



# Investor Presentation

November 2024

# 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. These statements relate to future events or future results and involve known and unknown risks, uncertainties and other factors that may cause the actual results, levels of activity, performance or achievements of Seer Inc. (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.

All statements other than statements of historical fact could be deemed forward-looking. 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.

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. The Company specifically disclaims any intention to update any forward-looking statements included in this presentation. 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 making any investment decision about any securities of the Company.

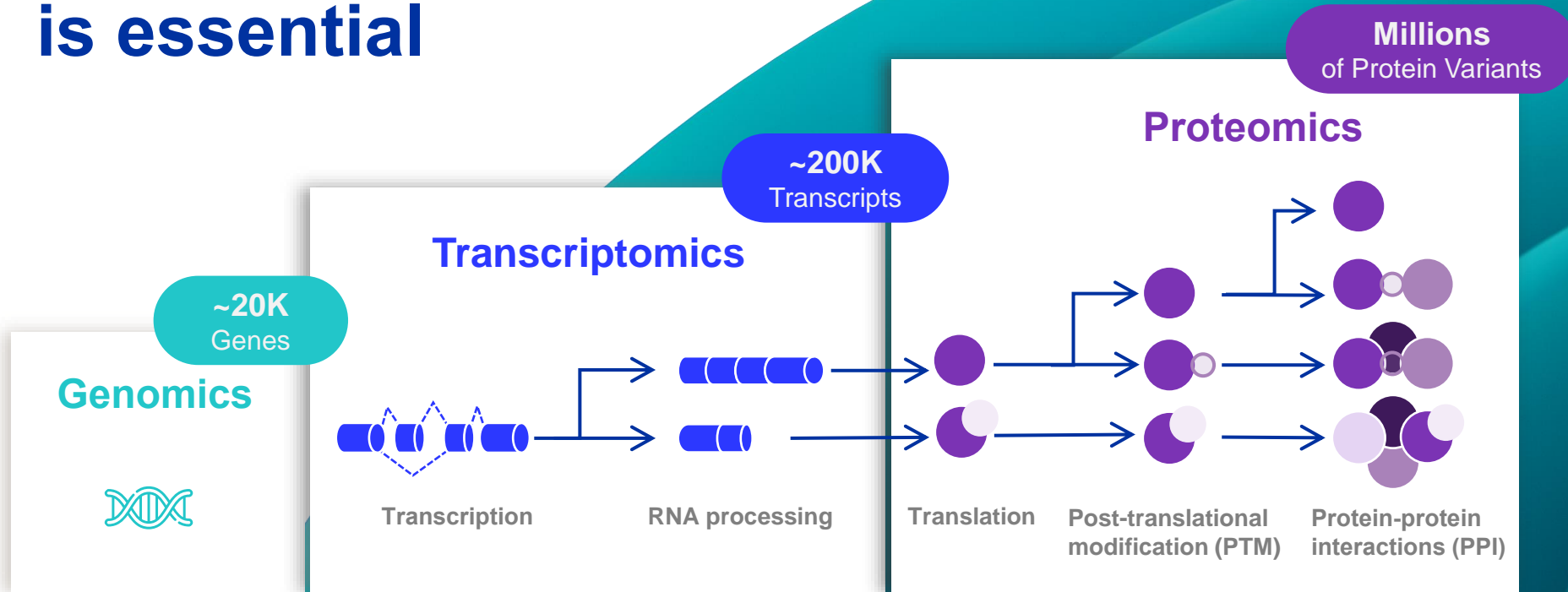


We imagine and  
pioneer new ways to

# **decode the biology of the proteome**

to improve human health

# Full characterization of the proteome is essential



>1.3 B genetic variants  
<0.2% characterized

Modest correlation of mRNA to proteins  
Distinct expression patterns in different cells

Protein variants can have distinct function  
Population proteomics will annotate genome variants

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

## Phenotype



Resource:  
**Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing**  
Xinying Yang<sup>1, 2, 3, 4, 17</sup>, Jasmin Coulombe-Huntington<sup>5, 17, 18</sup>, Shuli Kang<sup>6, 17, 18</sup>, Gloria M. Sheynkman<sup>1, 2, 3, 17</sup>, Tong Hae<sup>1, 2, 3, 17</sup>, Aaron Richardson<sup>1, 2, 3, 17</sup>, Song Sun<sup>7, 8, 9, 10</sup>, Fan Yang<sup>7, 8, 9</sup>, Yun A. Steen<sup>1, 2, 3</sup>, Ryan R. Murray<sup>2, 3, 17</sup>, Kristin Swoboda<sup>1, 2, 3</sup>, Richard E. Stearns<sup>1, 2, 3, 17</sup>, Michael Dumas-Fitzroth<sup>11</sup>, Andrew Stroobants<sup>12, 13, 14</sup>

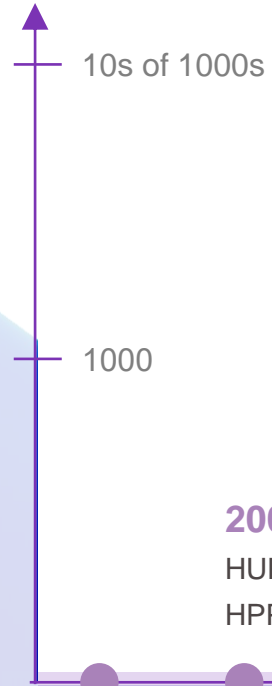
Science Translational Medicine  
HOME > SCIENCE TRANSLATIONAL MEDICINE > VOL. 13, NO. 605 > TGFβ2 AND TGFβ3 ISOFORMS DRIVE FIBROTIC DISEASE PATHOGENESIS  
RESEARCH ARTICLE | FIBROSIS  
**TGFβ2 and TGFβ3 isoforms drive fibrotic disease pathogenesis**  
TIANHE SUN<sup>1</sup>, ZHYU HUANG<sup>1</sup>, WELCHING LIANG<sup>1</sup>, JIANPING YIN<sup>1, 11</sup> AND JOSEPH R. ARRON<sup>1</sup> +30 authors | Authors Info & Affiliations  
SCIENCE TRANSLATIONAL MEDICINE • 9 Aug 2021 • Vol 13, Issue 605 • DOI: 10.1126/scitranslmed.aba0407

nature  
Article | Published: 04 November 2020  
**Combinatorial expression of GPCR isoforms affects signalling and drug responses**  
Maria Marti-Solano<sup>✉</sup>, Stephanie E. Crilly, Duccio Malinverni, Christian Munk, Matthew Harris, Abigail Pearce, Tezz Quon, Amanda E. Mackenzie, Xusheng Wang, Junmin Peng, Andrew B. Tobin, Graham Ladds, Graeme Milligan, David E. Gloriam, Manojkumar A. Puthenveedu & M. Madan Babu<sup>✉</sup>

