

Go From Data to Insight with the Proteograph™ Analysis Suite



Efficient Workflows

Intuitive Interface

Robust Assessment

Powerful Insights



Get a Clearer View of the Proteome

The Proteograph™ Product Suite is designed for unbiased, deep, and rapid proteomic analysis at scale. Whether you seek to survey thousands of human plasma proteins and discover new insights into the protein makeup of your sample or to dive into the biological meaning of your results by quantifying protein abundance differences between sample conditions, protein-protein interactions, and functional enrichment, Seer's Proteograph delivers quantitative, accurate, precise, and reproducible data for proteome studies of any size.

As an optional component of the automated Proteograph Product Suite, the Proteograph Analysis Suite (PAS) is a dedicated cloud-based software solution for processing, analyzing, and visualizing proteomics data sets generated by liquid chromatography-mass spectrometry (LC-MS). The software includes an integrated search engine for identification and annotation of LC-MS data and a variety of tools for evaluating data quality to ensure the highest confidence in your insights.



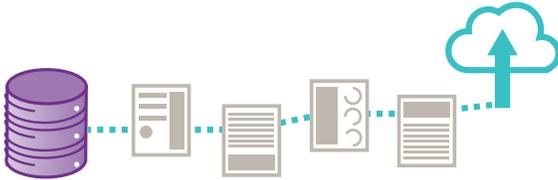
Figure 1: The Proteograph Product Suite includes the SP100 Automation Instrument, a 5-nanoparticle panel with associated consumables, and the Proteograph Analysis Suite of software (monitor not included).

From data to insight, the Proteograph Analysis Suite is intuitive and works out of the box, allowing you to maximize the performance of your experiments and the insights from your study. The software includes tools to perform quality control for both assay and instrument runs, as well as data analysis, allowing you to get insights quickly and efficiently.



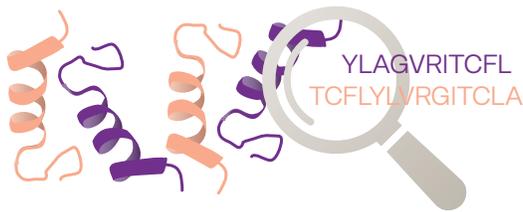
Search Engine and Automated Results Generation

Go from data to insight with PAS, a scalable, cloud-based pipeline for evaluation of Proteograph assay results.



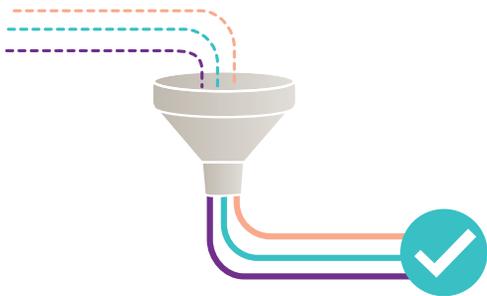
Automated Data Upload

Data may be automatically uploaded from LC-MS to PAS without manual intervention.



State-of-the-Field Peptide ID 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.

Figure 2: Seamless data analysis and results generation using PAS



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 3: 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.

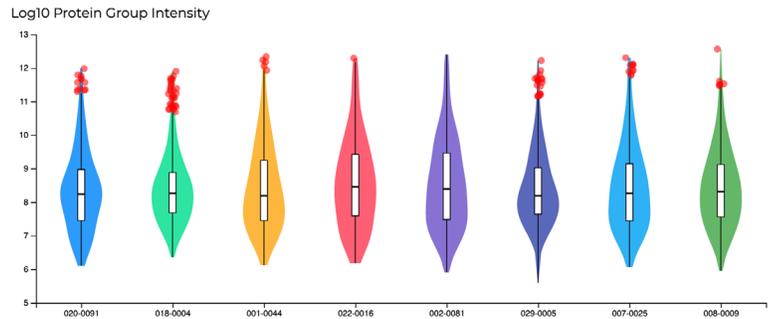


Figure 4: Distributions of protein group intensities and CVs across samples.

