Nature Genetics Study Validates Seer's Proteograph Platform as Essential for Turning Genetic Signals Into Reliable Drug Targets and Biomarkers

Large-scale GWAS across ~1,600 samples shows how peptide-level mass spectrometry distinguishes true protein changes from potential binding artifacts resulting from affinity-based approaches, establishing accuracy as the foundation for downstream discovery

REDWOOD CITY, Calif., Dec. 01, 2025 (GLOBE NEWSWIRE) -- Seer, Inc. (Nasdaq: SEER), the pioneer and trusted partner for deep, unbiased proteomic insights, today announced the publication in *Nature Genetics* of a large genome-wide association study (GWAS) that used the company's Proteograph® Product Suite to measure proteins at peptide-level resolution and map their genetic determinants. The study, led by Karsten Suhre, PhD, of Weill Cornell Medicine–Qatar, with collaborators from Harvard Medical School/Brigham and Women's Hospital, Seer, and TruDiagnostic, provides the strongest evidence to date that mass spectrometry validation is essential for turning genomic signals into reliable drug targets and clinical biomarkers. Without mass spectrometry validation, as many as one-third of protein–gene associations reported by affinity-based assays do not replicate, highlighting the necessity of accuracy in proteogenomics.

The analysis included ~1,600 blood samples representing multiple ethnic backgrounds. A discovery cohort of 1,260 and an independent replication cohort of 325 were profiled using Seer's Proteograph workflow. Across these samples, 5,753 proteins were detected, and 1,980 were quantified in at least 80 percent of participants.

From these data, the researchers identified 364 protein quantitative trait loci (pQTLs) genetic variants associated with protein abundance. Of these, 102 replicated in the independent cohort. 35 of the replicated signals were previously unreported, extending the catalog of genetic regulation of proteins.

Affinity reagents have been used in proteomics to measure a predetermined panel of proteins in large cohorts and have generated thousands of reported pQTLs. But when protein-altering genetic variants change the binding site of affinity reagents, these methods can register erroneous signals as the binding strength of the affinity reagent to the protein is diminished. These so-called epitope effects can produce apparent associations between protein expression and genetic variants that do not represent true biology.

By measuring proteins directly at the peptide level, the Proteograph's mass spectrometry approach made it possible to test whether a genetic variant truly altered protein expression, mitigating the confounding epitope effect.