Science Signaling  
**Opposing roles of RUBCN isoforms in autophagy and memory B cell generation**  
CHAO-YUAN TSAI<sup>1</sup>, SHUHEI SAKAKIBARA<sup>2</sup>, YUJIRO KIKUKAWA<sup>3</sup>, HIROKO ONDRE<sup>1, 4</sup> AND HITOSHI KUNITANI<sup>5</sup> +7 authors | Authors Info & Affiliations  
SCIENCE SIGNALING • 19 Sep 2023 • Vol 16, Issue 803 • DOI: 10.1126/scisignal.ade3592

# Changing the trajectory of deep unbiased proteomics

Deep Unbiased Study Size (# samples)



**1999**  
1<sup>st</sup> PubMed mention of Human Proteome Project

**2001**  
HUPO founded  
HPPP launched

**2015**  
Deepest study (16 samples; 5,300 proteins)

**2017**  
Seer founded

**2020**  
Seer study of 141 samples; 2,500 proteins  
First Proteograph™ shipped to customer

**2022**  
Multiple studies of >1,000 samples completed  
Deepest customer study >6,000 proteins

**2023**  
PrognomiQ begins 15,000 sample study  
Customers studies at scale with >8,000 proteins

**2024**  
Differentiated biological insights of unbiased proteomics for early cancer detection



**OPENING UP A NEW GATEWAY TO THE PROTEOME**

# Seer is positioned to lead the proteomics revolution

Deep,  
unbiased,  
high-  
throughput

Able to analyze 10,000+  
samples per year

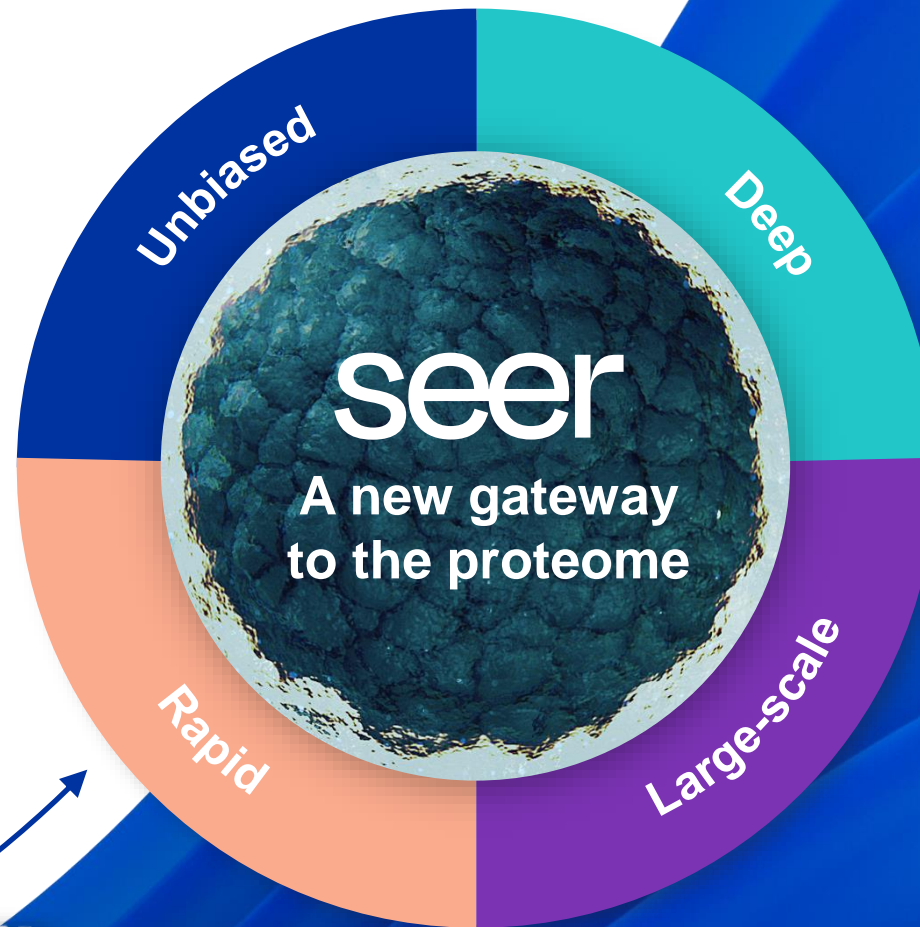
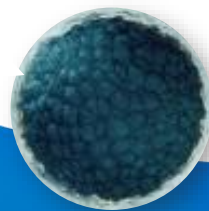