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.

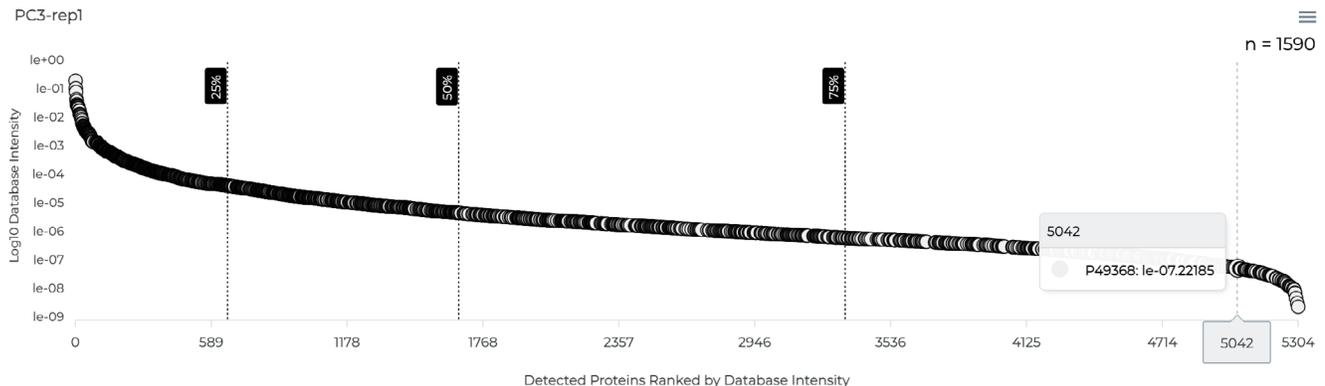


Figure 5: Plots show the dynamic range of identified proteins compared to the deepest reported human plasma proteome index.

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

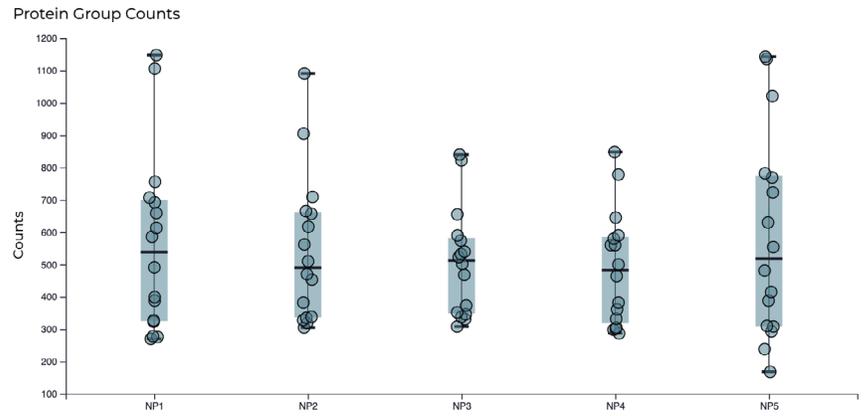


Figure 6: Box plots showing the number of protein groups identified across NPs. Hovering over a dot reveals the peptide or protein count, file, and sample name. Hovering over a box shows the quantile for the NP.

