Seers Announces Publication in Nature Communications Demonstrating Performance, Scalability and Utility of its Platform Technology for Deep, Unbiased Proteomics

Published results reveal differentiated ability of proprietary, engineered nanoparticle technology to enable large-scale proteomics studies to:

- Provide new insights into dynamic nature of the proteome
- Lead to discovery of potentially novel biomarkers
- Complement large-scale genomics datasets to advance overall understanding of human biology

Redwood City, CA, July 22, 2020 — Seer, Inc. announced the publication in *Nature Communications* today of a study demonstrating the power of its proprietary, engineered nanoparticle technology platform to discover novel proteins and biomarkers through an unprecedented combination of unbiased, deep, rapid, large-scale proteomics. The study brought together an interdisciplinary team of scientists, engineers and physicians from MIT, Harvard Medical School, Seer, and other organizations. The paper, entitled "*Rapid, Deep and Precise Profiling of the Plasma Proteome with Multi-Nanoparticle Protein Corona*," establishes the novel technology's ability to interrogate the plasma proteome across many orders of magnitude spanning highly abundant to rare proteins, and reproducibly capture and robustly quantify proteins in a rapid, automated workflow without the need for additional sample processing steps.

Omid Farokhzad, M.D., Chief Executive Officer at Seer, commented on the significance of the findings, "Measuring the vast amount of proteomic information across many individuals, many time points, and many diseases has long been a goal of scientific and industry researchers. But, that goal has not been achievable due to the complexity of the proteome and inherent challenges in measuring it. Essentially, researchers have had to sacrifice depth of profiling either for number of proteins or for speed. As the study published today demonstrates, this is the first technology to eliminate that trade-off – and, importantly, offer an unbiased view of the proteome."

The technology described in the *Nature Communications* paper forms the foundation for Seer's Proteograph™ suite of products, including reagents, instruments and software, which the company plans to begin commercializing next year.

Dr. Farokhzad continued, "This technology's unmatched combination of characteristics – unbiased, deep survey of the proteome with speed and at scale – set it apart, especially for large-scale proteomics studies. We are incredibly excited about its vast potential to empower researchers in both academia and industry to arrive at new insights that can transform our understanding of biology and health, and approaches to disease testing and treatment."

Seer's Proteograph product suite leverages the unique capabilities of the company's proprietary engineered nanoparticles to offer an automated and scalable workflow that can provide researchers with a clearer view of the proteome and its dynamic and complex nature. Leveraging an optimized panel of nanoparticles, engineered to embody diverse biochemical properties necessary to survey a broad range of proteins without bias, the Proteograph removes much of the complexity of proteomic studies by eliminating the need for separation columns, cumbersome protocols, and lengthy workflows standard with other technologies. This, in turn, enables the unbiased profiling of large numbers of study subjects with a combination of depth and speed previously not possible in proteomics but standard in genomics and transcriptomics.

"The full power of the proteome has been untapped for far too long. The data from this study signal that we are on the cusp of changing that trajectory," said Robert S. Langer, Sc.D., Institute Professor and a faculty member at the Koch Institute for Integrative Cancer Research at MIT, and a co-author of the study and co-founder of Seer.

Dr. Langer continued, "We believe that unbiased, large-scale proteomics can shed light on the complex, dynamic nature of the proteome. This completely novel technology will enable researchers to comprehensively and accurately capture and analyze the proteome as it exists in individuals, at various points in time. This approach holds the potential to ignite an era of extraordinary proteomics exploration, discoveries, and transformative outcomes."

About the Study Findings

The published study demonstrated the ability of the technology to differentially interrogate the proteome on an individual protein and biological pathway level. In contrast to conventional peptide-based fractionation workflows, engineered nanoparticles addressed the dynamic range challenge in complex biological samples by leveraging the unique interaction of a panel of optimized nanoparticle surfaces with intact proteins, forming intricate protein coronas.

The study also revealed the platform technology's performance in terms of accuracy, precision, and reproducibility of protein quantification. Compared to conventional plasma proteomics studies, this technology yielded more proteins with better precision at greater depth, in terms of the orders of magnitude of protein abundance in the plasma proteome observed. Unlike conventional deep proteomic techniques requiring extensive depletion and fractionation workflows, often requiring days to weeks for equivalent depth of protein coverage, the technology's method was performed in a highly parallel, multiplexed, automated seven-hour sample preparation in a scalable 96-well format.

In a clinical pilot study outlined in the *Nature Communications* paper demonstrating the utility of the platform, the platform technology enabled robust quantification of >2,000 plasma proteins from 141 patients, including early-stage non-small cell lung cancer (NSCLC) patients and matched controls in less than three weeks. The unbiased quantification of plasma proteins achieved with this platform enabled the identification of novel combinations of known and unknown protein biomarkers that discriminated early NSCLC patients from matched controls, suggesting potential application of the proteomic technology for sensitive early detection. This pilot study demonstrated the unique capabilities of this novel technology platform for a broad range of large-scale proteomics studies that can accelerate fundamental understanding of biology.

About Seer

Seer is a life sciences company focused on empowering exceptional scientific outcomes by removing multiple technological limitations that stand between breakthrough ideas and the deep, unbiased proteomics information that can make them a reality. Seer is developing its Proteograph™ suite of products, which includes reagents, instruments and software, to give researchers an automated and simple-to-scale solution to access and mine the richness of the proteome, a capability not currently available. We believe that unbiased, large-scale proteomics can, and must, become a reality for us to advance what is possible in biology and disease treatment. Our solutions will enable basic and translational researchers to see the proteome through an entirely new lens, one that does not compromise their ability to see the proteome's richness and diversity as it appears in individuals – and that is where transformative biological breakthroughs can begin. Visit www.seer.bio to learn more.

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