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Investor Presentation

January 2026

Safe harbor disclosures

Certain statements in this presentation and the accompanying oral commentary are forward-looking statements within the meaning of the federal securities laws. All statements other than statements of historical fact could be deemed forward-looking. These forward-looking statements relate to future events or results of Seer, Inc. (the “Company”) and involve known and unknown risks, uncertainties and other factors that may cause the actual results, levels of activity, performance or achievements of the Company or its industry to be materially different from those expressed or implied by any forward-looking statements. In some cases, forward-looking statements can be identified by terminology such as “may,” “will,” “could,” “would,” “should,” “to,” “target,” “expect,” “plan,” “anticipate,” “intend,” “believe,” “estimate,” “predict,” “potential” or other comparable terminology. These forward-looking statements include, but are not limited to, statements regarding the Company's projections of market opportunities and the Company’s business and industry; statements regarding the Company’s business strategy, product development, operations, results of operations, financial needs, and financial condition; and statements regarding the Company’s long-term expectations and future performance.

These forward-looking statements are subject to a number of risks, uncertainties and assumptions, including, among other things, the risk factors described in the Company’s filings with the Securities and Exchange Commission (“SEC”) and other documents that the Company subsequently files with the SEC from time to time. You should read these documents for more complete information about us. You may obtain these documents for free by visiting EDGAR on the SEC website at www.sec.gov.

While the Company believes these expectations, assumptions, estimates and projections are reasonable, such forward-looking statements are only predictions and involve known and unknown risks and uncertainties, many of which are beyond the Company's control. These and other important factors may cause actual results, performance, or achievements to differ materially from those expressed or implied by these forward-looking statements. The forward-looking statements in this presentation are made only as of the date hereof. For a further description of the risks and uncertainties that could cause actual results to differ from those expressed in these forward-looking statements, as well as risks relating to the business of the Company in general, are described more fully in the Company’s filings with the SEC and other documents that the Company subsequently files with the SEC from time to time. These risks are not exhaustive. New risk factors emerge from time to time, and it is not possible for our management to predict all risk factors, nor can we assess the impact of all factors on our business or the extent to which any factor, or combination of factors, may cause actual results to differ materially from those contained in, or implied by, any forward-looking statements. The Company specifically disclaims any intention to update any forward-looking statements included in this presentation, except as required by law. If one or more of these statements is updated or corrected, investors and others should not conclude that additional updates or corrections will be made.

In light of the foregoing, investors are urged not to rely on any forward-looking statement in reaching any conclusion or prediction of future events or making any investment decision about any securities of the Company.

Proteomics is critical to enabling precision medicine

	Genomics	Proteomics
‘RIGHT DRUG’	✗ Only a **small percentage of drugs** target genes	✓ Most drug targets **are proteins**
‘RIGHT PATIENT’	✗ Genetics has **unproven utility** for stratification of complex diseases	✓ Blood proteins are **routinely used** as diagnostics in clinical practice (e.g., ApoB)
‘RIGHT TIME’	✗ DNA is temporally **static**	✓ Proteins are temporally **dynamic**

“Genomics is not fully compatible with the principles of precision medicine, **but proteomics is.**”

Chris Whelan, Ph.D.
Founder, UKB-PPP

Biological discovery is at an inflection point and proteomic content will be a key enabler

Biological insight is shifting from focused hypothesis-driven experiments to broad, large-scale data-driven discoveries

AI models are progressively capable of drawing novel biological insights from vast amounts of multimodal data

AI models are only as effective as the quality of the data they are fed

Data-driven discoveries require data that is **complete**, **precise**, and **scalable**

Seer is uniquely positioned to power the next era of AI-driven precision medicine

Complete

Peptide-level resolution

Precise

Accurate and reproducible

Scalable

Population-scale studies

Complete characterization of the proteome is essential

~20K Genes

Genomics

~200K Transcripts

Transcriptomics

Transcription

RNA processing

Millions of Protein Variants

Proteomics

Translation

Post-translational modification (PTM)

Protein-protein interactions (PPI)

Static → Dynamic

>1.3B genetic variants <0.2% characterized	Modest correlation of mRNA to proteins Distinct expression patterns in different cells	Protein variants have distinct structure and function Millions of allelic and post-translational variants

Source: Isabell Bludau et al. Proteomic and interactomic insights into the molecular basis of cell functional diversity. Nature Reviews Molecular Cell Biology (2020).

Complete

455,000 exomes sequenced
6,345,457 potential deleterious variants

Source: Backman, J.D. et al. Exome sequencing and analysis of 454,787 UK Biobank participants. *Nature* 599, 628–634 (2021)

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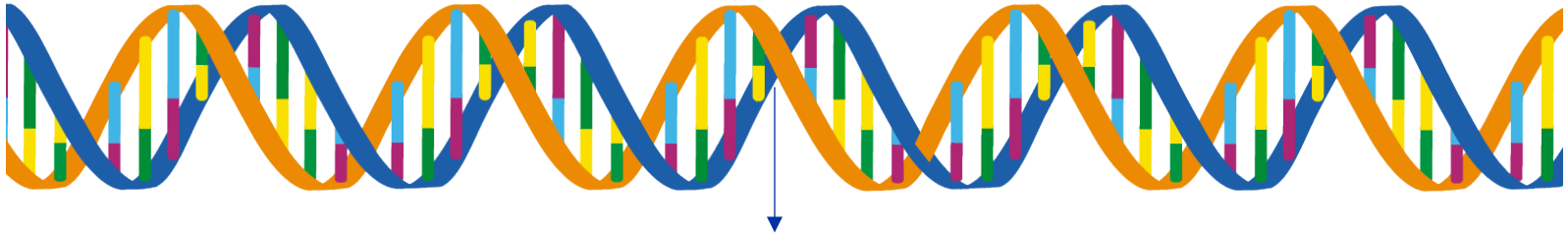
Molecular diversity explodes at the level of the proteome

