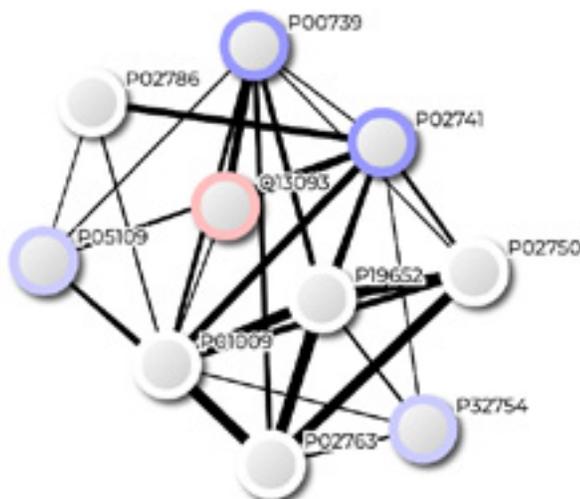
**Sequence Coverage:** Visualize where peptides map relative to the protein sequence



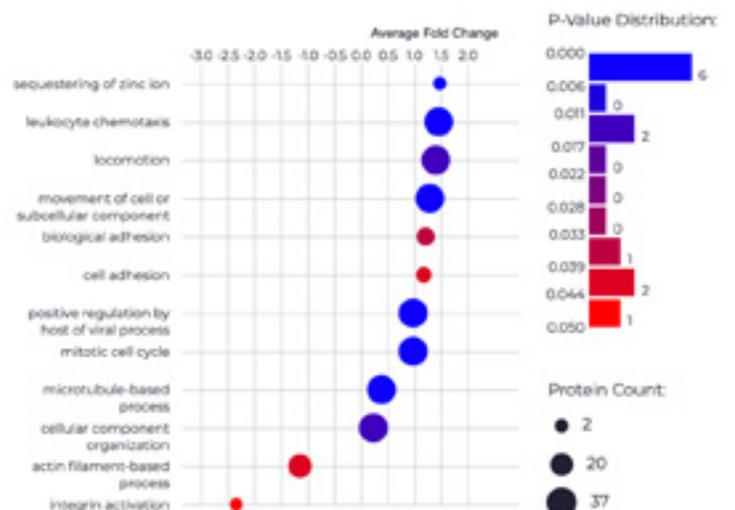
**Intensity Comparison:** View how the intensity of a protein of interest differs between groups



**Protein-Protein-Interactions Comparison:** Build a PPI network using the STRING database<sup>4</sup> to visualize possible protein interactions



**Gene Ontology (GO) Enrichment:** Perform GO enrichment analysis<sup>5</sup> to explore how proteins associated with a group differ functionally<sup>6,7</sup>



## Identify and Explore Variant Peptides with the Proteogenomics Workflow

Proteograph Analysis Suite now includes a Proteogenomics workflow to identify and explore peptide variants arising from allelic variation or other user-defined protein sequence altering variants, through the integration of Proteograph proteomics data with NGS variant information (Figure 8). The workflow offers a scalable and easy-to-use solution to a typically computationally intensive bioinformatics pipeline.

### Build a custom peptide database

Upload a custom or sample-specific variant call file (VCF) to predict protein altering variants not captured in the canonical reference database. Personalized variant peptides are automatically combined with the canonical reference database to generate a customized database.

### Perform a search for variant peptides

Using the customized protein sequence database, search your LC-MS/MS Data Dependent Acquisition (DDA) data for variant peptides utilizing MSFragger search algorithms in PAS.

### Browse and explore your variant peptide results

Variant peptide results are summarized in an interactive table and plots. Browse peptide and variant peptide data maps in genomic space at nucleic acid/amino acid resolution (Figure 8). Visualize gene structure, protein domain information, and region information with respect to identified peptides.

