Seer and Collaborators Unveil Broad New Data Demonstrating the Translational Power of Deep Proteomics at HUPO 2025

November 7, 2025

Studies spanning cardiovascular, aging, and cancer biology highlight how Seer's Proteograph® platform is enabling discovery at population scale

REDWOOD CITY, Calif., Nov. 07, 2025 (GLOBE NEWSWIRE) -- Seer, Inc. (Nasdaq: SEER), the pioneer and trusted partner for deep, unbiased proteomic insights, today announced new data to be featured at the Human Proteome Organization (HUPO) World Congress 2025, underscoring how deep, scalable proteomics is transforming the study of human disease. Through a combination of Seer-led, collaborative, and independent studies, the company's Proteograph Product Suite is powering a growing body of research across cardiovascular, oncology, and aging biology. Collectively, these findings demonstrate how Seer's technology is enabling scientists worldwide to translate complex biological signatures into actionable understanding, bringing proteomics to the forefront of translational and population-scale research.

Seer's presence at HUPO 2025 represents one of the most comprehensive demonstrations of its technology to date, with more than a dozen scientific presentations, including two invited talks in the company's breakfast symposium and sixteen posters presented across three days of sessions. Together, these studies highlight the accelerating adoption of Seer's Proteograph platform and its growing impact across diverse biological and clinical research areas.

"The studies presented at HUPO demonstrate that proteomics has reached a new stage of scalability and relevance," said Omid Farokhzad, Chair and CEO of Seer. "We are seeing proteomics move from specialized studies to population-scale discovery that bridges molecular insights to real clinical translation. Seer's Proteograph platform continues to be the catalyst making that possible, empowering researchers to go deeper, broader, and faster than ever before."

Seer Breakfast Symposium

Proteomic Breakthroughs in Cardiac Dysfunction and Aging-Related Decline
Date: November 10, 2025 | Time: 8:00–9:00 a.m. ET | Location: Room Pier 2+3

Speakers:

Nathan Basisty, PhD, NIH Distinguished Scholar and Investigator, National Institute on Aging
Uros Kuzmanov, PhD, Senior Research Associate, University of Toronto and Ted Rogers Centre for Heart Research

This session will highlight the use of deep plasma and tissue proteomics to illuminate disease mechanisms and reveal clinically relevant biomarkers in cardiovascular and aging biology. Dr. Basisty will share how deep proteomic analysis of mouse serum uncovered paracrine mediators of physical dysfunction caused by senescent cells. Dr. Kuzmanov will present findings from a proteomic study of paired myocardial and serum samples from patients with end-stage heart disease that identified candidate biomarkers of right ventricular failure. Together, these talks showcase the power of Seer's technology to uncover novel biomarkers, link circulating proteins to disease mechanisms, and accelerate translational insights for cardiovascular failure and aging-related decline.

Scientific Presentations Featuring Seer Technology

Scalable Plasma Proteomics Workflow Reveals Disease Insights Using the Seer Proteograph Workflow and the Thermo Scientific Orbitrap Astral Mass Spectrometer — Presenter: S. Maity | Poster Viewing I | November 10, 1:15–3:15 p.m.

Comprehensive and High-Throughput Plasma Proteome Profiling for Biomarker Discovery Using a Modified Orbitrap Astral Mass Spectrometer — Presenter: S. Samra | Poster Viewing I | November 10, 1:15–3:15 p.m.

Tools to Explore Complex Glycoproteomics Data — Presenter: N. Riley | Poster Viewing I | November 10, 1:15–3:15 p.m.

Deep Proteomic Profiling of Paired Myocardial and Serum Samples Identifies Biomarkers of Right Ventricular Failure in LVAD Patients — Presenter: D. Davoudpour | Poster Viewing II | November 11, 1:15–3:15 p.m.

Plasma Proteome Profiling in Acute Decompensated Heart Failure Reveals Biomarkers Predictive of Readmission Risk — Presenter: M. Di Paola | Poster Viewing II | November 11, 1:15–3:15 p.m.

Expanding the Landscape of Biomarker Discovery in a Multi-Cancer Cohort — Presenter: D. Gutierrez | Poster Viewing II | November 11, 1:15–3:15 p.m.

LC-MS Workflows for Diverse Omics Analysis of Plasma Samples in a Mini Cancer Cohort Using the Orbitrap Astral Mass

Spectrometer — Presenter: S. Peterman | Poster Viewing II | November 11, 1:15–3:15 p.m.

Alternative Protein Isoform Biomarkers Predicting Differential Survival in Idiopathic Pulmonary Fibrosis — Presenter: J. Korchak | Poster Viewing II | November 11, 1:15–3:15 p.m.

Ultra-Deep and Reproducible Proteomic Profiling of Extracellular Vesicles with the Proteograph® Platform: Uncovering the Hidden Landscape of EV Biology — Presenter: A. Gajadhar | Poster Viewing II | November 11, 1:15–3:15 p.m.

A Fast, Sensitive and Accurate Search Engine for Quantitative DIA Proteomics — Presenter: L. Cantrell | Poster Viewing II | November 11, 1:15–3:15 p.m.

Systematic Evaluation of Enrichment and Analytical Methods for CSF Proteomics — Presenter: A. Aastha | Poster Viewing III | November 12, 1:15–3:15 p.m.

Comparative Analysis of Enrichment Workflows for Optimized Profiling of EVs in Plasma — Presenter: M. Bok | Poster Viewing III | November 12, 1:15–3:15 p.m.

An Update on the Fundamental Biological Determinants of the Plasma Proteome Using Proteograph Assay and Murine Models — Presenter: M. Chang | Poster Viewing III | November 12, 1:15–3:15 p.m.

Investigating the Role of NETosis in the Migration and Invasion of Bladder Cancer Cells — Presenter: E. Bang | Poster Viewing III | November 12, 1:15–3:15 p.m.

Deep Plasma Proteomics Using Bead-Based Approaches in Combination with LC-MS/MS Analysis: How Is the Next Generation of Technologies Performing — Presenter: C. Kluger | Poster Viewing III | November 12, 1:15–3:15 p.m.

Characterization of the Mechanism of Resistance to EZT Treatment in Prostate Cancer Using Secretome Analysis — Presenter: M. Kim | Poster Viewing III | November 12, 1:15–3:15 p.m.

For more information, please visit booth #801 or contact us at pr@seer.bio.

About Seer, Inc.

Seer, Inc. (Nasdaq: SEER) sets the standard in deep, unbiased proteomics—delivering insights with scale, speed, precision, and reproducibility previously unattainable by other proteomic methods. Seer's Proteograph Product Suite uniquely integrates proprietary engineered nanoparticles, streamlined automation instrumentation, optimized consumables, and advanced analytical software to solve challenges conventional methods have failed to overcome. Traditional proteomic technologies have struggled with inconsistent data, limited throughput, and prohibitive complexity, but Seer's robust and scalable workflow consistently reveals biological insights that others do not. Seer's products are for research use only and are not intended for diagnostic procedures. For more information about Seer's differentiated approach and ongoing leadership in proteomics, visit www.seer.bio.

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