Complete

Tau Protein

MAPT Tau Gene



Tau Protein Variants at Isoform and PTM Levels

Variants only visible with peptide-level resolution

Signals shift in early Alzheimer's pathology

pTau118

pTau217

Associated with advanced Alzheimer's pathology

1 MAPT tau gene that is static during lifetime	>768 dynamic tau protein variants during health and disease	Distinct tau protein variants drive different biology

Source: Technology Networks. Mapping 768 Tau Proteoforms Could Advance Alzheimer's Research

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Mass spectrometry is the gold standard for proteomics

Complete

Unbiased Seer + MS methods

- Not restricted to a binding epitope or a known protein
- Measurements are made along the length of the protein
- Protein variants are detected and do not confound analysis
- Broad coverage of proteins of sufficient abundance in sample

Targeted ligand-based methods

- Binding epitope represents < 2% of protein length
- Changes to the remaining ~98% of the protein are unable to be analyzed
- Protein variants can impact the binding epitope and result in false measurement
- Only protein epitopes that are targeted can be measured

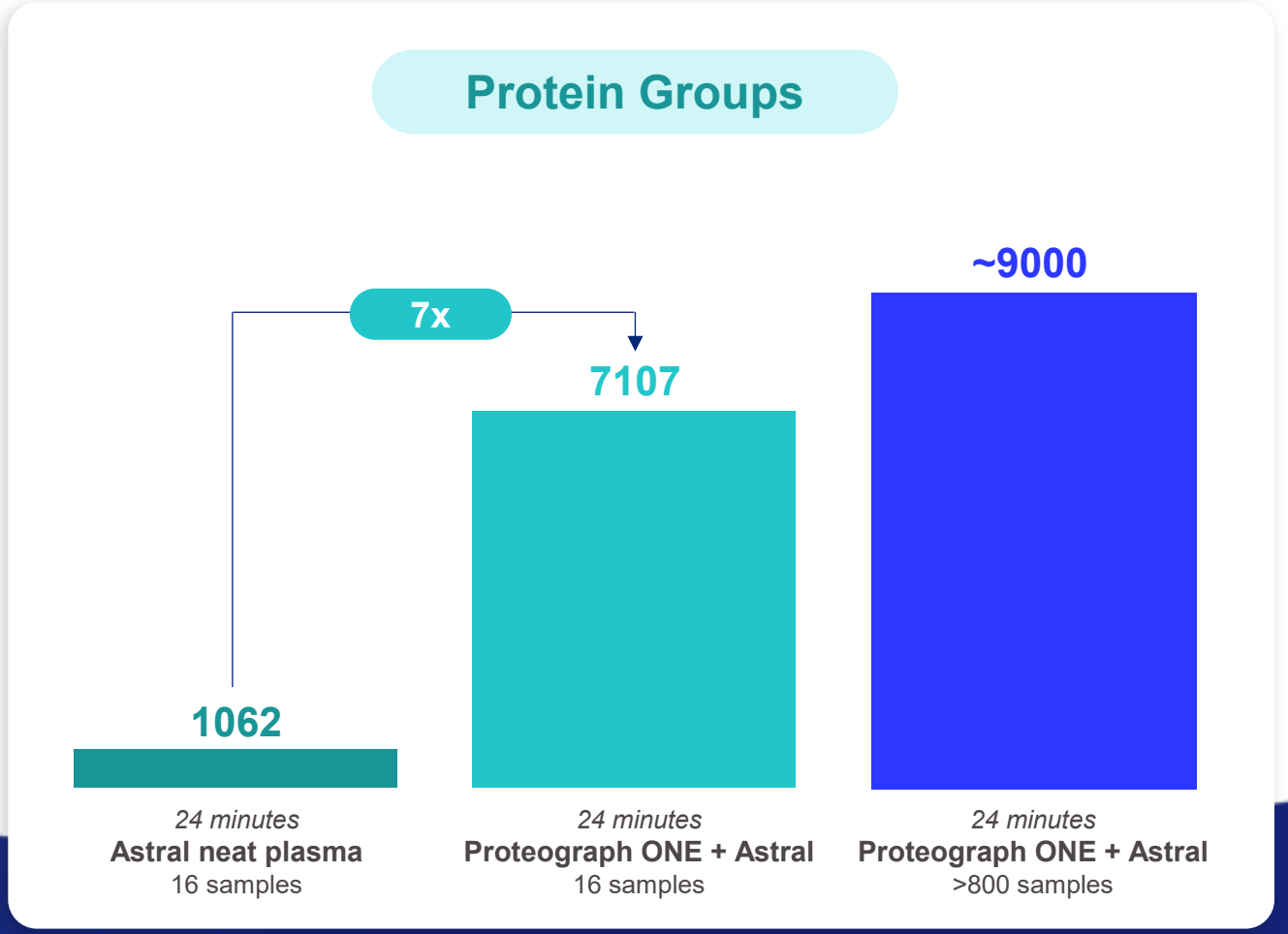
Complete

Proteograph ONE + Astral enables the deepest proteomic discovery research

Significantly more proteins detected by mass spec with Seer technology

~7X Avg proteins detected with Seer compared to neat

~9K Proteins reproducibly measured in studies at scale



Source: Seer, Inc. *Advancing Analytical Throughput and Depth in Plasma Proteomic Studies with the Proteograph® ONE Workflow* [Technical Note].

