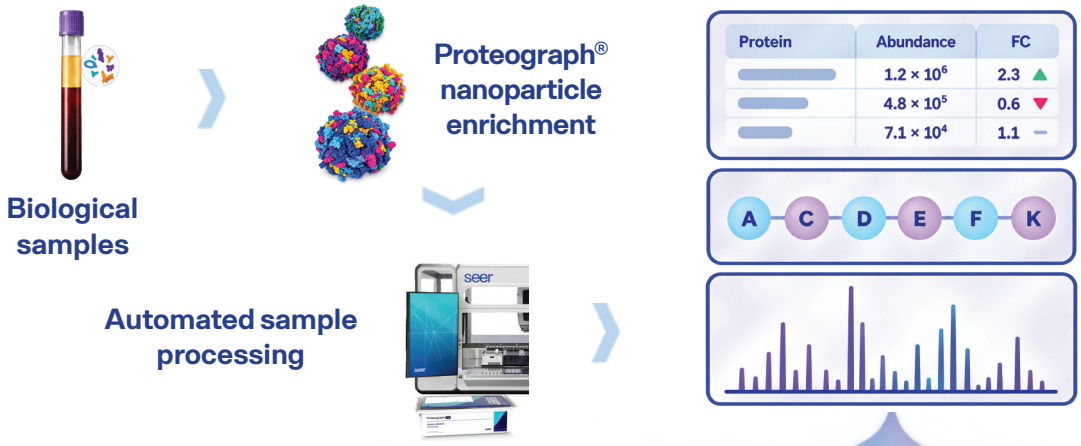
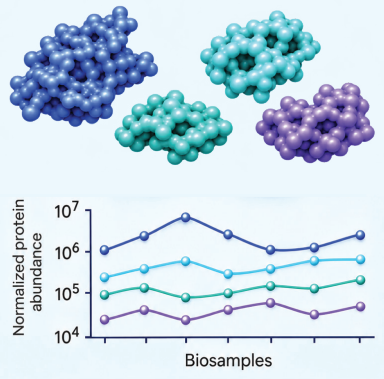
One Experiment Yields Multiple Layers of Proteomic Information



Proteograph-enabled MS produces multiple dimensions of information

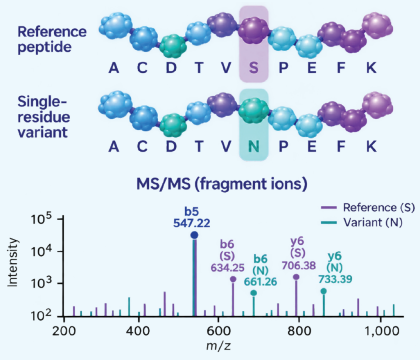
Different Proteograph-enabled data layers provide different analytical opportunities

1 Protein-Level Data
Biological Interpretation



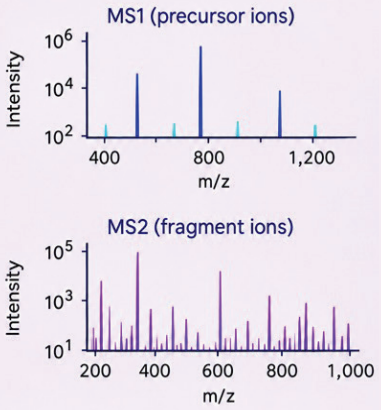
Protein identification and quantification support pathway analysis, disease biology, and biomarker discovery. Aggregated protein results simplify interpretation but can obscure peptide-specific differences.

2 Peptide-Level Data
Molecular Resolution



Sequence-resolved peptides provide greater molecular granularity, enabling resolution of variants, modifications, and molecular heterogeneity that protein summaries may not capture.

3 Raw Spectral Data
Underlying Measurements



MS1 and MS2 data preserve raw ion and fragmentation signals overlooked by conventional workflows, providing a foundation for reanalysis and emerging identification-free computational methods.

Explore Proteomic Data for AI-Driven Precision Medicine

Discover how researchers are applying deep, reproducible proteomics to computational discovery, disease research, and precision medicine.

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Better Models Begin with Better Biological Data

The value of proteomic data depends on more than the number of measurements collected. Biological coverage, molecular resolution, and reproducibility determine what researchers can reliably learn. Seer's Proteograph® technology expands access to the proteome before mass spectrometry, while standardized processing supports consistent data generation across samples and cohorts.

Seer's Proteograph® Product Suite Enables

Broader Biological Access

Engineered nanoparticles create complementary views of the proteome, expanding the molecular diversity sampled from complex biological specimens.

Information-Rich Measurements

High-resolution mass spectrometry captures peptide and spectral information that can support both established identification-based analysis and emerging computational methods.

Reproducibility at Scale

Automated sample processing helps generate consistent measurements across large biological cohorts, supporting comparisons and computational modeling.

Different Data Representations Support Different Research Questions

Interpret Disease Mechanisms	Protein-level associations and pathway analyses.
Investigate Molecular Heterogeneity	Peptide-specific differences, variants, and modifications.
Explore New Computational Approaches	Spectral feature extraction and emerging identification-free analysis.

Broader proteomic sampling, molecularly resolved measurements, and reproducible data generation provide a stronger foundation for computational discovery.

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