seer

# Investor Presentation

September 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.

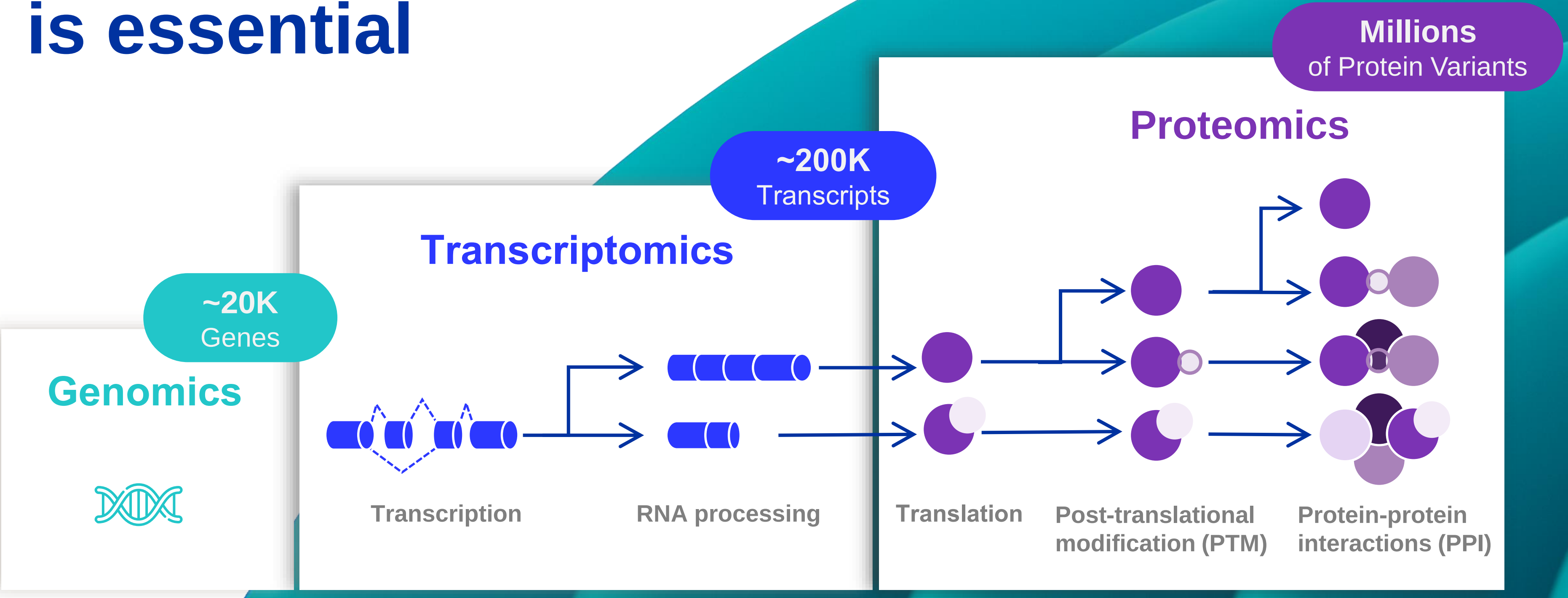
In light of the foregoing, investors are urged not to rely on any forward-looking statement in reaching any conclusion or making any investment decision about any securities of the Company.

We imagine and
pioneer new ways to

# decode the biology of the proteome

to improve human health

# Full characterization of the proteome is essential



**~20K**
Genes

## Genomics

**~200K**
Transcripts

## Transcriptomics

**Millions**
of Protein Variants

## Proteomics

Static → **Dynamic**

>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

Resource

Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing

Xinping Yang[1, 2, 3, 4, 17], Jasmin Coulombe-Huntington[5, 17, 19], Shuli Kang[6, 17, 18], Gloria M. Sheynkman[1, 2, 3, 17], Tong Hao[1, 2, 3, 17], Aaron Richardson[1, 2, 3], Song Sun[2, 8, 9, 10], Fan Yang[2, 8, 9], Yun A. Shen[1, 2, 3], Ryan R. Murray[2,