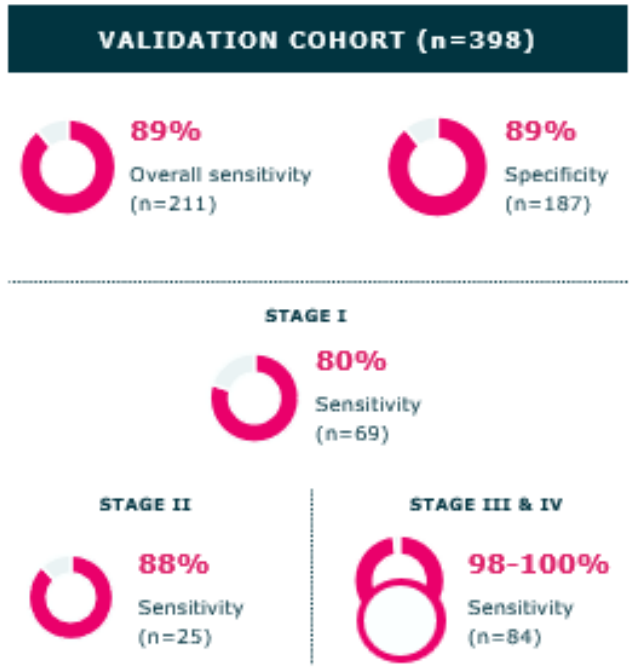
Seer's proprietary, unbiased proteomics platform has enabled the development of a clinical test

Complete

prognomiQ
Lung cancer screening

ProVue LUNG

Strong Discovery Classifier Performance



> Our proprietary multi-omics approach, with deep unbiased proteomics at its core, enables best-in-class test performance, and we're excited to launch our first product in lung cancer detection.
>
> **Philip Ma,** CEO, PrognomiQ

PrognomiQ has developed a transformative early detection / screening platform for lung cancer

Addressing a critical screening gap for 14M[1] high-risk individuals in the U.S.

Based on a proprietary unbiased proteomics-first approach (leveraging Seer's Proteograph) to discover novel multi-omic content and biomarkers

1. American Lung Association 'Lung Health Barometer' (2024)

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First large-scale pQTL study using the Proteograph for peptide-level resolution in decoding biology

Complete

Weill Cornell Medicine-Qatar

True pQTL identification

Up to one third of strongest pQTLs identified with affinity-based proteomics technologies in two cohorts are likely false due to epitope effects

Follows Nature Communications publication demonstrating the Proteograph's ability to properly account for variant peptides

Source: Suhre K, Venkataraman GR, Guturu, H et al. Nanoparticle enrichment mass-spectrometry proteomics identifies protein-altering variants for precise pQTL mapping. Nat Communications 15, 989.

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Drs. Langenberg and Pietzner demonstrate the unique value of Seer data in the Genes & Health cohort

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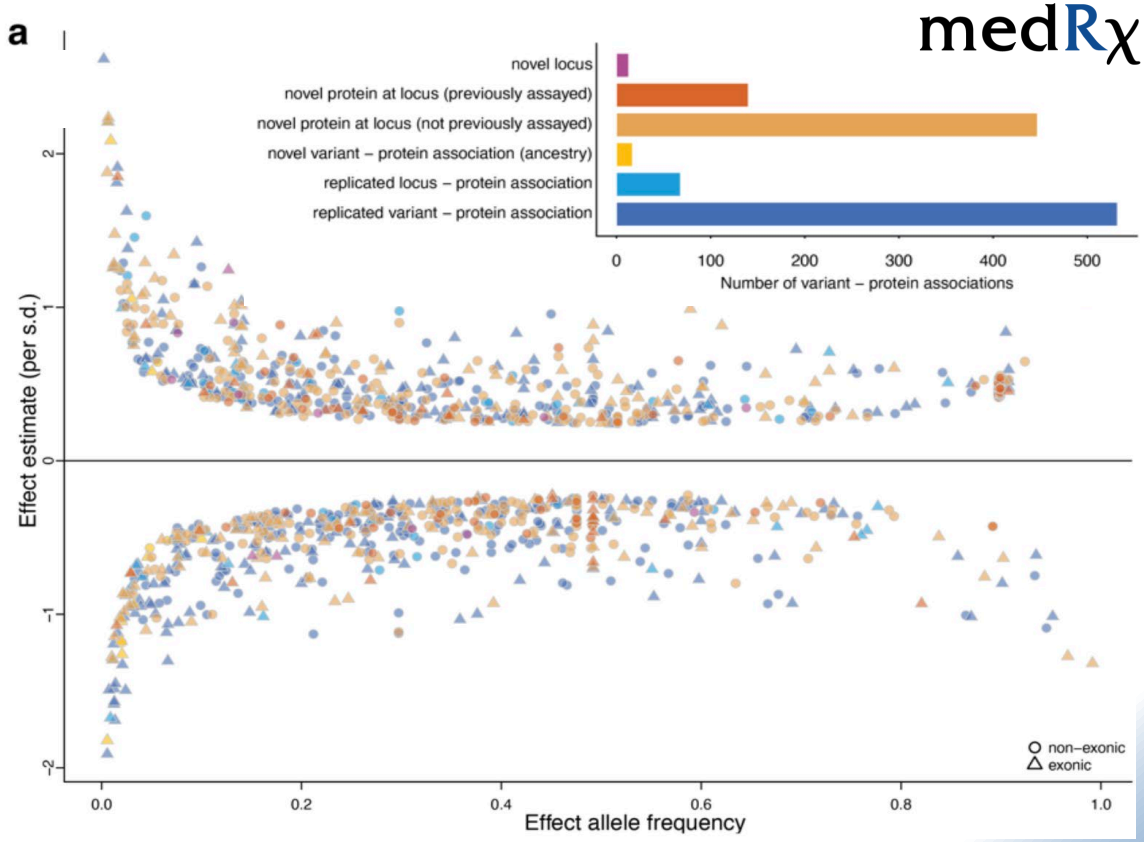
Queen Mary University of London

