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.

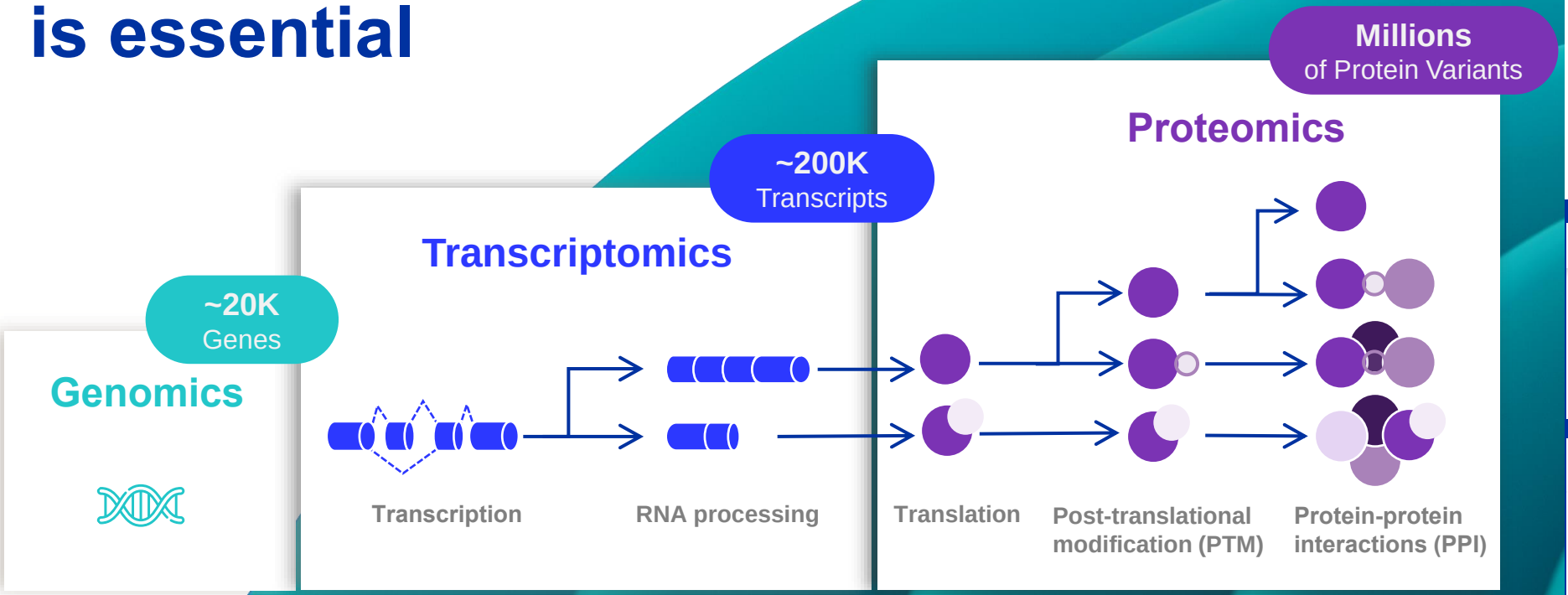
We imagine and pioneer new ways to

decode the biology of the proteome

to improve human health

seer

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

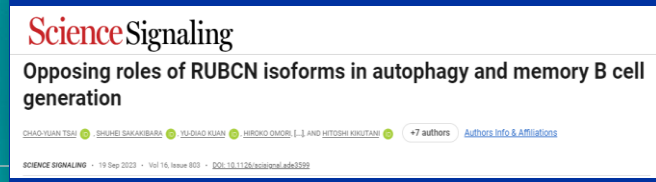
Source: Isabell Bludau et al. Proteomic and interactomic insights into the molecular basis of cell functional diversity. Nature Reviews Molecular Cell Biology (2020).

Phenotype


Cell
Volume 164, Issue 4, 11 February 2016, Pages 805-817
CellPress
Resource
Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing


Science Translational Medicine
RESEARCH ARTICLE | FIBROSIS
TGFβ2 and TGFβ3 isoforms drive fibrotic disease pathogenesis


nature
Article | Published: 04 November 2020
Combinatorial expression of GPCR isoforms affects signalling and drug responses
Maria Marti-Solano, 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


Science Signaling
Opposing roles of RUBCN isoforms in autophagy and memory B cell generation

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Changing the trajectory of deep unbiased proteomics

Deep Unbiased
Study Size
(# samples)