Science Translational Medicine

HOME > SCIENCE TRANSLATIONAL MEDICINE > VOL. 13, NO. 605 > TGFB2 AND TGFB3 ISOFORMS DRIVE FIBROTIC DISEASE PATHOGENESIS

RESEARCH ARTICLE | FIBROSIS

TGFβ2 and TGFβ3 isoforms drive fibrotic disease pathogenesis

TIANHE SUN, ZHIYU HUANG, WEI-CHING LIANG, JIANPING YIN, [...], AND JOSEPH R. ARRON +30 authors Authors Info & Affiliations

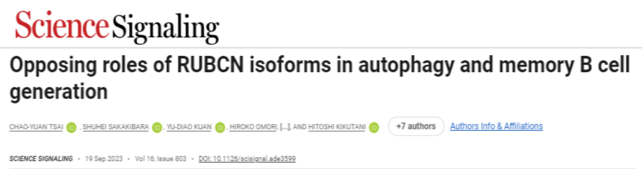
SCIENCE TRANSLATIONAL MEDICINE • 3 Aug 2021 • Vol 13, Issue 605 • DOI: 10.1126/scitranslmed.abe0407

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

CHAO-YUAN TSAI, SHUHEI SAKAKIBARA, YU-DIAO KUAN, HIROKO OMORI, [...], AND HITOSHI KIKUTANI +7 authors Authors Info & Affiliations

SCIENCE SIGNALING • 19 Sep 2023 • Vol 16, Issue 803 • DOI: 10.1126/scisignal.ade3599

# 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**

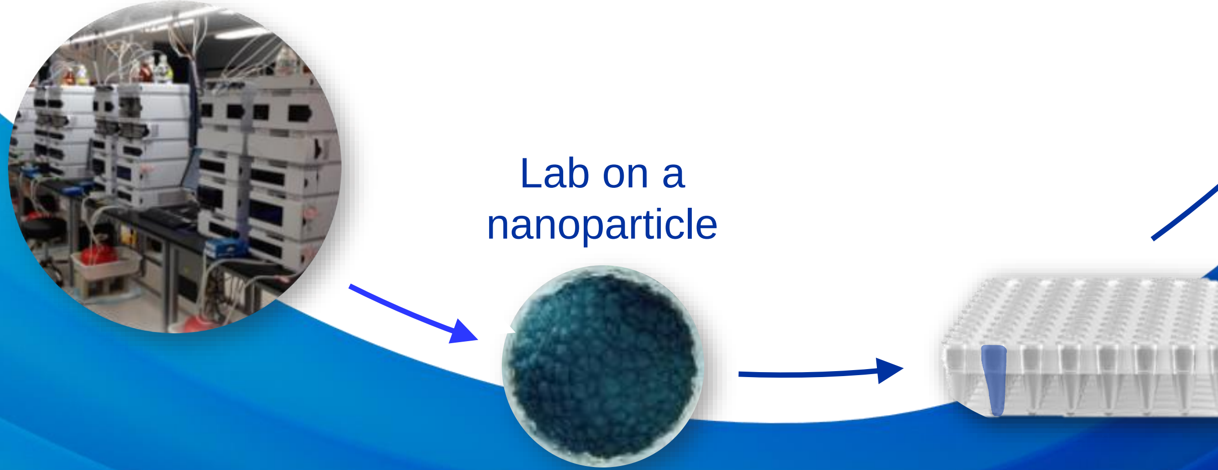
# Seer is positioned to lead the proteomics revolution