Disease-associated protein detection



- >1,200 variant protein associations, half of which are novel
- Seer detected a high number of proteins previously not found by affinity-based technologies
- Seer detected a high number of pQTLs that were previously not found by affinity-based technologies
- Seer uniquely confirmed absence of some proteins in plasma that had lost their function

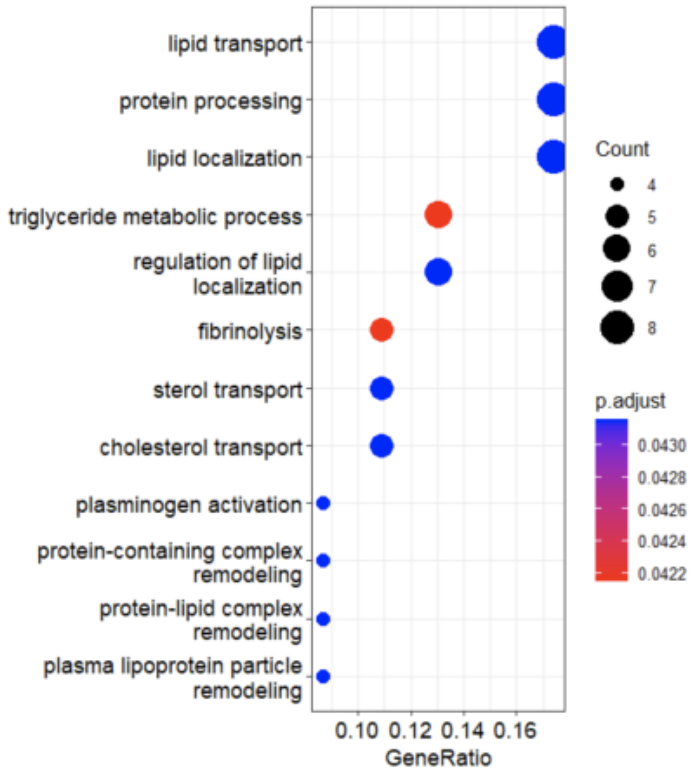
Source: https://www.medrxiv.org/content/10.1101/2025.08.12.25333522v1.full

Complete

Unbiased discovery proteomics used to develop circulating aging signatures in mice

NIH National Institute on Aging

Aging & longevity



Identified pathways related to lipid and triglycerides transport and metabolism

896 samples, >4,300 protein groups

64 proteins were differentially abundant in initial 30 sample pilot program of mice

None of these proteins are on the high-plex affinity-based mouse panel

Proteograph enables deep, unbiased proteomics and is species-agnostic

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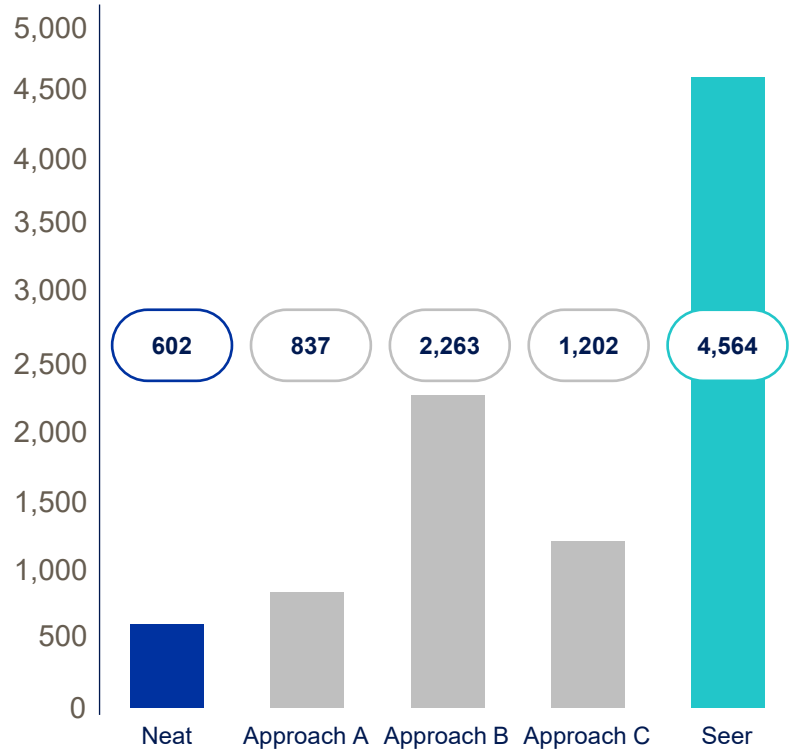
Precise

Seer has pioneered the method that others are trying to follow

Protein Group IDs



A Technical Evaluation of Plasma Proteomics Technologies

William F. Beimers, Katherine A. Overmyer, Pavel Sinitcyn, Noah M. Lancaster, Joshua J. Coon

doi: https://doi.org/10.1101/2025.01.08.632035

This article is a preprint and has not been certified by peer review [what does this mean?].