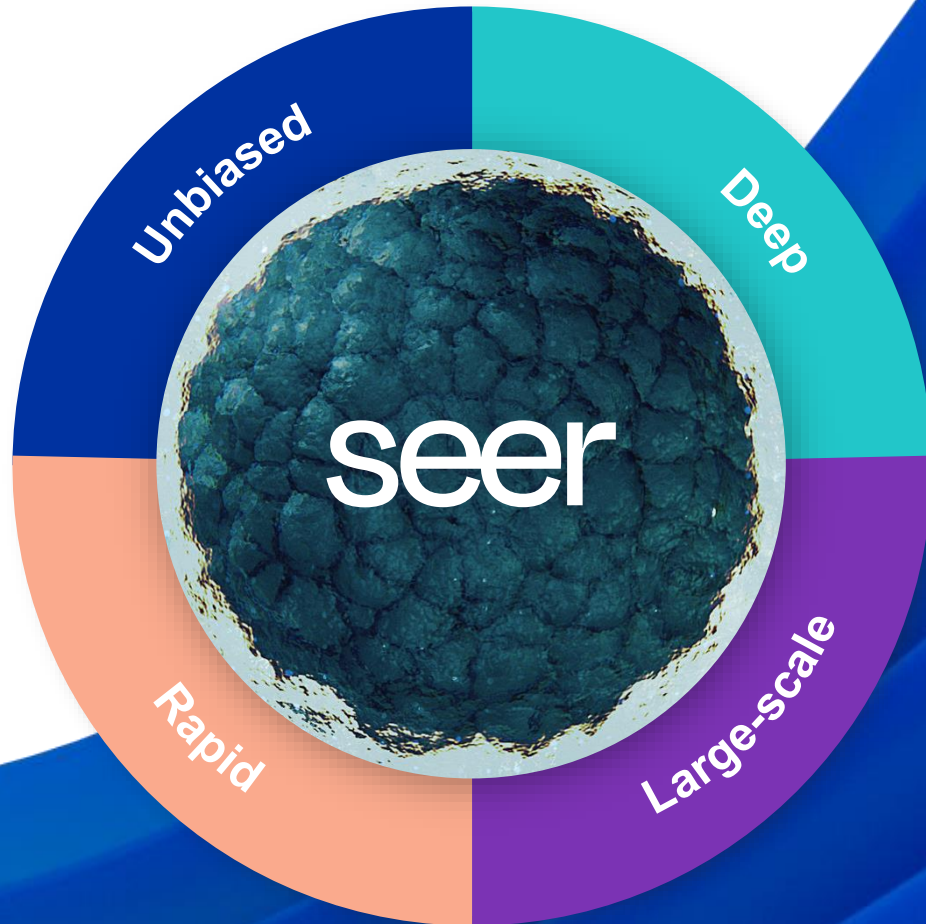
# Seer enables unbiased, deep and rapid proteomic analysis at scale

Taking advantage of the way proteins interact



Lab on a nanoparticle





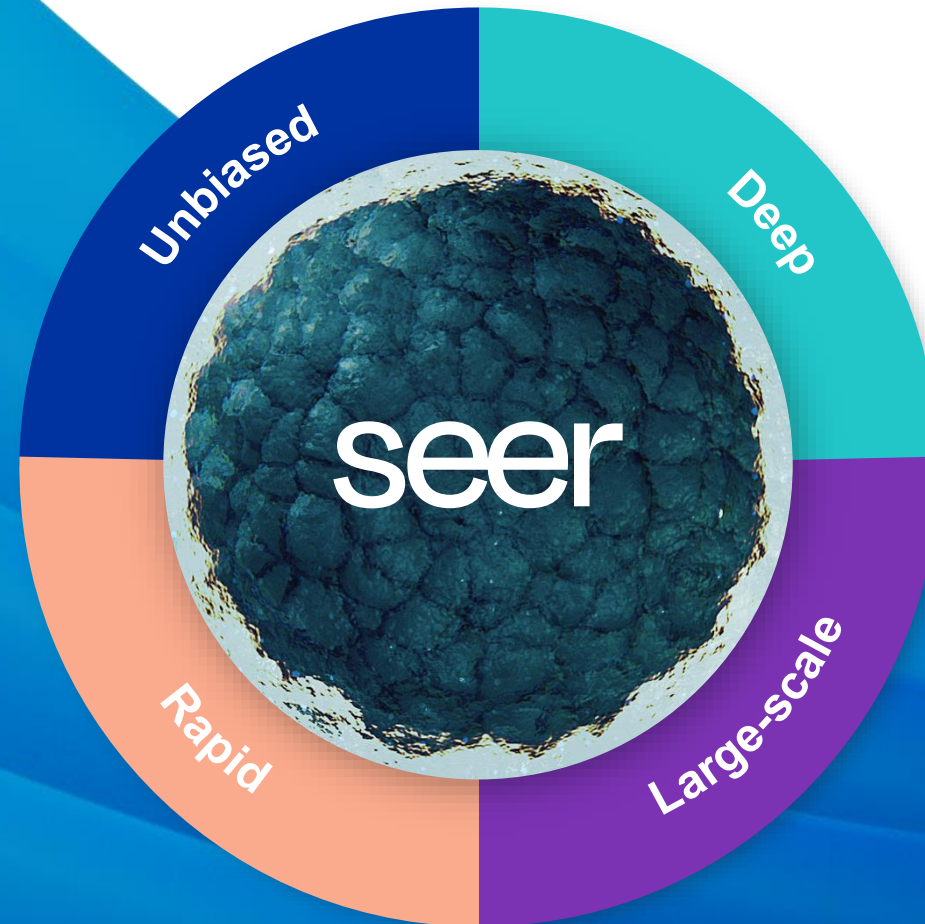
## Exceptional performance and flexibility

- High accuracy and reproducibility
- Quantitative measurement
- Broad dynamic range
- 1% false discovery rate (FDR)
- Wide range of sample types
- Species agnostic



# Differentiated biological insights and applications

- Protein isoforms
- Protein variants
- pQTLs
- Biomarker discovery
- Drug target discovery
- Model organisms
- QC of biomanufacturing