**Deep, unbiased, high-throughput**

Able to analyze 10,000+ samples per year

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

Taking advantage of the way proteins interact



Unbiased

Deep

Large-scale

Rapid

seer

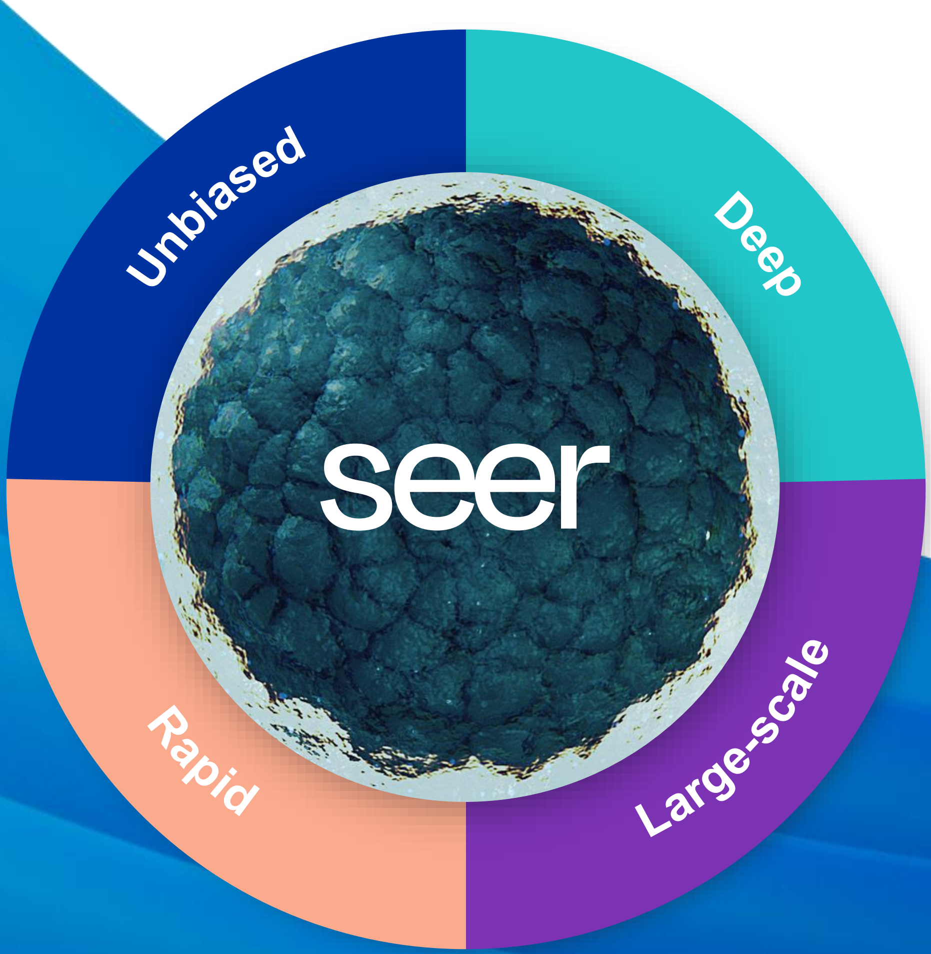
A new gateway to the proteome

# 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

Genomics

~$28B

Proteomics

~$27B

Academic

Translational

Commercial

Pharma

Applied

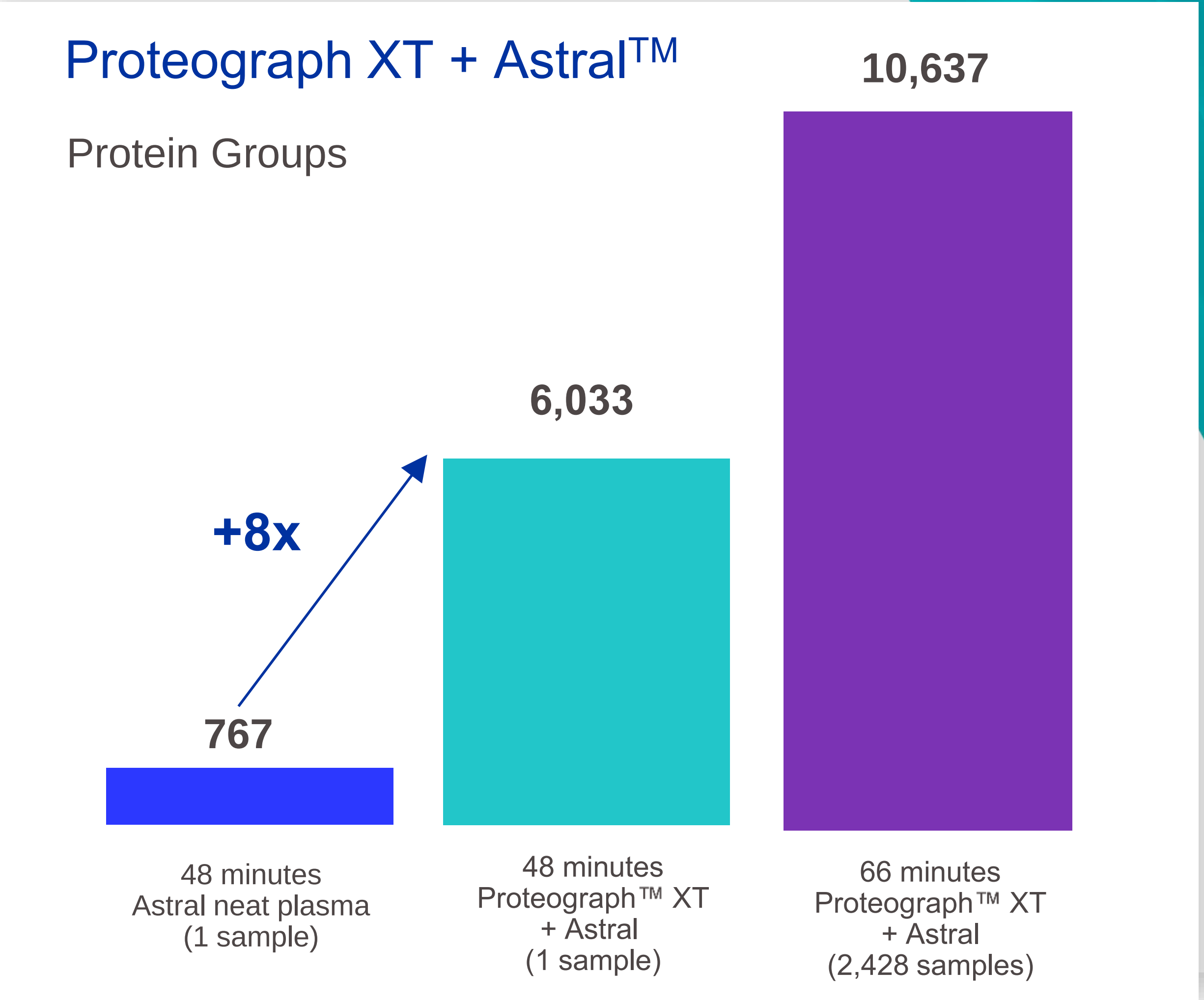
Sources: Allied Market Research, Technavio estimates for 2022