Abstract | Info/History | Metrics | Preview PDF

Abstract

Plasma proteomic technologies are rapidly evolving and of critical importance to the field of biomedical research. Here we report a technical evaluation of six notable plasma proteomic technologies - unenriched (Neat), Acid depletion, PreOmics ENRICHplus, Mag-Net, Seer Proteograph XT, Olink Explore HT. The methods were compared on proteomic depth, reproducibility, linearity, tolerance to lipid interference, and limit of detection/quantification. In total we performed 618 LC-MS/MS experiments and 93 Olink Explore HT assays. The Seer method achieved the greatest proteomic depth (~4,500), while Olink detected ~2,600 proteins. Other MS-based methods ranged from ~500-2,200. Neat, Mag-Net, Seer, and Olink had strong reproducibility, while PreOmics and Acid showed higher variability. All MS methods showed good linearity with spiked-in C-Reactive Protein (CRP); CRP was surprisingly not in the Olink assay. None of the methods were affected by lipid interference. Seer had more than double the number of quantifiable proteins (4,800) for both LOD and LOQ than the next best method. Olink was comparable to Neat and Mag-Net for LOD, but worse for LOQ. Finally, we tested the applicability of these methods for detecting differences between healthy and cancer groups in a non-small cell lung cancer (NSCLC) cohort.

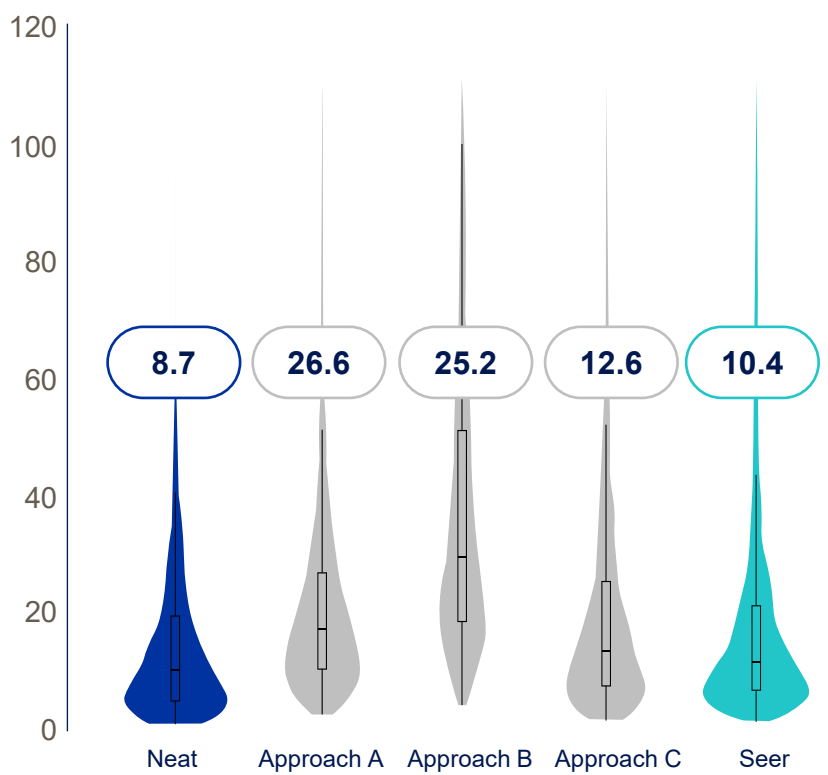
Competing Interest Statement

Note that JJC is on the Scientific Advisory Board of Seer. He is a consultant for Thermo Fisher Scientific and a founder of CeleramAb Inc.

Joshua Coon, Ph.D.

Professor of Chemistry and Biomolecular Chemistry at University of Wisconsin-Madison

Reproducibility



Source: Joshua J. Coon. A Technical Evaluation of Plasma Proteomics Technologies. Biorxiv. https://doi.org/10.1101/2025.01.08.632035

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Dr. Sheynkman leveraged the Proteograph's peptide-level resolution to identify potential biomarkers in IPF

Precise

University of Virginia School of Medicine

Biomarker identification

Seer Insights Grant Program

Identification of potential biomarkers in idiopathic pulmonary fibrosis (IPF)

Two protein isoforms were identified using the Proteograph that were preferentially expressed in the sicker patient population relative to healthy patient population

Uniquely identified isoform differences in these populations using the Proteograph when no significant difference was seen at the protein group level

Study demonstrates the critical role that protein isoforms may play in disease and the need for peptide-level resolution to glean important biological insights