# Significant need for unbiased proteomics at scale



Academic

Translational

Commercial

Pharma

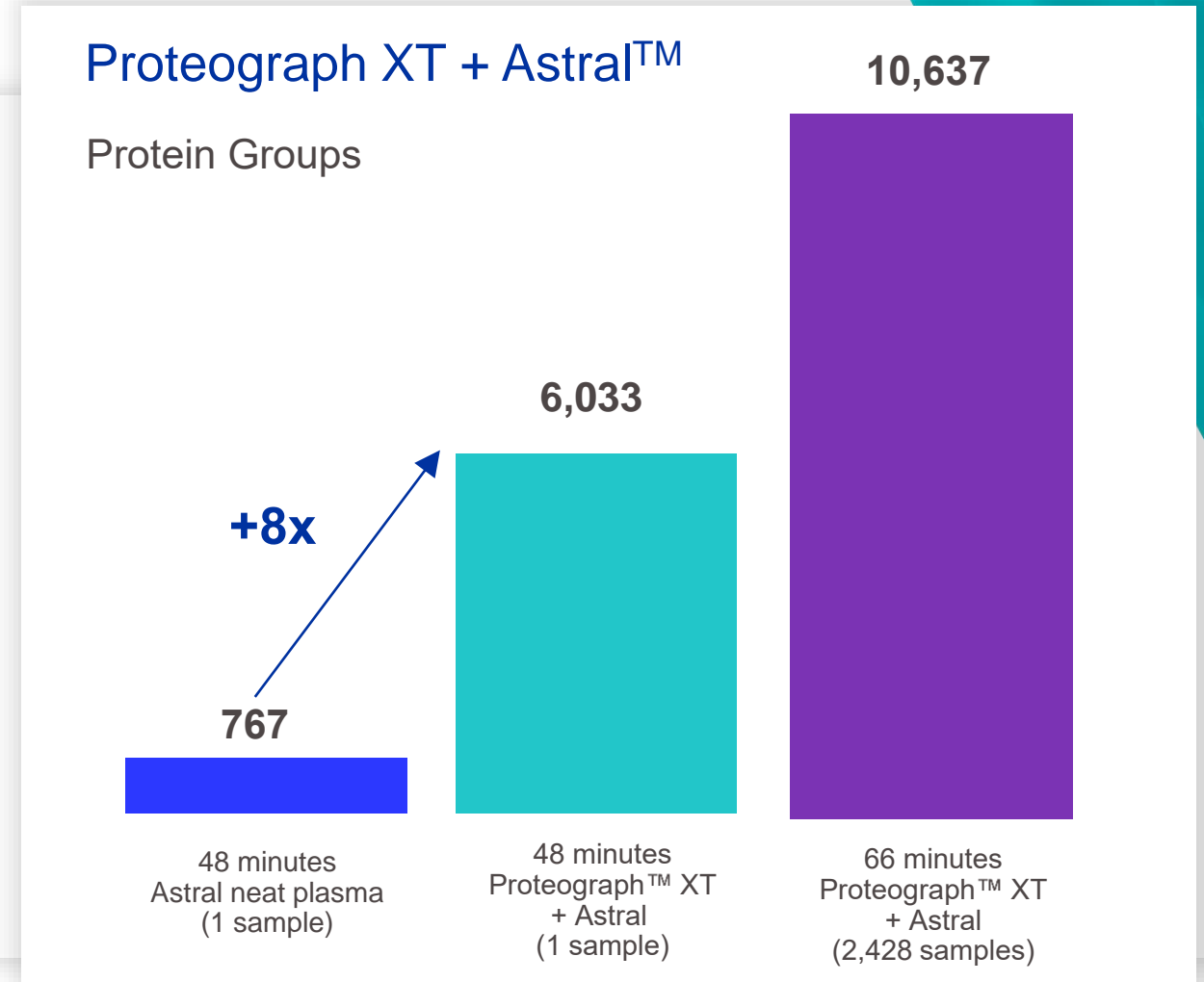
Applied

# Customers are excited about the expanded protein coverage and throughput of XT

**2.5x sample throughput**  
without sacrificing depth

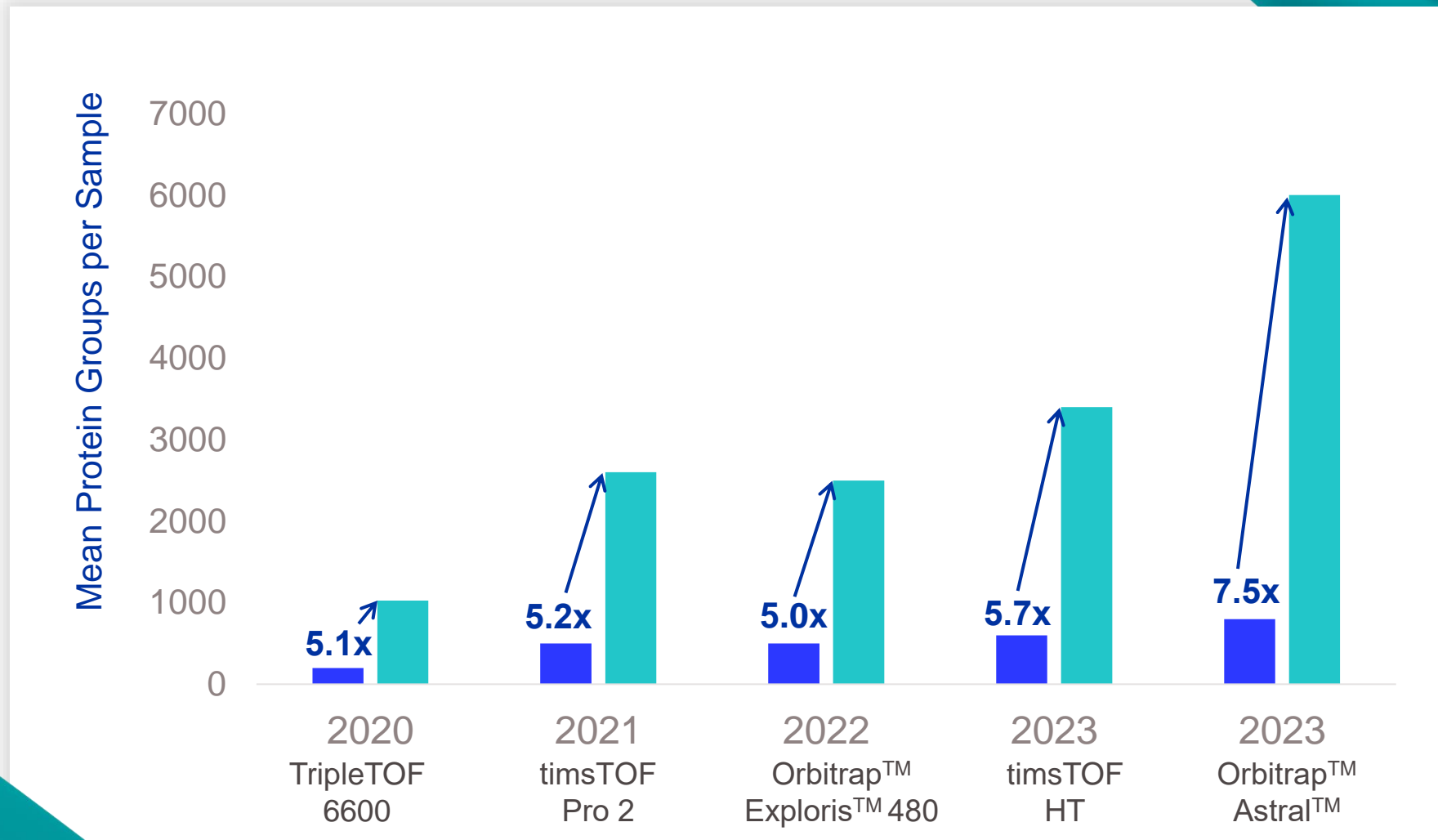
**Significantly more proteins detected** by mass spec with Seer technology