10s of 1000s

1000

1999
1st PubMed mention
of Human Proteome Project

2001
HUPO founded
HPPP launched

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

2017
Seer founded

2019
Largest study
(48 samples; 1,835 proteins)

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

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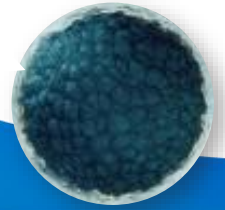
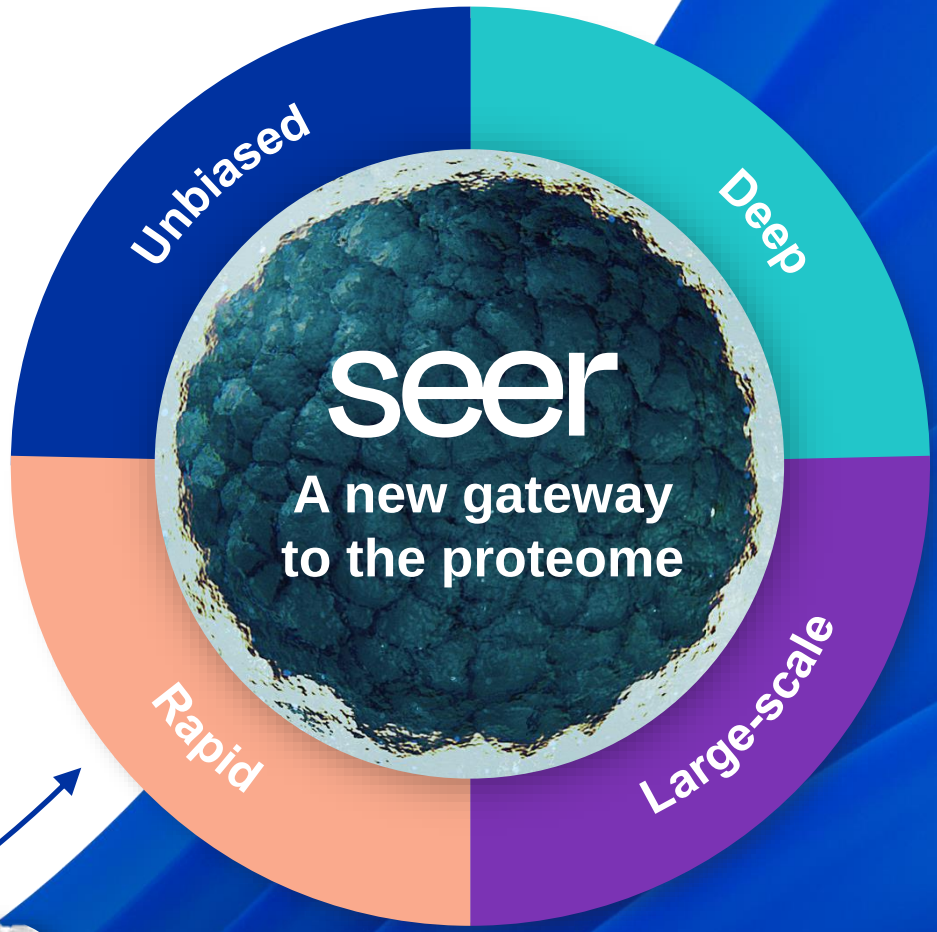
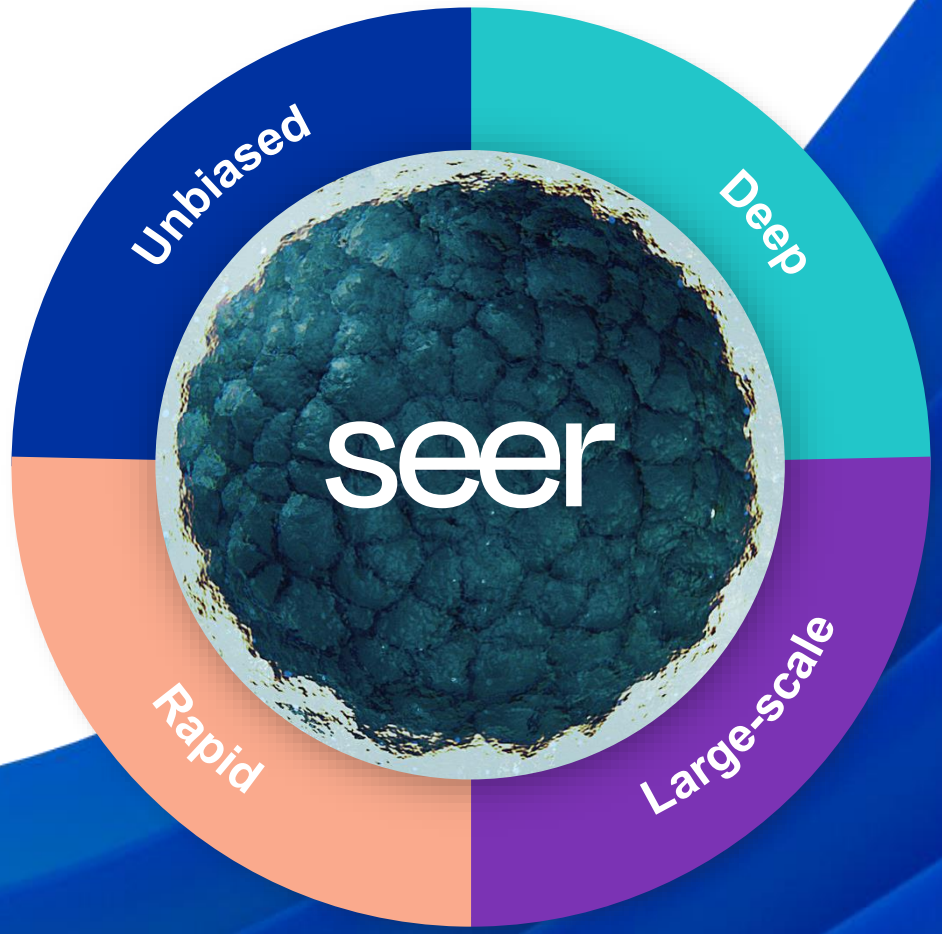
Seer enables unbiased, deep and rapid proteomic analysis at scale