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

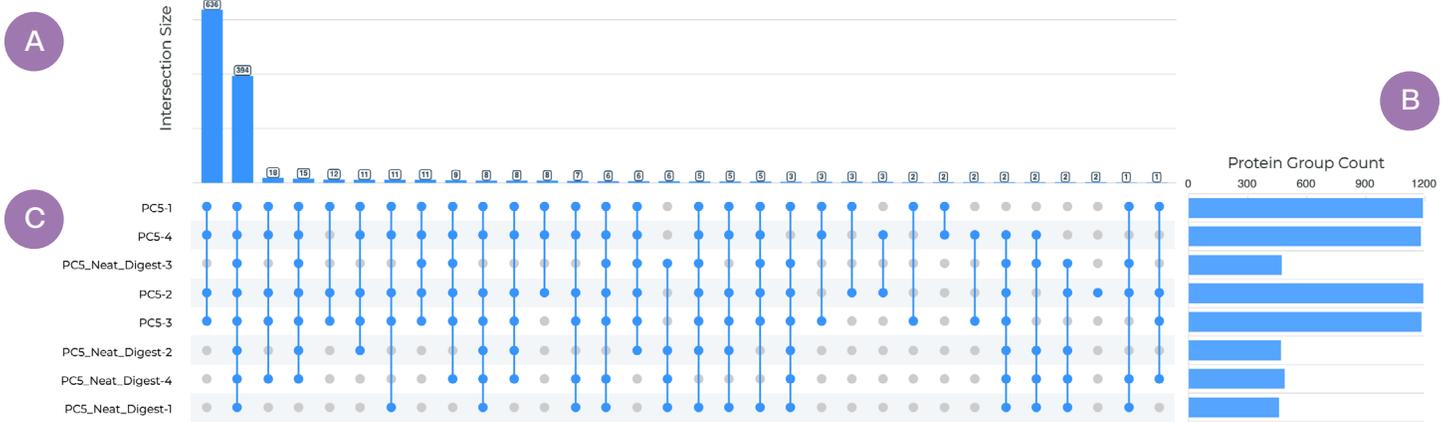


Figure 7: (A) Graphs and a matrix show protein group overlaps; Intersection Size bar graph (B) Protein group count bar graph (C) Matrix.

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

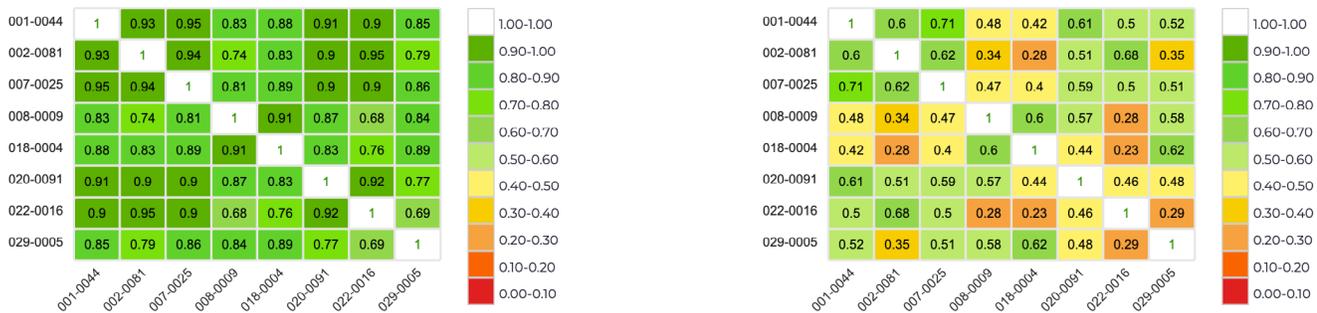


Figure 8: A color-coded matrix displays sample comparability data using PCC (left) or the Jaccard index (right). Samples on the green end of the spectrum have high correlation, while samples on the red end of the spectrum have low correlation.



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.