~80% of installed base  
using **Proteograph XT**



# Seer's Proteograph consistently improves mass spec performance

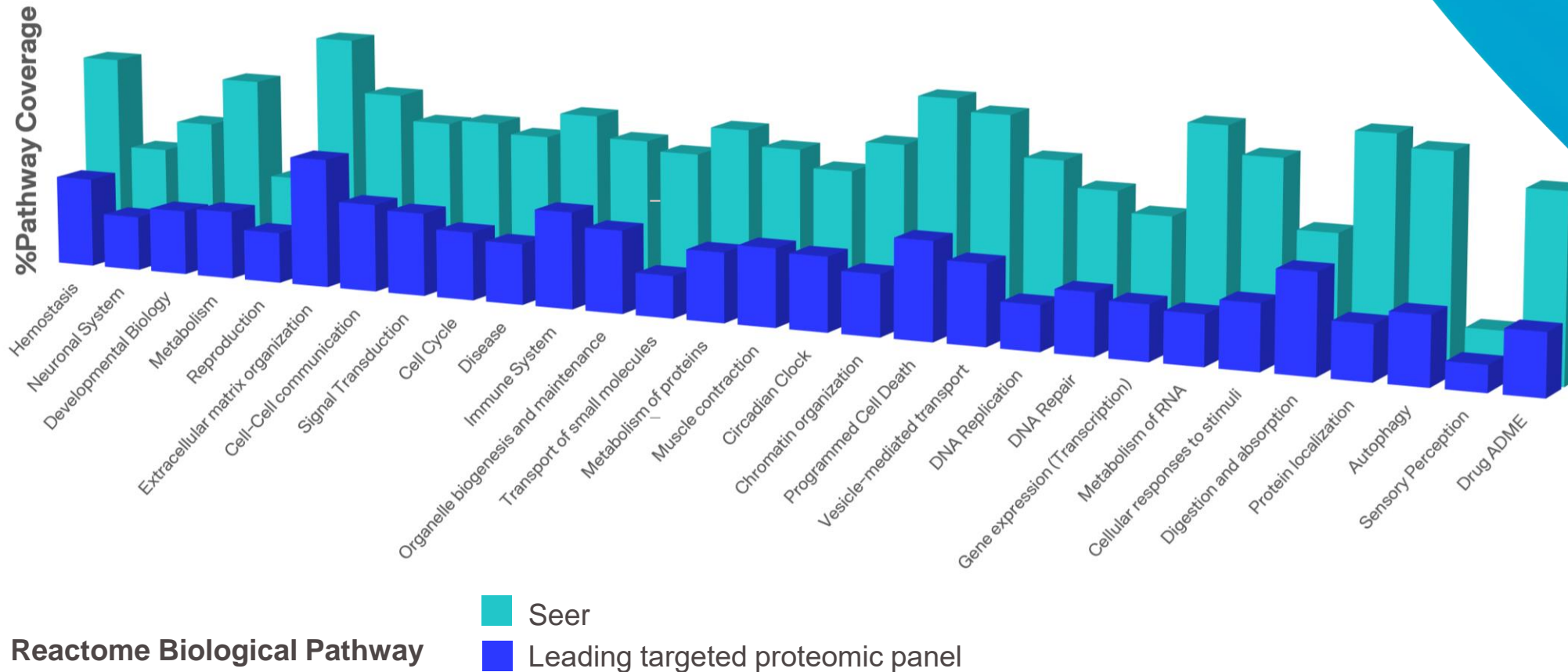
■ Neat Plasma  
■ Proteograph



These are representative numbers achieved on these platforms in these years. This is not a direct head-to-head evaluation

# Proteograph XT provides industry-leading measurement depth

150,000+ peptides,  
10,000+ human proteins,  
>1,900 biological pathways



# Strong demand for STAC services exemplifying the power of the Proteograph XT and accelerating adoption

Partnership with Thermo Fisher Scientific provides access to newly launched **Proteograph XT + Orbitrap Astral LC-MS**