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

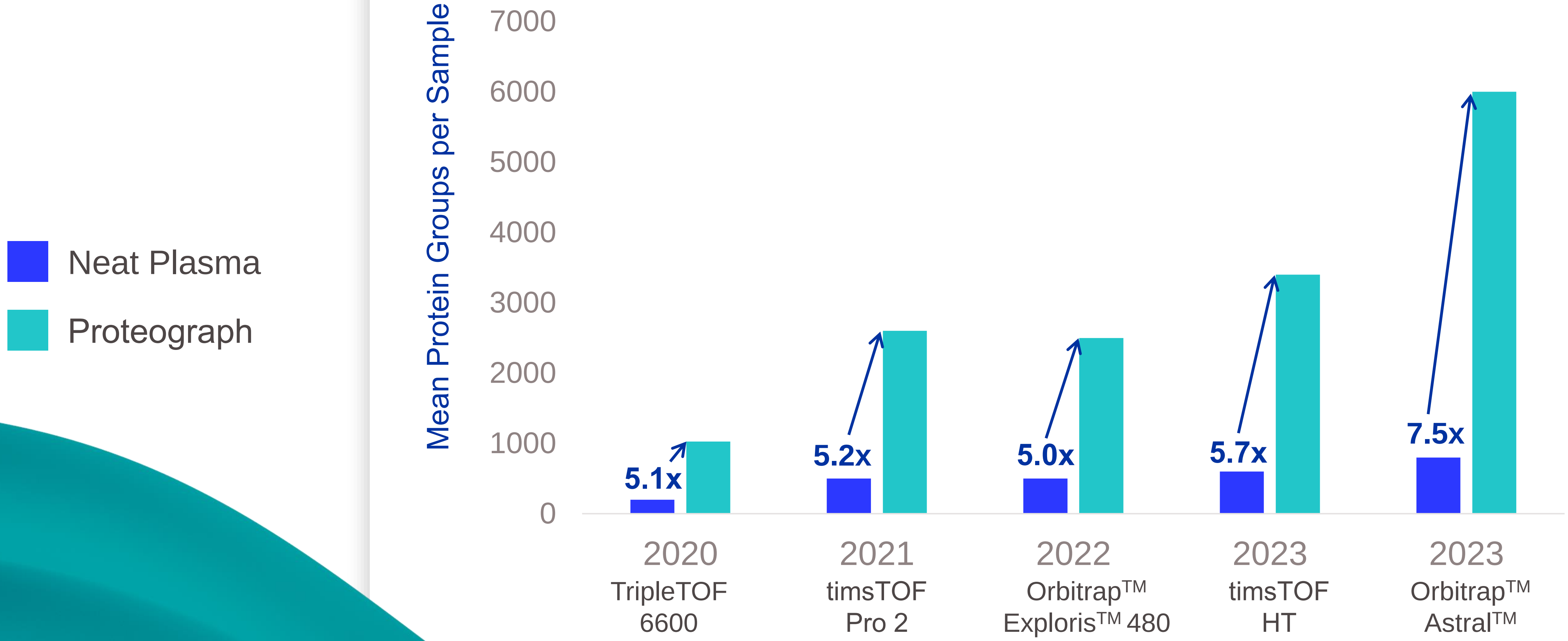
**2.5x sample throughput** without sacrificing depth