Taking advantage of the way proteins interact

Lab on a nanoparticle





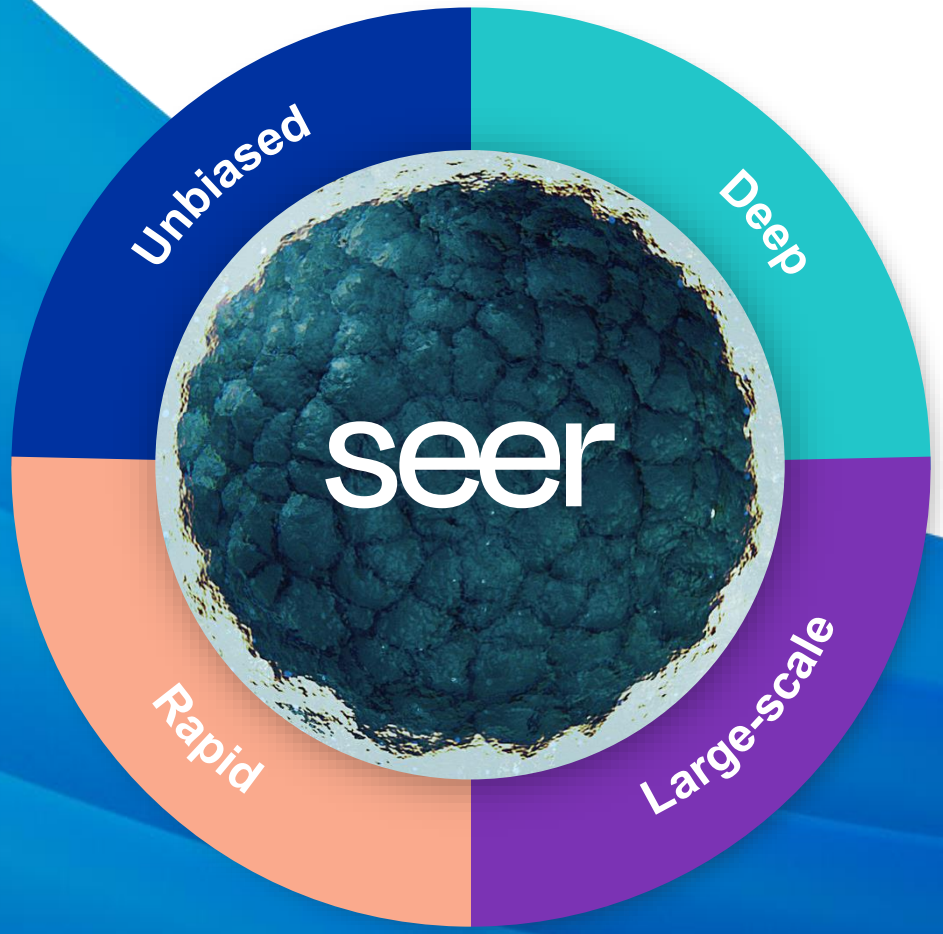


Exceptional performance and flexibility

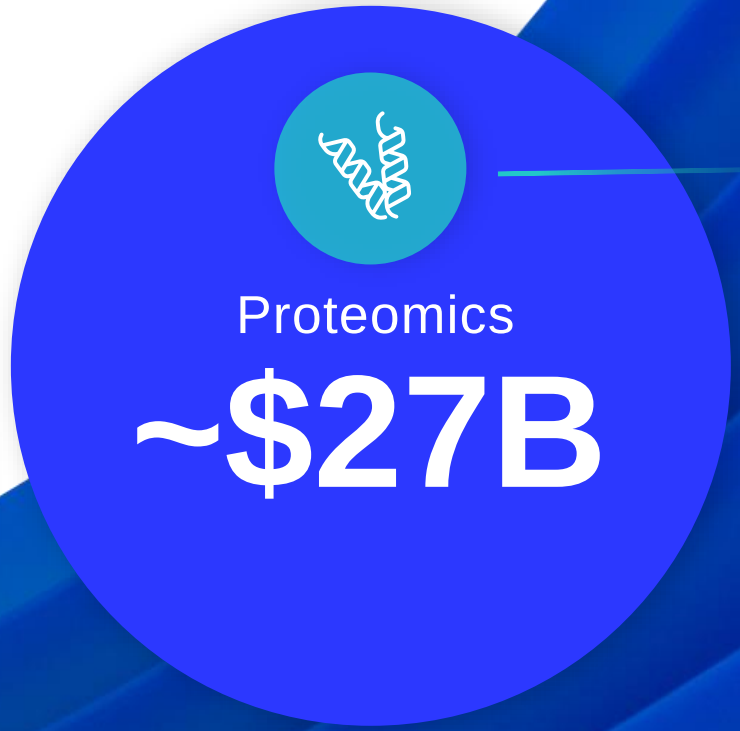
- High accuracy and reproducibility
- Quantitative measurement
- Broad dynamic range
- 1% false discovery rate (FDR)
- Wide range of sample types
- Species agnostic

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

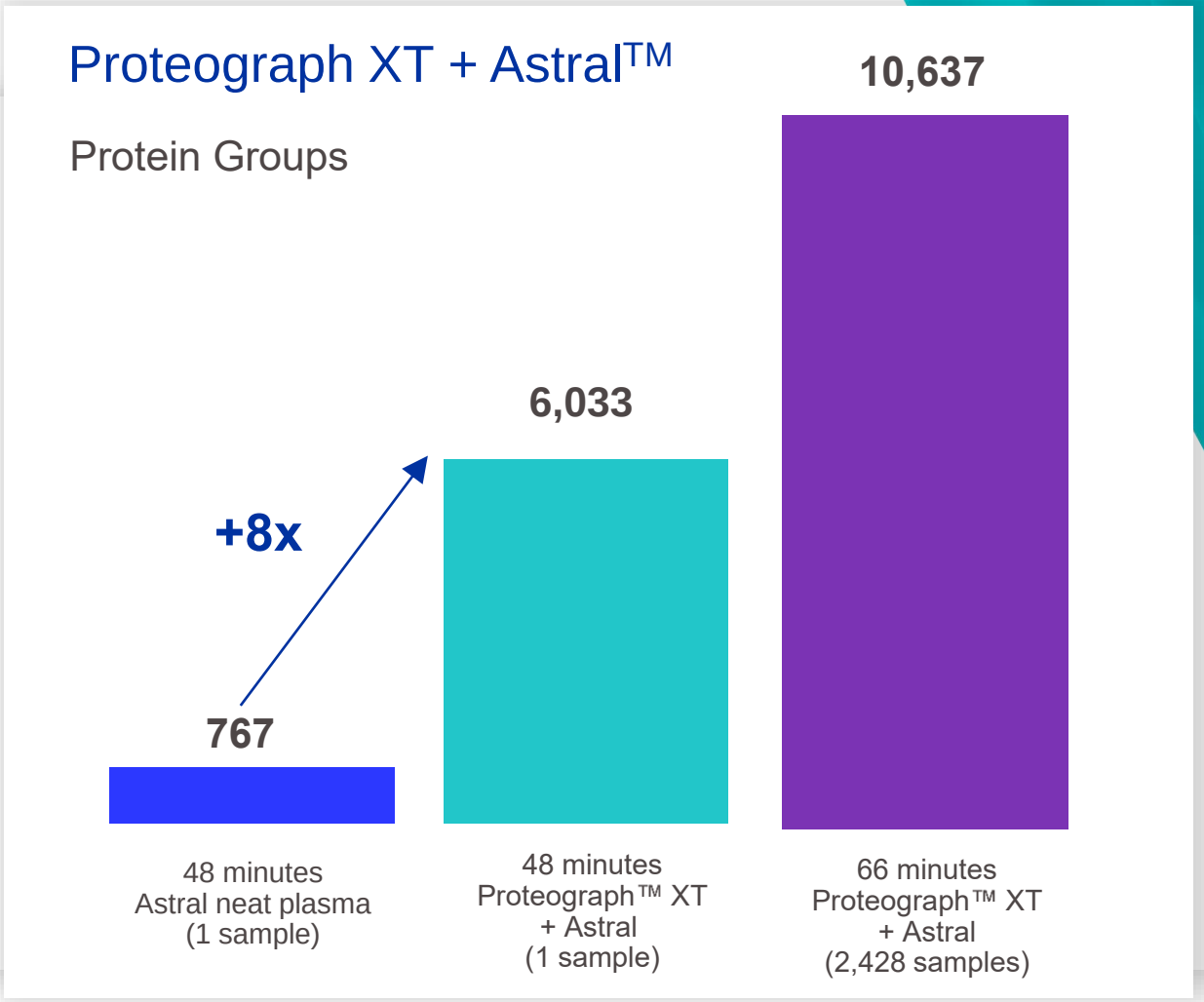
Sources: Allied Market Research, Technavio estimates for 2022