STAC (Seer Technology Access Center) available in the U.S. and Europe



**66** Organizations served



**10** Large pharma customers



**6,000** Average protein groups per plasma sample



**6x** Average fold improvement over neat plasma

# Market development to broad scale adoption

Revenue inflection point

Phase 4

Widespread adoption and revenue growth

Phase 3

We are here

Biological insight

Phase 2

Facilitate scaling

Phase 1

Content discovery

Growth

Time

# Growing validation of Seer technology

PNAS RESEARCH ARTICLE | APPLIED BIOLOGICAL SCIENCES OPEN ACCESS

## Engineered nanoparticles enable deep proteomics studies at scale by leveraging tunable nano-bio interactions

Shao Fengsi<sup>1</sup>, Betzad Tangirani<sup>1</sup>, Tristan R. Brown<sup>1</sup>, Francis A. Evens<sup>1</sup>, Michael Goff<sup>1</sup>, Matthew McGraw<sup>1</sup>, Eshwar M. Elgeran<sup>1</sup>, Xiaoyan Zhao<sup>1</sup>, Veda<sup>1</sup>, Garca<sup>1</sup>, Triany Wang<sup>1</sup>, Matthew E. K. Chang<sup>1</sup>, Kalyana Reddy<sup>1</sup>, Jessica Xu<sup>1</sup>, Max Makarewicz<sup>1</sup>, Hongwei Xia<sup>1</sup>, Evan S. O'Brien<sup>1</sup>, Craig Stoczka<sup>1</sup>, Camran Hamirani<sup>1</sup>, Theodore J. Platt<sup>1</sup>, Wang Ma<sup>1</sup>, Martin Grotzer<sup>1</sup>, Robert Lange<sup>1</sup>, Mark R. Flory<sup>1</sup>, Ryan Benz<sup>1</sup>, Wei Tao<sup>1</sup>, Juan Cruz Corrales<sup>1</sup>, Seanan Rodriguez<sup>1</sup>, John E. Blum<sup>1</sup>, Ashim Siddiqui<sup>1</sup>, Daniel Hornburg<sup>1</sup>, and Omer C. Faruqi<sup>1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100</sup>

Edited by Chi-Hang Ho, University of Hong Kong, Hong Kong, China, received March 31, 2023; accepted December 17, 2023

March 11, 2022 | 119 (11) e2106553119 | https://doi.org/10.1073/pnas.2106553119

**Significance**  
Deep profiling of the plasma proteome at scale has been a challenge for traditional approaches. We achieve superior performance across the dimensions of precision, depth, and throughput using a panel of surface-functionalized superparamagnetic nanoparticles (SPNs) in combination with deep proteomics automated workflow leverages competitive nanoparticle-protein quantitative mass spectrometry. We dissect the contribution of individual properties of nanoparticles to the composition of protein coronas. Competitive nanoparticle functionalization can be tailored to protein sets. This feasibility of deep, precise, unbiased plasma proteomics at a scale genomic enables multi-proteomic studies.

**Deep interrogation of plasma proteome on a large scale is a challenge and concentration of proteins, which span a dynamic range magnitude. Current plasma proteomics workflows employ latent combining abundant protein fragments and sample fractionation demonstrated the superiority of multiproteinase (multi-PP) on the plasma proteome in terms of proteome depth compared to 1**

**An Infection Point in High-Throughput Proteomics with Orbitrap Astral: Analysis of Biofluids, Cells, and Tissues**  
Nathan C. Hendricks, Samim D. Bhowik, Angil J. Kesavap, Joseph Onto, Akshank Soodani, Saad Soudki, Muhammad, Ch. D. L. Nigro, Jonathan T. Bai, Anne Mersbach, Susan M. Meekins, and Jennifer E. Van Eyk<sup>1</sup>

**ABSTRACT:** The traditional Nano proteomics workflow is not well suited for the analysis of complex biofluids, cells, and tissues. Current workflow is the integration of Adaptive Fusion Ion-Trap (AFIT) technology for ion optics and ion mobility for separation and detection. However, AFIT technology is not well suited for the analysis of complex biofluids, cells, and tissues. We have developed a workflow that combines the strengths of AFIT technology with the strengths of Orbitrap technology. This workflow is well suited for the analysis of complex biofluids, cells, and tissues. It provides a CV less than 20%, and a 4.4 min run time with a 100% duty cycle. This workflow is well suited for the analysis of complex biofluids, cells, and tissues. It provides a CV less than 20%, and a 4.4 min run time with a 100% duty cycle. This workflow is well suited for the analysis of complex biofluids, cells, and tissues. It provides a CV less than 20%, and a 4.4 min run time with a 100% duty cycle.

# 10 19

## Manuscripts in bioRxiv Peer-reviewed articles

**Nanoparticle enrichment mass-spectrometry proteomics identifies protein-altering variants for precise pQTL mapping**  
Kavita Balun<sup>1,2</sup>, Oshin Kulkarni<sup>1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100</sup>

**A second space age spanning omics, platforms and medicine across orbits**  
The recent acceleration of commercial, private and multi-national spaceflight has created unprecedented opportunities for omics research in space. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease.

**Resistance training rejuvenates the mitochondrial methylene in aged human skeletal muscle**  
Bradley A. Ruple<sup>1</sup>, Joshua S. Godwin<sup>1</sup>, Paulo H. C. Mesquita<sup>1</sup>, Shelby C. Osburn<sup>1</sup>, Christopher C. Vann<sup>1</sup>, Donald A. Lamb<sup>1</sup>, Casey L. Sexton<sup>1</sup>, Darren G. Candow<sup>1</sup>, Scott C. Forbes<sup>1</sup>, Andrew D. Zumbo<sup>1</sup>, Andrew N. Kavasi<sup>1</sup>, Kaelin C. Young<sup>1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100</sup>

**A novel deep proteomic approach in human skeletal muscle unveils distinct molecular signatures affected by aging and resistance training**  
Michael D. Roberts<sup>1</sup>, Bradley A. Ruple<sup>1</sup>, Joshua S. Godwin<sup>1</sup>, Mason C. McIntosh<sup>1</sup>, Shao-Yang Chen<sup>1</sup>, Nicholas J. Kontos<sup>1</sup>, Anthony Aguin-Birikang<sup>1</sup>, Max Michael<sup>1</sup>, Daniel L. Plotkin<sup>1</sup>, Madison L. Mattingly<sup>1</sup>, Brooks Mobley<sup>1</sup>, Tim J. Ziegenfuss<sup>1</sup>, Andrew D. Fruge<sup>1</sup>, Andrea N. Kavasi<sup>1</sup>

**The Space Omics and Medical Atlas (SOMA) and international astronaut biobank**  
Spaceflight induces molecular, cellular and physiological shifts in astronauts and crew members. These shifts are complex and multifaceted, and understanding them is critical for the development of space medicine and the optimization of human health in space. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease.