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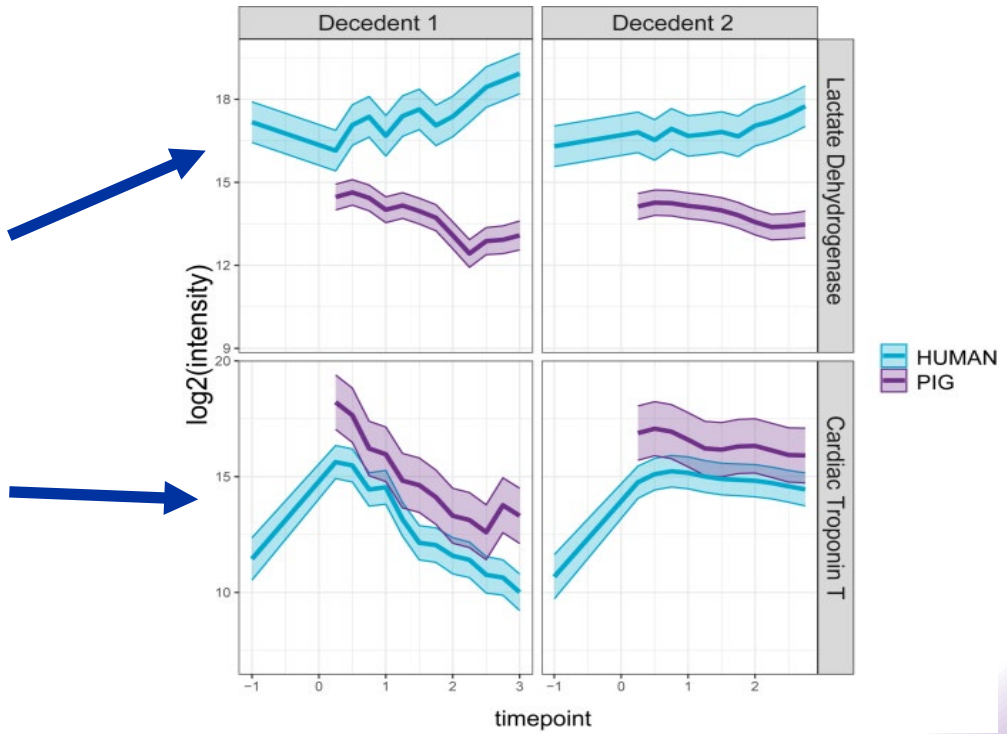
Precise

Deep protein profiling in xenotransplant enables simultaneous profiling of human and pig proteins

NYU Grossman School of Medicine

Xenotransplantation



Transplant Operation at Timepoint 0

2 decedent humans received a pig heart transplant

Levels of human proteins and their pig ortholog are separately monitored

Proteograph delivers unique value even for the most complex and unusual sample types

>6,850 human proteins

>1,850 pig proteins

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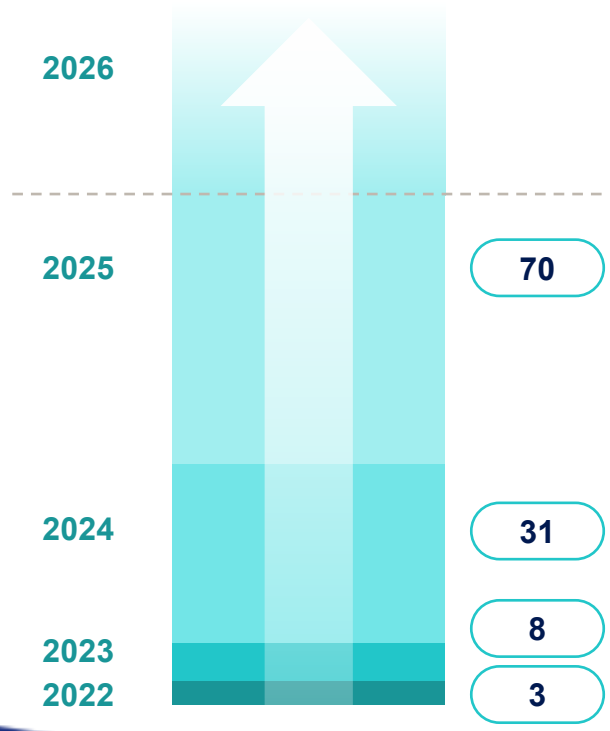
Precise

Growing validation of platform makes us a trusted partner for customers

Accelerating adoption of Proteograph Product Suite

More than half of cumulative publications and preprints were produced in 2025

Cumulative peer-reviewed publications[2]



As of January 9, 2025, includes publications, preprints and reviews

Increasing presence in high-impact journals

nature
AGING
Journal of proteome research
nature communications
FASEB Federation of American Societies for Experimental Biology
PNAS
nature genetics