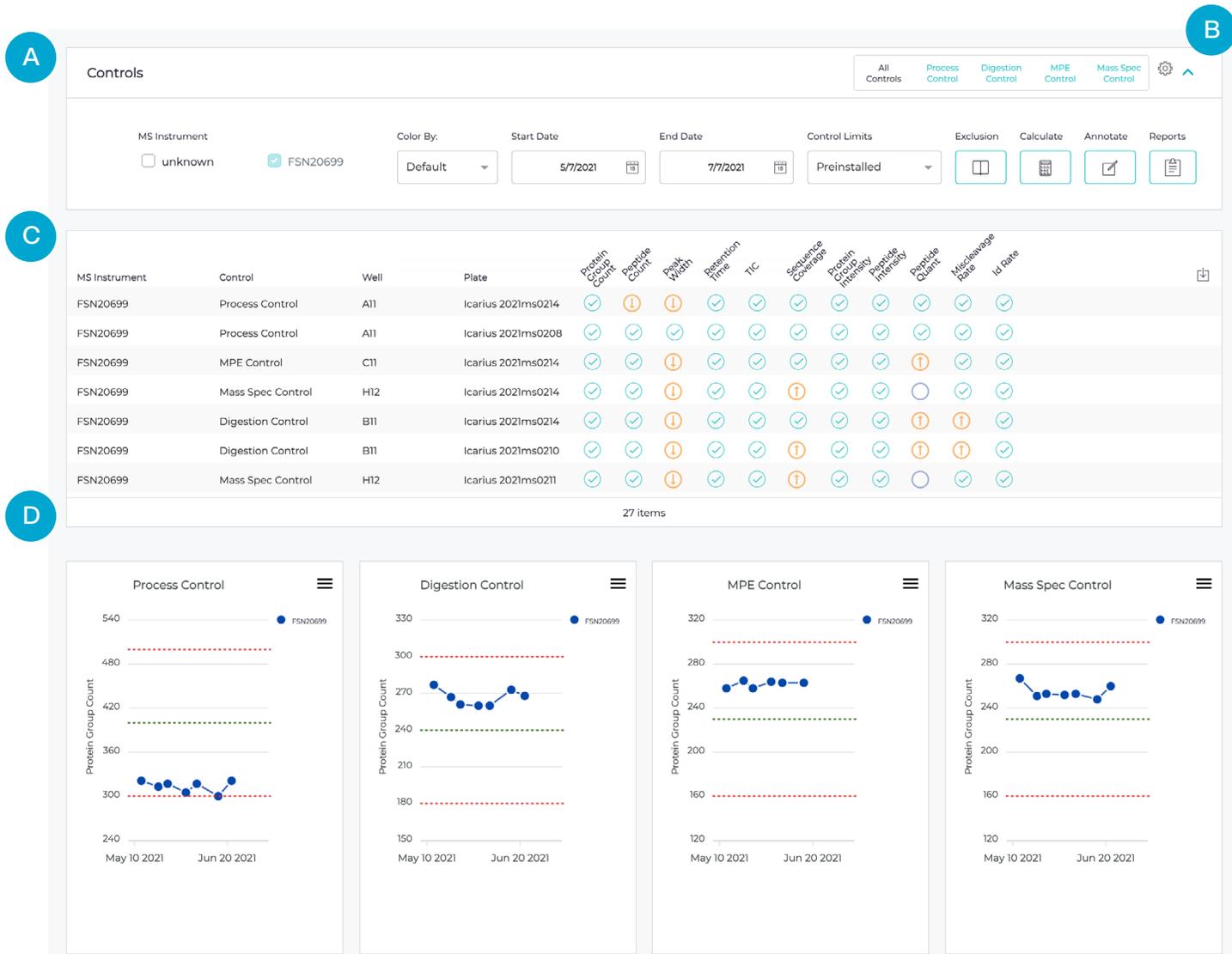


Figure 9: Control Results: (A) Filters for viewing charts for all controls or a selected control type. (B) Toolbar with additional filters and functions. (C) Summary of control data for the selected analysis time frame. (D) QC charts with metrics for each control.