**Secretome profiling reveals acute changes in oxidative stress, brain homeostasis, and coagulation following short-duration spaceflight**  
A spaceflight becomes more common with commercial crew, blood-based measures of crew health can guide both astronaut biomedical and countermeasures. By profiling plasma proteomics, metabolites, and metabolite levels, we can identify acute changes in oxidative stress, brain homeostasis, and coagulation following short-duration spaceflight.

Large-scale studies of the plasma proteome using mass spectrometry have advanced significantly over the past decade. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease.

Deep interrogation of plasma proteome on a large scale is a challenge and concentration of proteins, which span a dynamic range magnitude. Current plasma proteomics workflows employ latent combining abundant protein fragments and sample fractionation demonstrated the superiority of multiproteinase (multi-PP) on the plasma proteome in terms of proteome depth compared to 1

**Abstract**  
Resistance training (RT) dramatically alters the skeletal muscle mitochondrial methylene. However, no study has examined RT effects on the mitochondrial DNA (mtDNA) methylene. Herein, we used a novel, sensitive, and specific method to measure mtDNA methylene in skeletal muscle. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease.

**Abstract**  
The skeletal muscle proteome alterations to aging and resistance training have been reported in prior studies. However, conventional proteomics in skeletal muscle typically yields wide protein abundance ranges that mask the detection of lowly expressed proteins. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease.

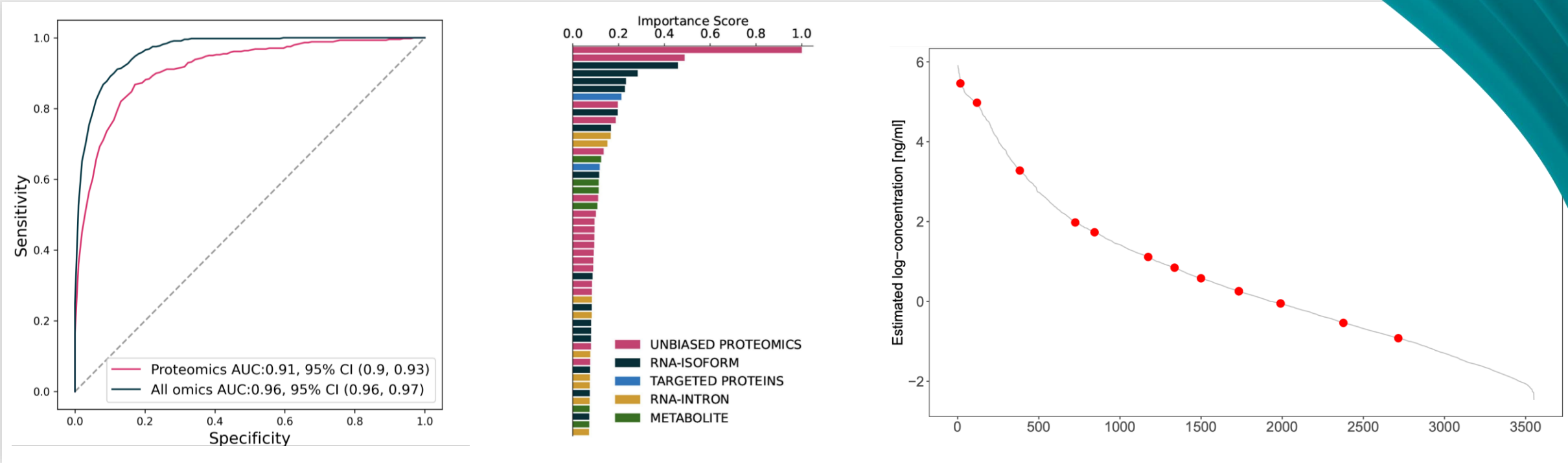
Spaceflight induces molecular, cellular and physiological shifts in astronauts and crew members. These shifts are complex and multifaceted, and understanding them is critical for the development of space medicine and the optimization of human health in space. This research is the largest ever undertaken in space, and is expected to lead to significant advances in our understanding of human biology and disease.

A spaceflight becomes more common with commercial crew, blood-based measures of crew health can guide both astronaut biomedical and countermeasures. By profiling plasma proteomics, metabolites, and metabolite levels, we can identify acute changes in oxidative stress, brain homeostasis, and coagulation following short-duration spaceflight.



# Deep, unbiased proteomics at scale powers a breakthrough advance in early lung cancer detection

Multi-omics profiling detected >13,000 proteins groups, >200,000 RNA transcripts, and >1,000 metabolites