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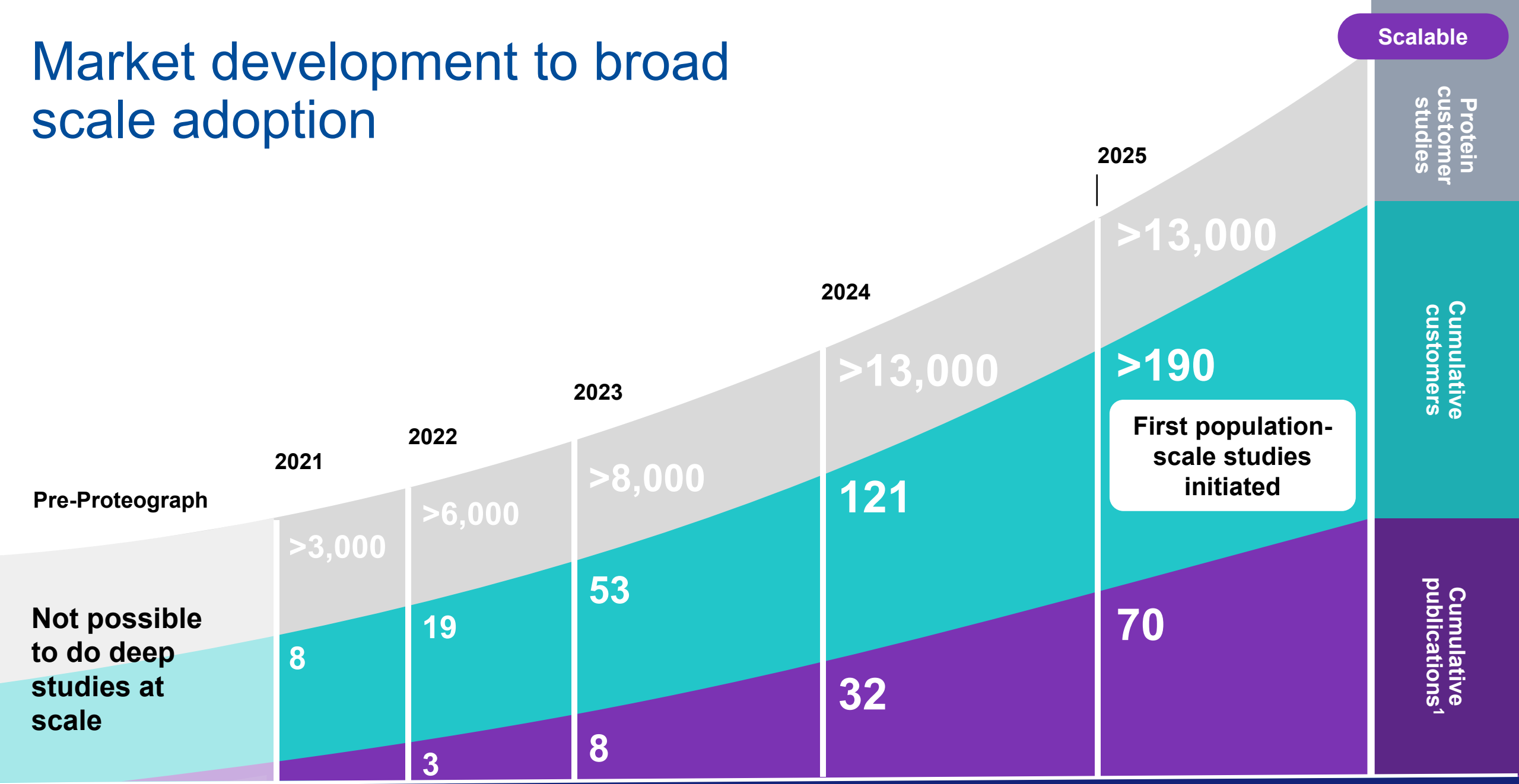
Market development to broad scale adoption



Scalable

Innovation across depth, scale, and reproducibility drove significant performance improvements

2021

Instrument

SP100 Launch

Assay

RiSE

2022

2023

Assay

XT

Software

PAS 2.0

2024

Software

PAS 3.0

2025

Instrument

SP200 Launch

Assay

ONE

Software

PAS 3.3

Unlocking Scale

112

samples per week[1]

2.5X

280

samples per week[1]

>3.6X

>1,000

samples per week[2]

~10X IMPROVEMENT IN THROUGHPUT

1One 8-hour run per day
2Two 5-hour runs per day
PAS = Proteograph Analysis Suite

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Scalable

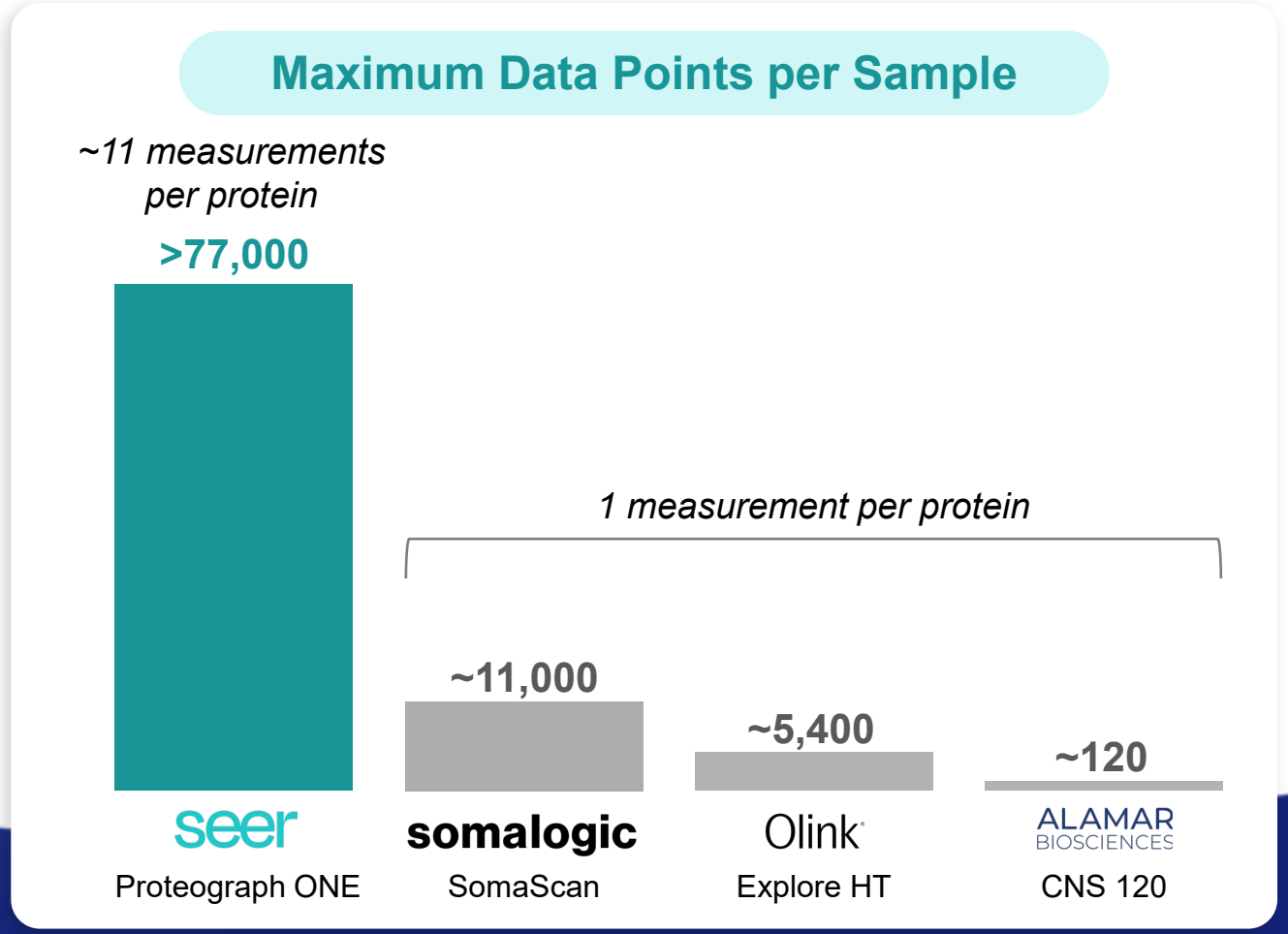
Seer is uniquely positioned to generate massive amounts of data needed for AI