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

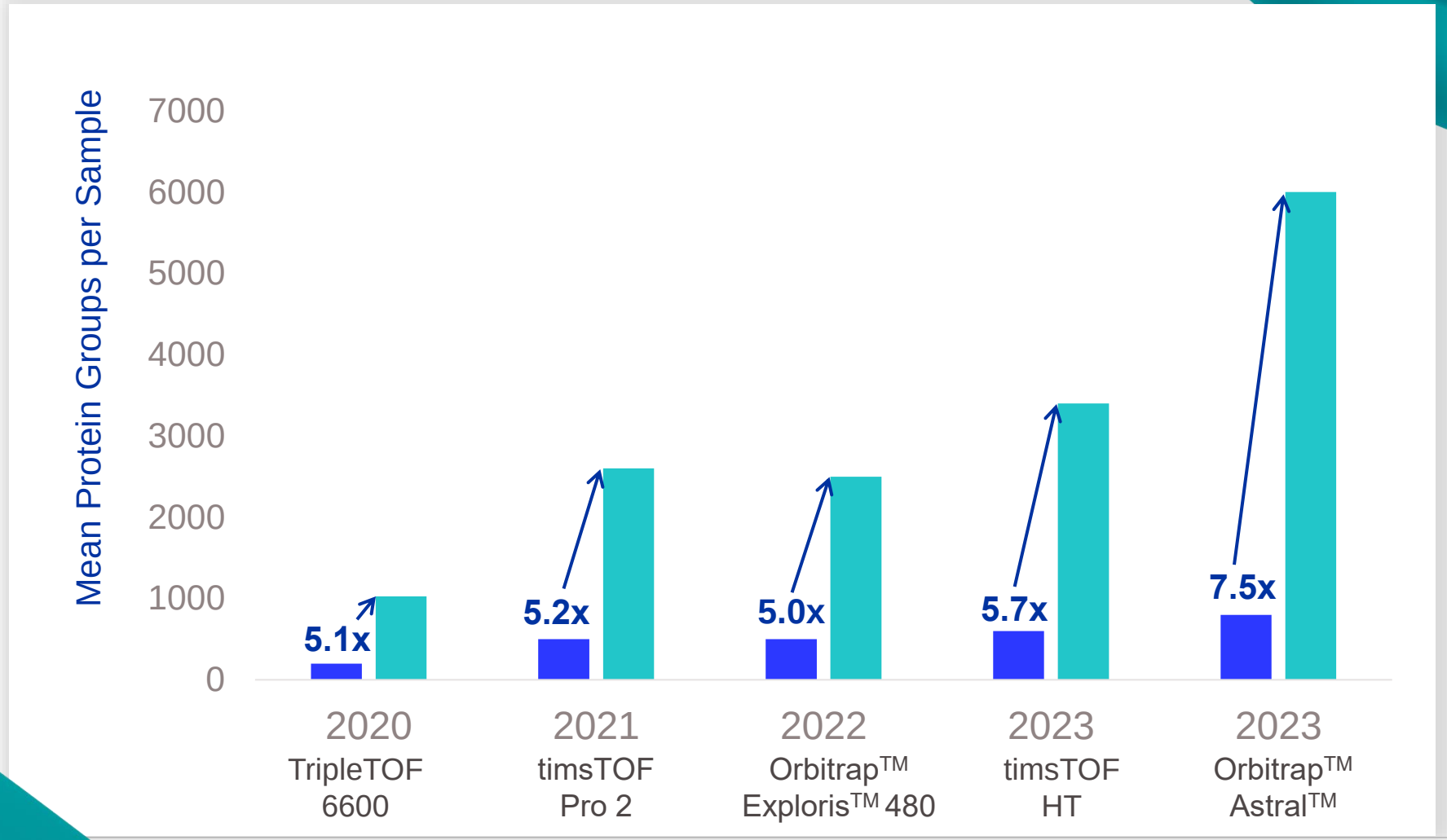
2.5x sample throughput without sacrificing depth