Differential Expression Analysis

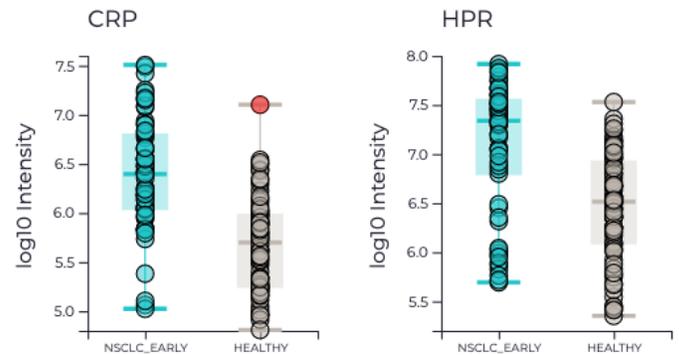
Interactive plots enable functional and biological interpretation of results. Seamlessly evaluate expression differences between study samples using Group Analysis or output raw and processed protein expression tables for custom analyses. To support Group Analysis, PAS provides a variety of MS database search engines including MaxQuant¹ for DDA-based analyses, and either EncyclopeDIA² or DIA-NN³ for DIA-based analyses.

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

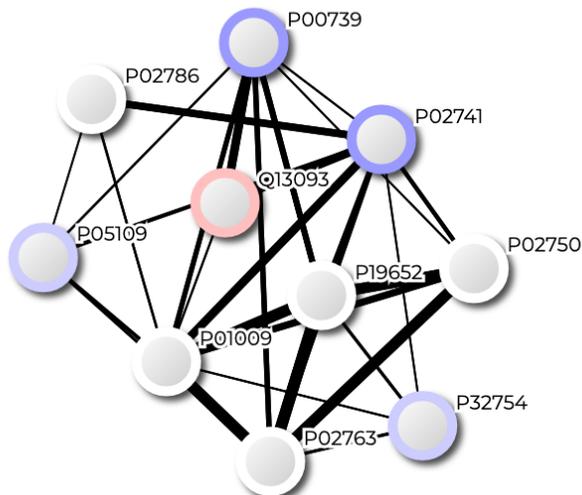


Intensity Comparison: View how the intensity of a protein of interest differs between groups

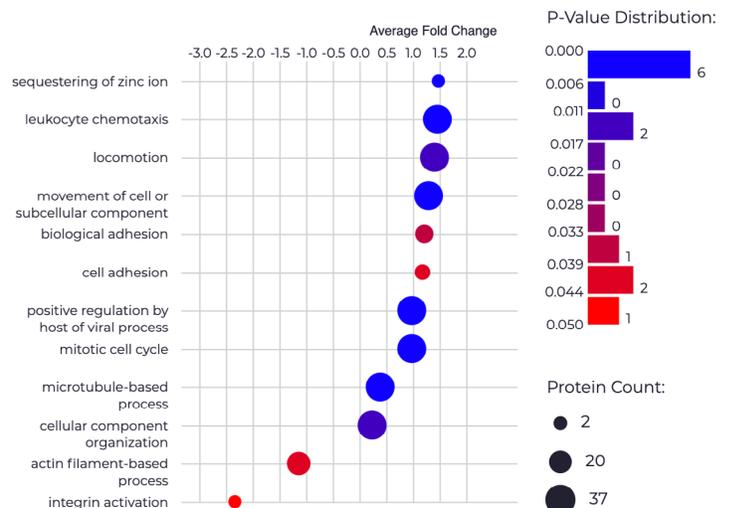
Box Plots



Protein-Protein-Interactions Comparison: Build a PPI network using the STRING database⁴ to visualize possible protein interactions