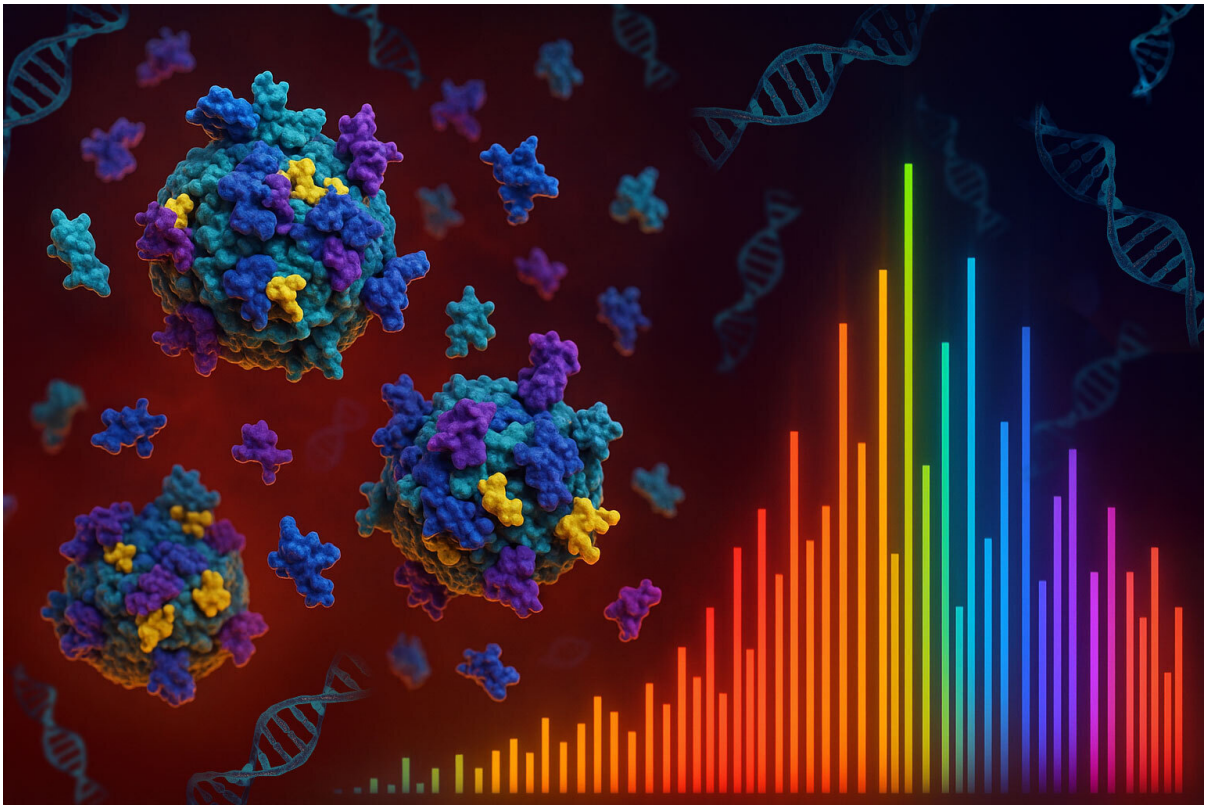
"The Proteograph platform made it possible to perform population-scale mass spectrometry proteomics with the depth and reproducibility needed for genetic association studies," said Dr. Suhre. "By measuring proteins directly at the peptide level, we could distinguish true biological effects from assay artifacts—yielding a more reliable map from genes to proteins to disease pathways."

To contextualize the findings, the study compared mass spectrometry results with two of the largest affinity-based proteomics resources. The comparison revealed a clear pattern:

- pQTLs consistently reported across multiple affinity platforms were confirmed by mass spectrometry.
- Up to one-third of associations reported by a single affinity platform did not replicate when tested by mass spectrometry.

"This study demonstrates that mass spectrometry-based analysis is crucial for proteomics," said Serafim Batzoglou, PhD, Chief Data Officer at Seer. "By providing peptide-level confirmation at scale, the Proteograph establishes protein measurements that lead to novel genetic associations and help annotate the accuracy of affinity-based pQTL predictions."

For academic researchers conducting GWAS and Mendelian randomization studies, the message is direct: datasets built only on affinity reagents may contain a substantial fraction of associations that do not represent true protein abundance. Without validation, downstream analyses risk drawing causal inferences from epitope-induced artifacts.



For drug discovery and biomarker development, peptide-level validation strengthens confidence that selected targets represent genuine biology, not technical noise. Reliable associations reduce wasted effort and increase the likelihood that preclinical findings will hold in clinical settings.

For translational research, the study demonstrates how mass spectrometry and affinity reagents can be used together, with mass spectrometry stratifying the level of reliability of affinity-based predictions.

For patients, this rigor means a higher probability that tomorrow's therapies are built on real biology. Together, they create a path toward comprehensive and trustworthy protein–genetic maps.

This publication marks the validation stage. The *Nature Genetics* study provides peer-reviewed evidence that mass spectrometry can systematically resolve artifacts and confirm which associations are robust.

The transformation comes in what this enables. As proteomics expands to larger populations and integrates with genomics, epidemiology, and clinical records, the utility of those datasets depends on accuracy. By anchoring discovery on peptide-level confirmation, Seer positions proteomics to become a population-ready science that supports drug targets, biomarkers, and translational medicine with the rigor required for clinical impact.

Article information

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About Seer

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