Significantly more proteins detected by mass spec with Seer technology

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



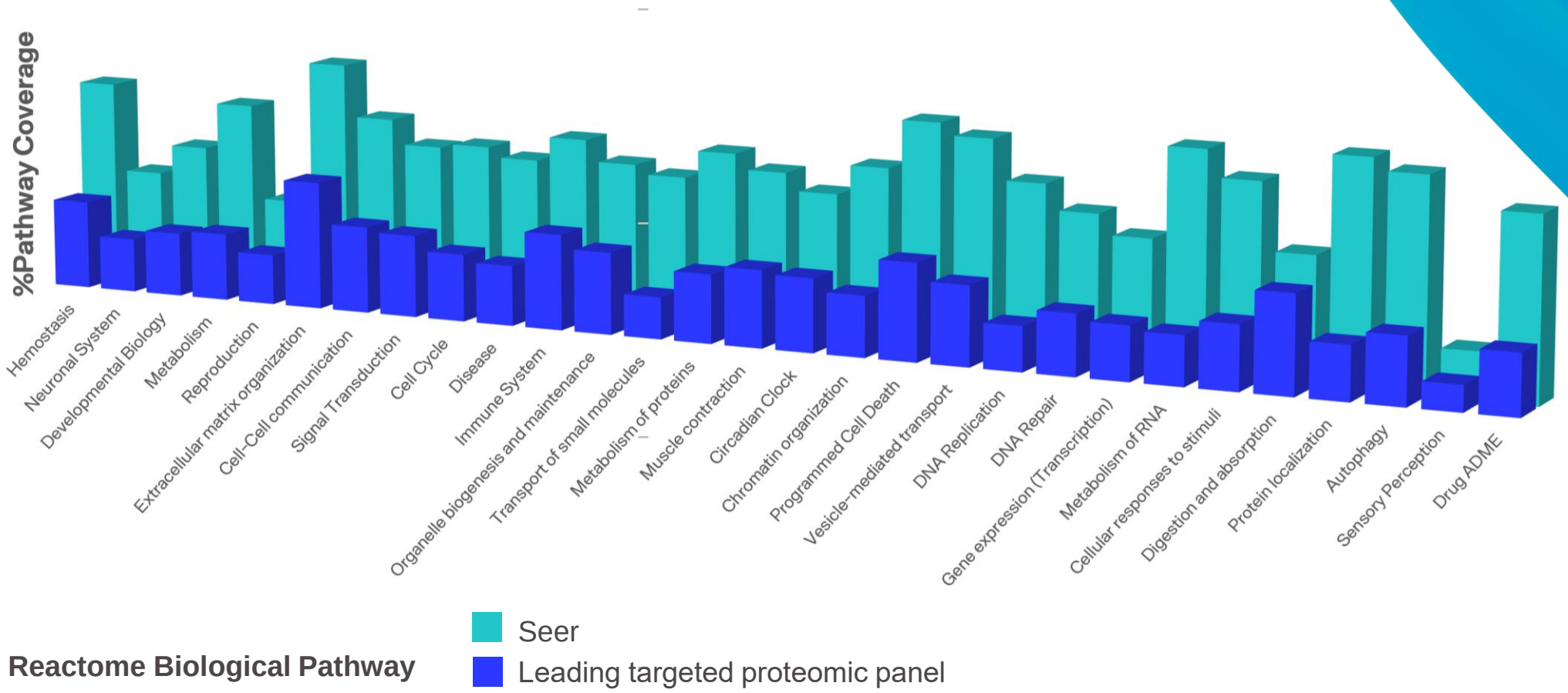
Seer's Proteograph consistently improves mass spec performance



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



Sources: seer.bio/protein-discovery-catalog/; olink.com/products-services/exploreht/olink-explore-ht-assay-list-2023-10-03.xlsx