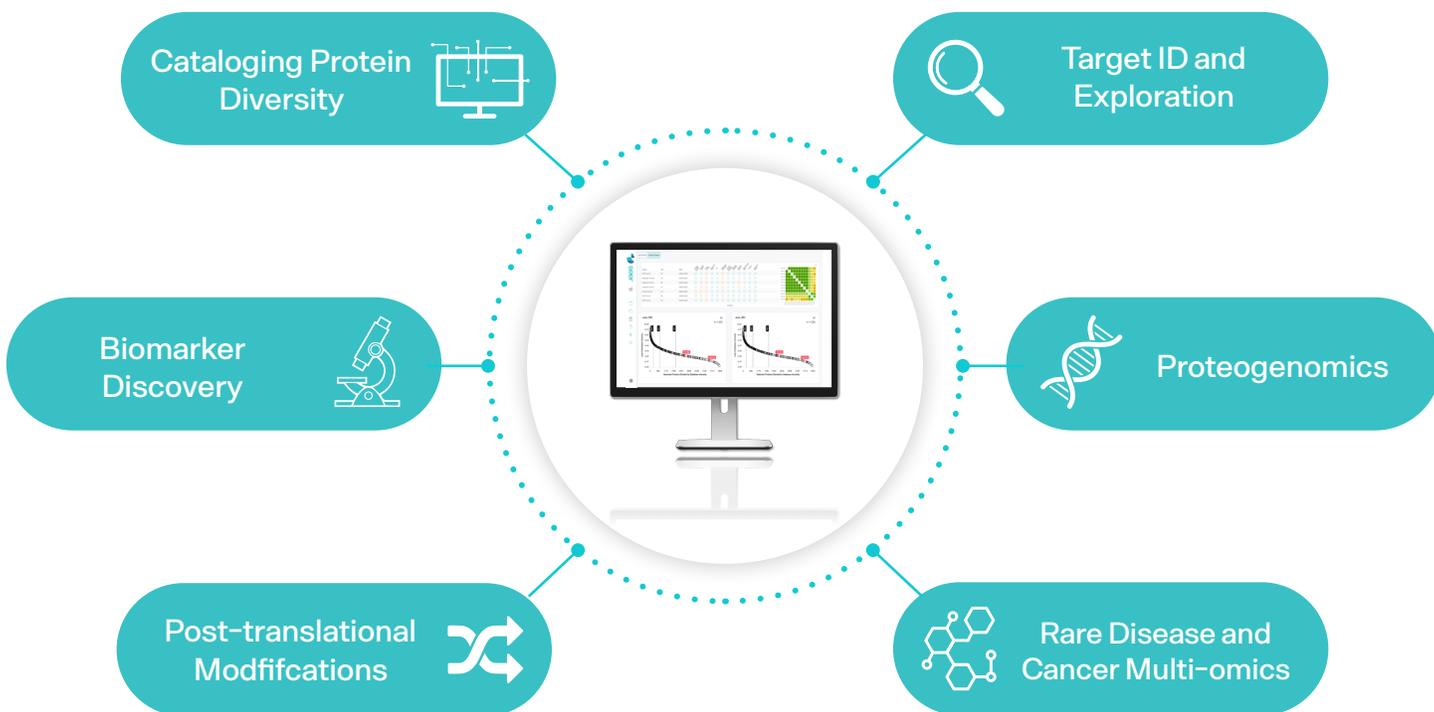


Gene Ontology (GO) Enrichment: Perform GO enrichment analysis⁵ to explore how proteins associated with a group differ functionally^{6,7}



Get Started With Proteograph Analysis Suite

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



Become a PAS User



Contact a Representative

References

1. Cox et al., *Nat Biotechnol* 2008; 1367–1372
2. Searle et al., *Nat Commun* 2018; 5218
3. Demichev et al., *Nat Methods* 2020; 41–44
4. Szklarczyk et al. *Nucleic Acids Res* 2015;43 D447–52
5. Faria, D. GOEnrichment, (2017). <https://github.com/DanFaria/GOEnrichment>
6. Ashburner et al., *Nat Genet* 2000;25(1):25–9.
7. The Gene Ontology resource: enriching a GOld mine. *Nucleic Acids Res* 2021;49(D1):D325–D334.

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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3200 Bridge Pkwy #102
Redwood City, CA 94065

info@seer.bio | 650.453.0000 | seer.bio