Significantly more data to train foundation models and reveal deeper insights

>7X More data points per sample versus other proteomic platforms

11X More avg measurements per protein with peptide-level resolution

77K Protein measurements per sample



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Scalable

Enabling multiple deep, unbiased population-scale studies, with several more discussions ongoing

NIH

$50M multi-institutional large-scale multiomics study over five years

KOREA UNIVERSITY

20,000 subject proteomics biomarker discovery for early detection of multiple cancers

DISCOVERY LIFE SCIENCES

Human cadaver multi-organ proteomic benchmarking study totaling over 10,000 samples

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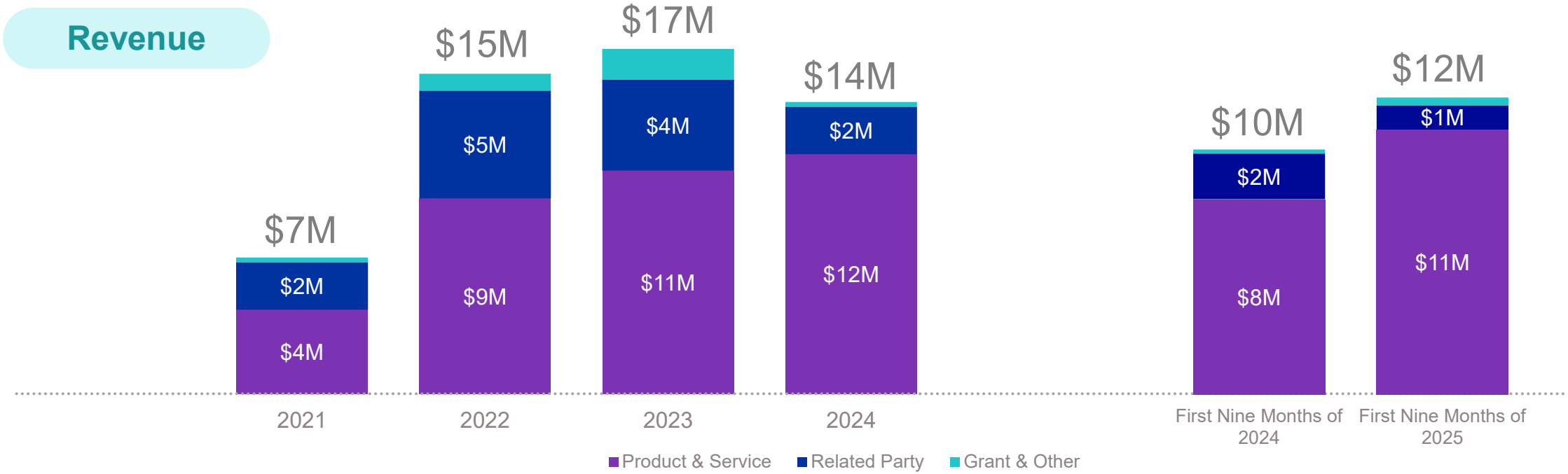
Disciplined financial execution with strong cash runway to achieve profitability



~$251M

Cash, cash equivalents and investments**, no debt**[1]

~11.7M

Shares repurchased through open-market share repurchase program, reducing shares outstanding by ~14% to 55.8M shares[1]

Significantly reduced cash burn

1. As of September 30, 2025

2026 growth catalysts

Expand addressable market through new product innovation

Win additional population-scale cohort programs

Grow and drive utilization of rapidly expanding installed base

Establish leadership position as preferred proteomic data platform for AI-driven biology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