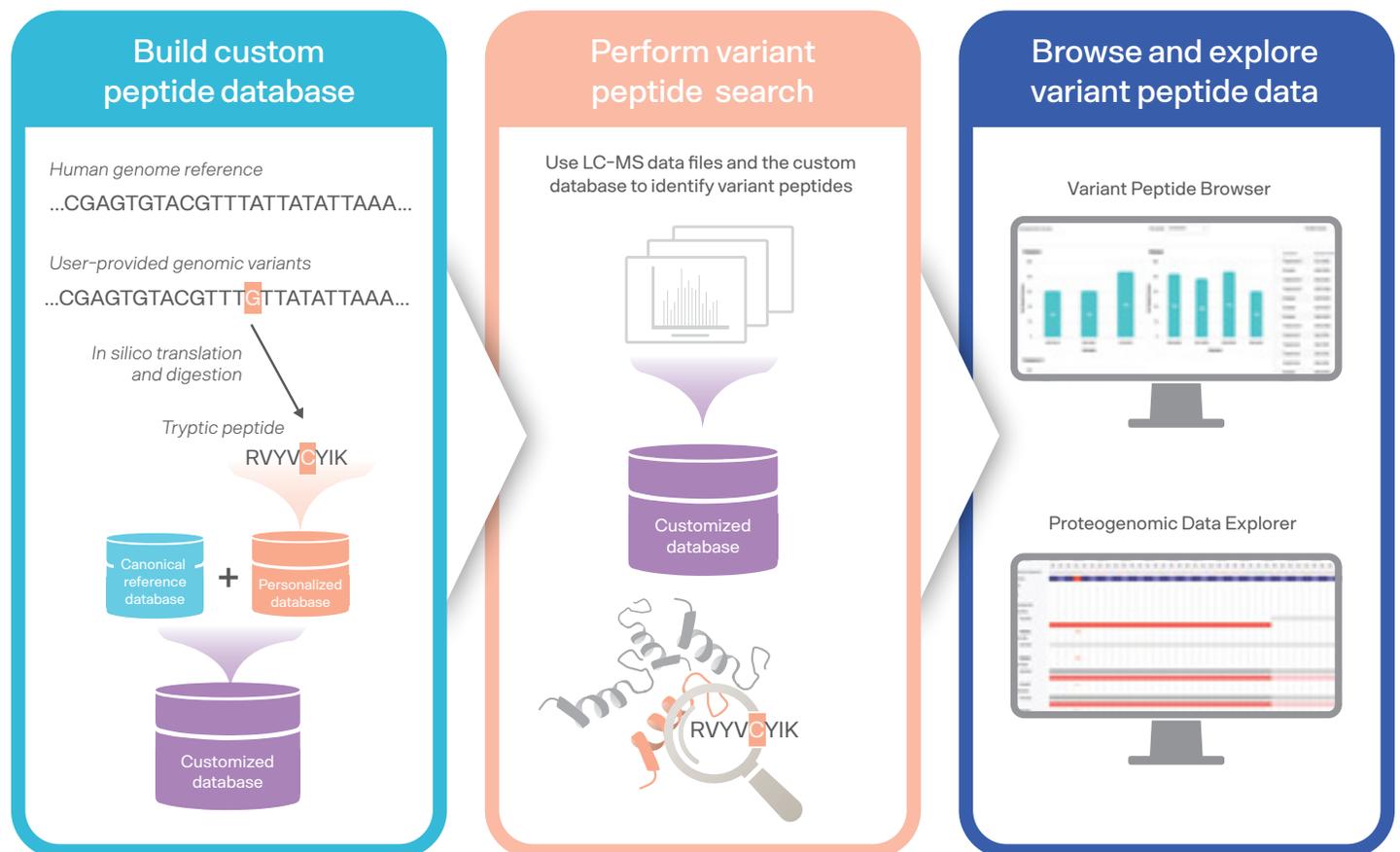
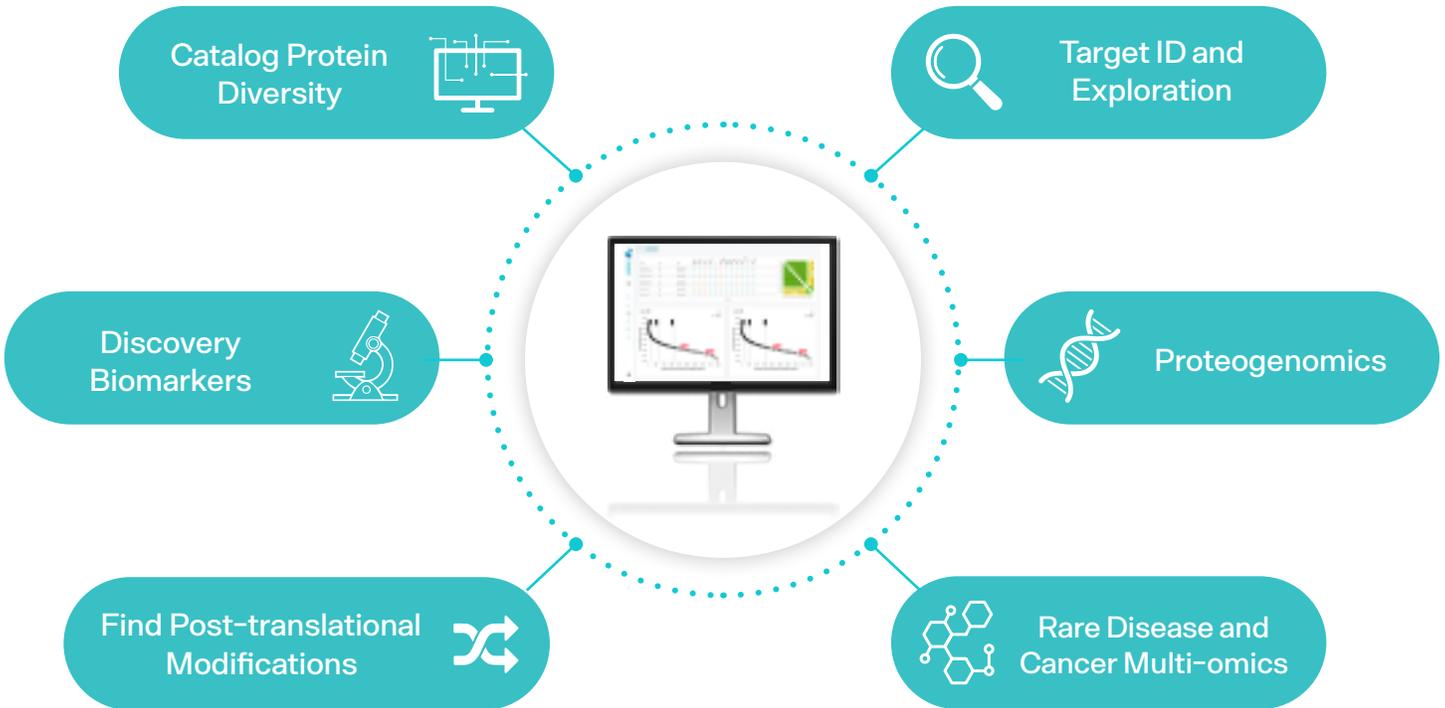


Figure 8: Proteograph™ Analysis Suite Proteogenomics Workflow

# Get Started With Proteograph Analysis Suite

Seamless QC and data analysis designed for speed and reproducibility, enabling powerful biological insights.



## Become a PAS User



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## References

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To learn more about the Proteograph Product Suite or to be kept up to date on recent information – visit our website or follow us on social.

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