✓ Extremely strong performance

✓ Unbiased proteomics is the key driver

✓ Classifier proteins fall across the dynamic range

# ~1,800 sample cohort identifies markers of Alzheimer's Disease, fast and slow cognitive decline

**138**

identified markers of Alzheimer's Disease vs normal

**55%**

are not present on high-plex affinity panel

**94/138**

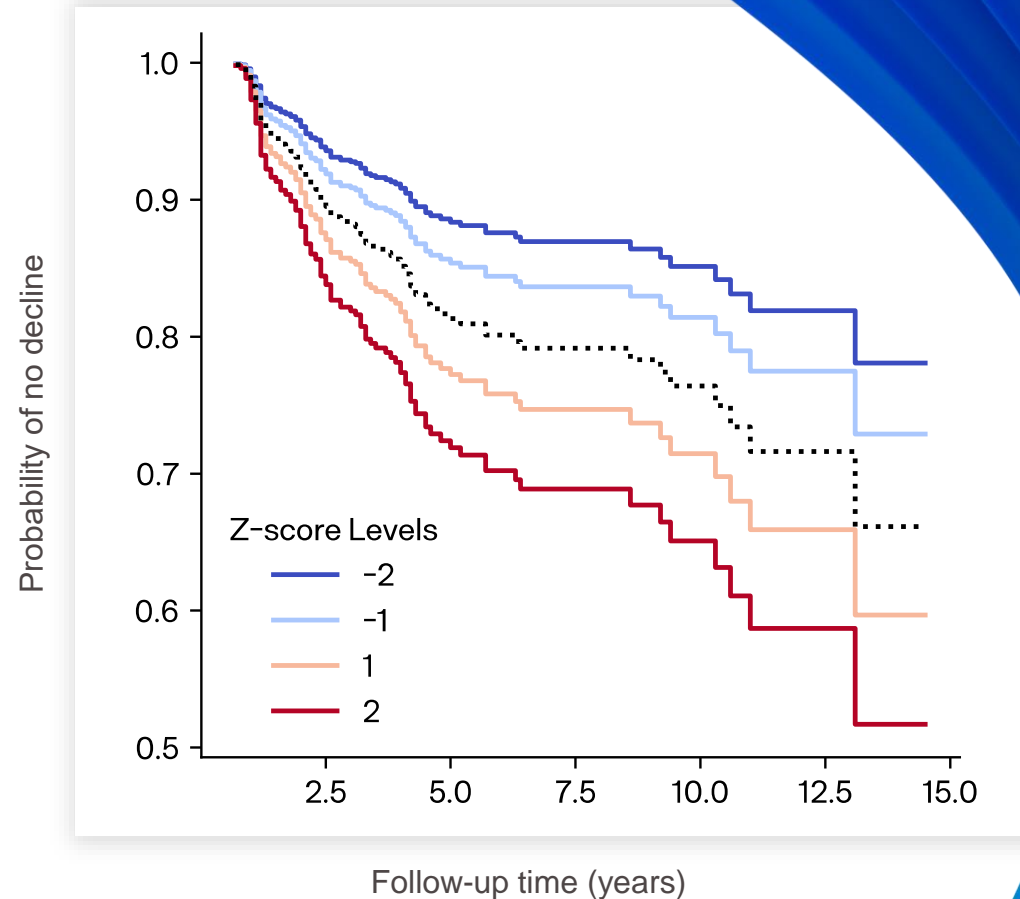
putative novel Alzheimer's disease biomarkers

**8**

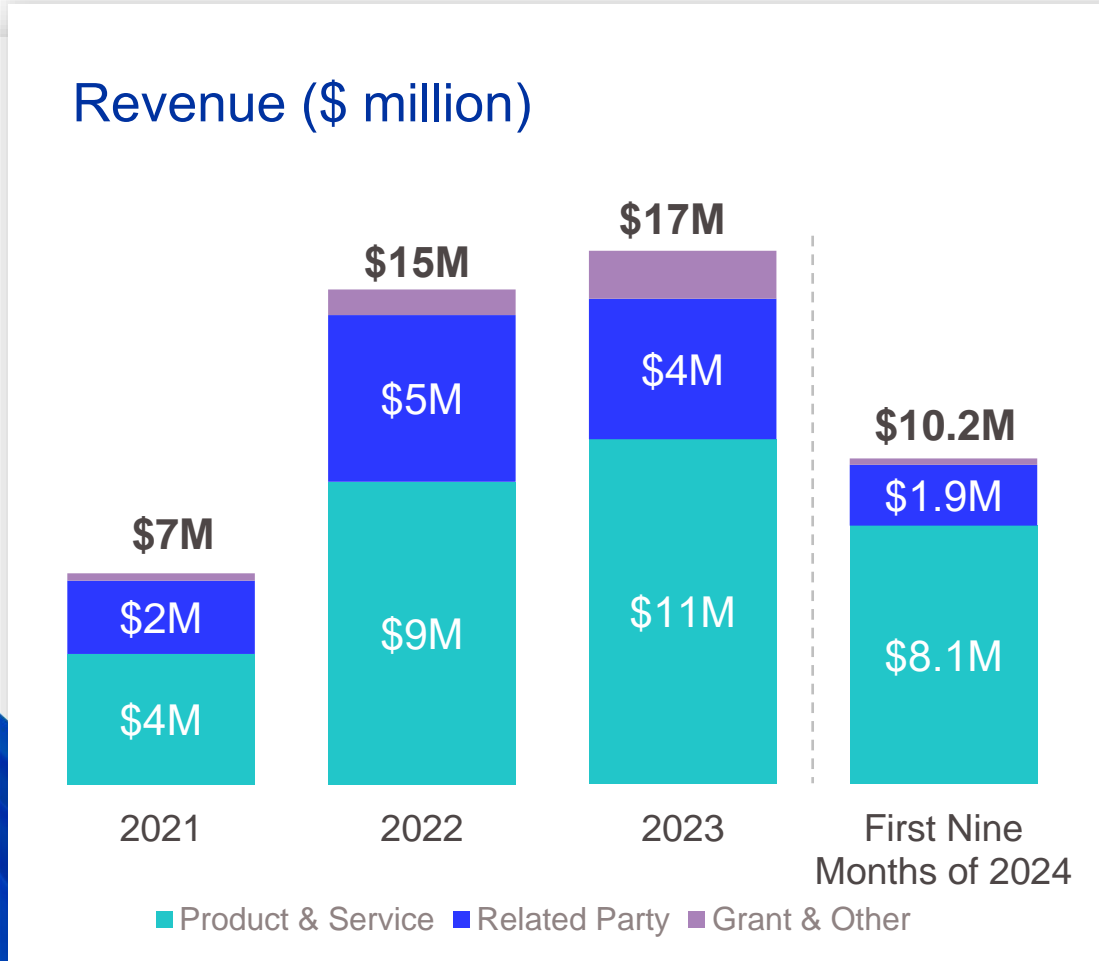
identified markers distinguishing fast and slow progressors of cognitive decline

**75%**

are not present on high-plex affinity panel



# Enhancing access to Proteograph while preserving strong balance sheet



**\$312.5 million**

cash, cash equivalents and investments,  
no debt as of September 30, 2024

**49.5% gross margin** in first nine months of 2024

**Reduced operating cash burn**  
with increased cost efficiency

**Authorized \$25 million**  
open-market repurchase program in Q2 2024



seer