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

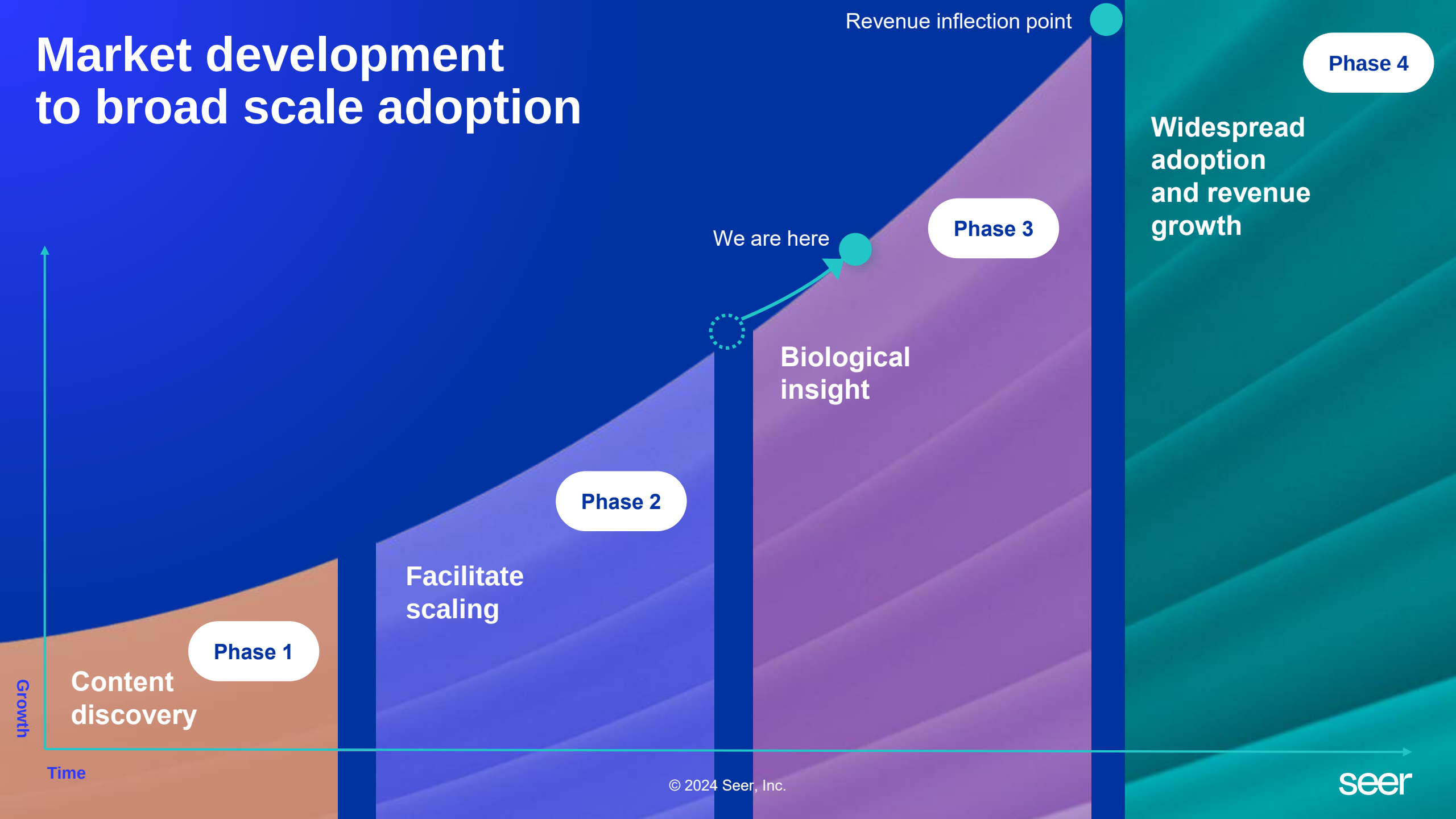
66 Organizations served

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



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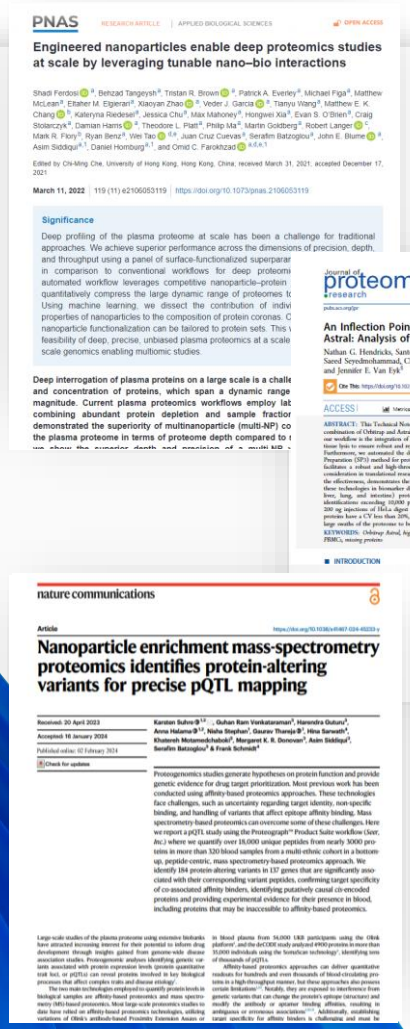
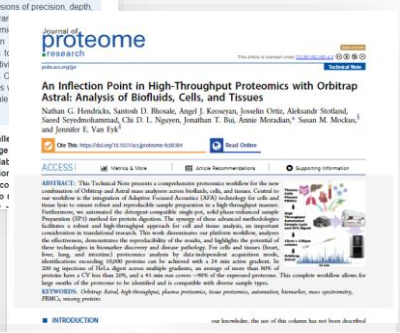
Growing validation of Seer technology

10 Manuscripts in bioRxiv

19 Peer-reviewed articles


PNAS

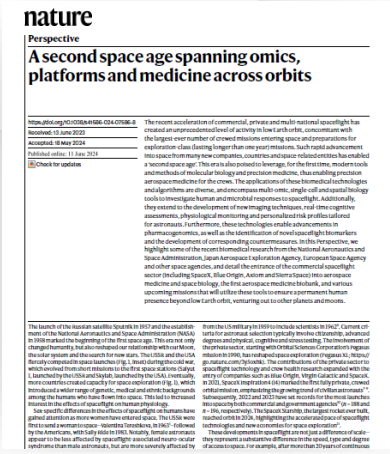
Engineered nanoparticles enable deep proteomics studies at scale by leveraging tunable nano–bio interactions


Journal of proteome research

An Inflection Point in High-Throughput Proteomics with Orbitrap Astral: Analysis of Biofluids, Cells, and Tissues

nature communications

Nanoparticle enrichment mass-spectrometry proteomics identifies protein-altering variants for precise pQTL mapping


nature

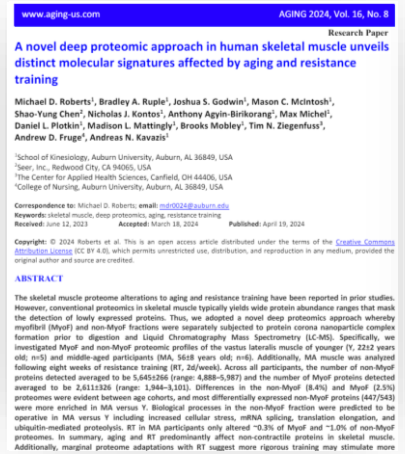
Perspective

A second space age spanning omics, platforms and medicine across orbits


RESEARCH ARTICLE

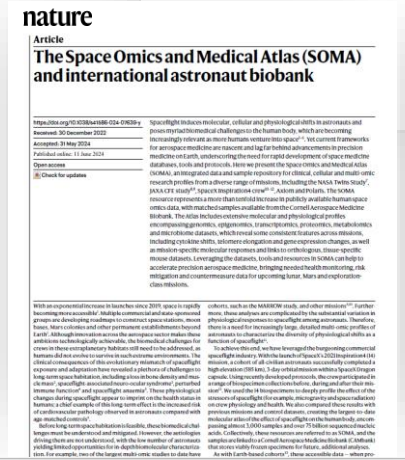
FASEB Journal

Resistance training rejuvenates the mitochondrial methylome in aged human skeletal muscle


www.aging-us.com AGING 2024, Vol. 16, No. 8

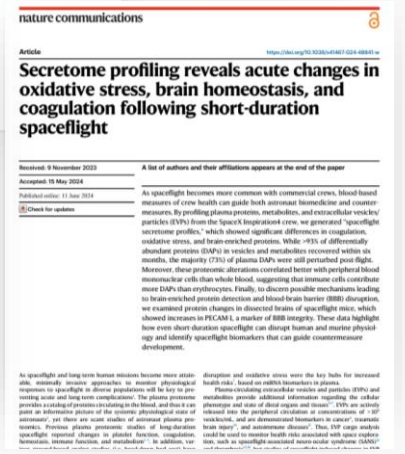
Research Paper

A novel deep proteomic approach in human skeletal muscle unveils distinct molecular signatures affected by aging and resistance training


nature

Article

The Space Omics and Medical Atlas (SOMA) and international astronaut biobank


nature communications

Article

Secretome profiling reveals acute changes in oxidative stress, brain homeostasis, and coagulation following short-duration spaceflight


nature COMMUNICATIONS

ARTICLE

Rapid, deep and precise profiling of the plasma proteome with multi-nanoparticle protein corona

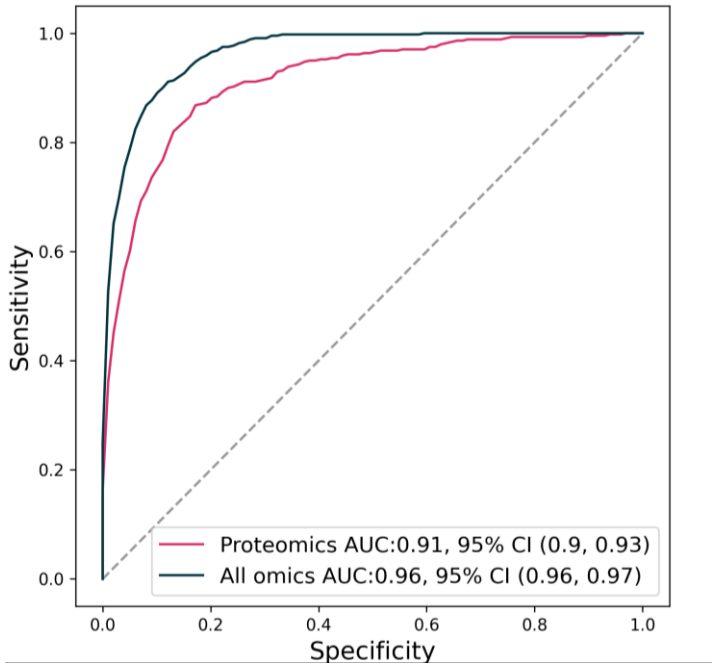

Journal of proteome research

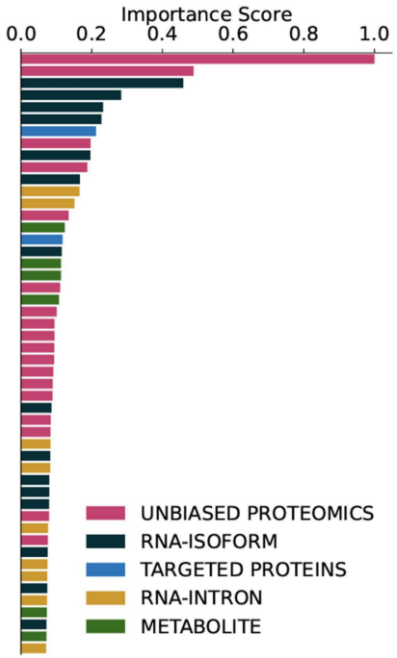
timsTOF HT Improves Protein Identification and Quantitative Reproducibility for Deep Unbiased Plasma Protein Biomarker Discovery

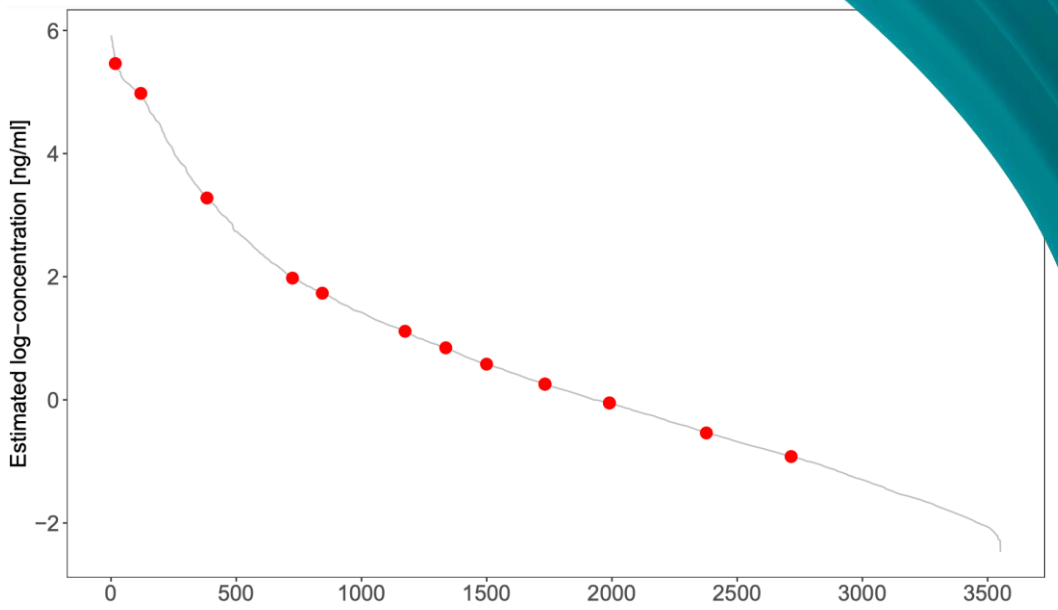
seer

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

Source: https://www.medrxiv.org/content/10.1101/2024.01.03.24300798v1

~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

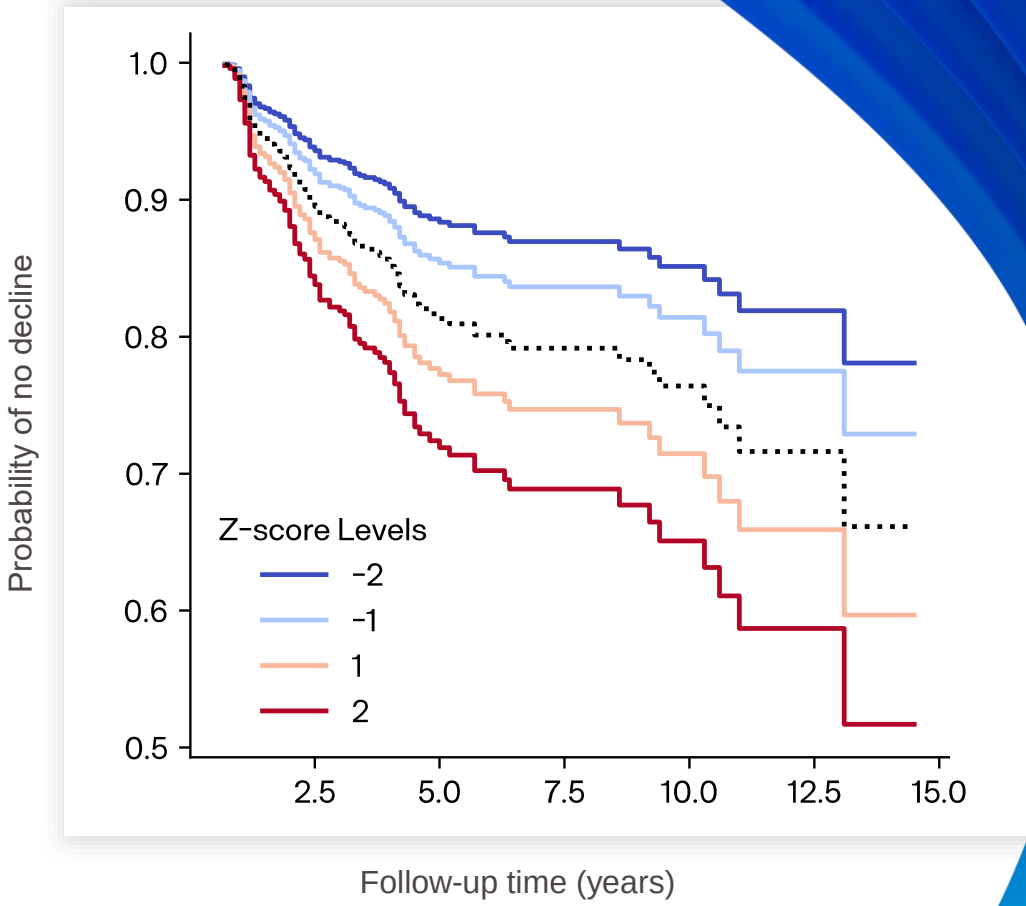
putative novel Alzheimer's disease biomarkers

8

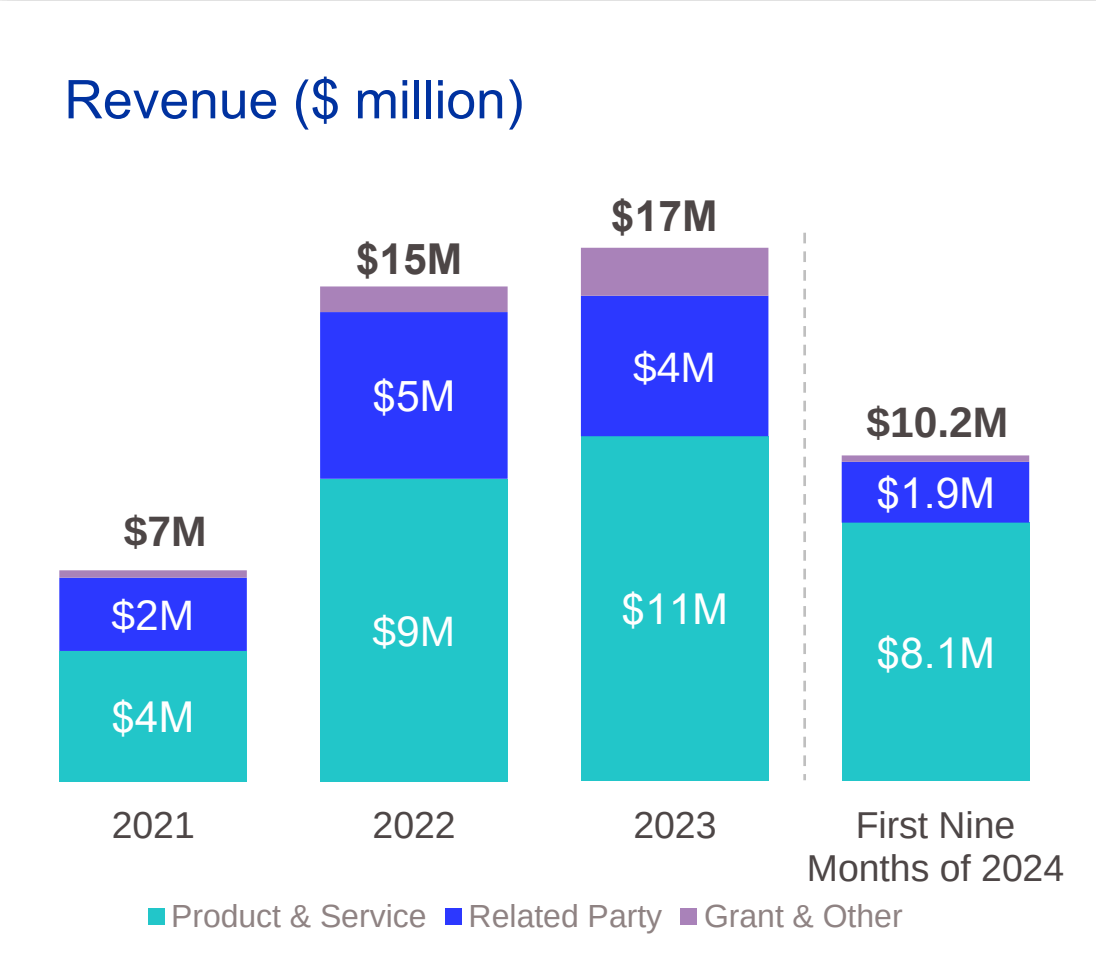
identified markers distinguishing fast and slow progressors of cognitive decline

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