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

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



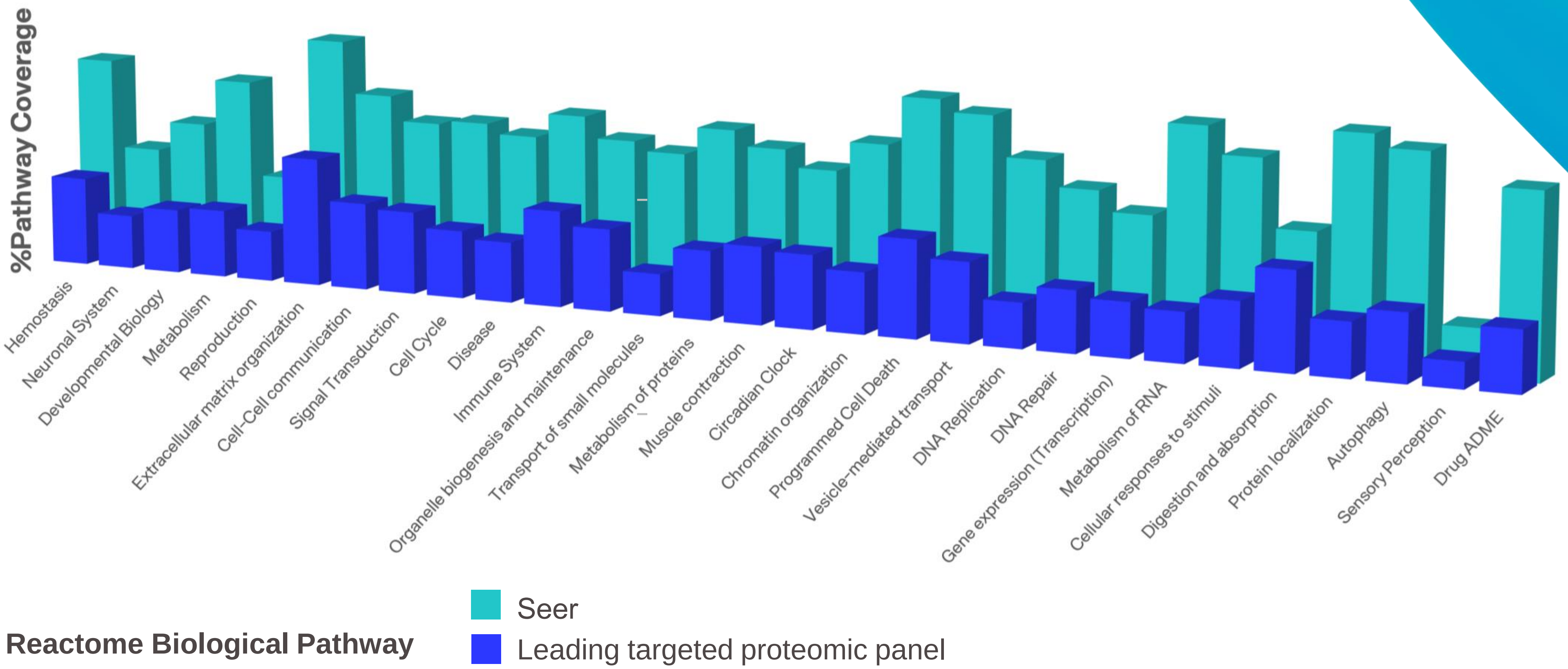
# Seer’s Proteograph consistently improves mass spec performance



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

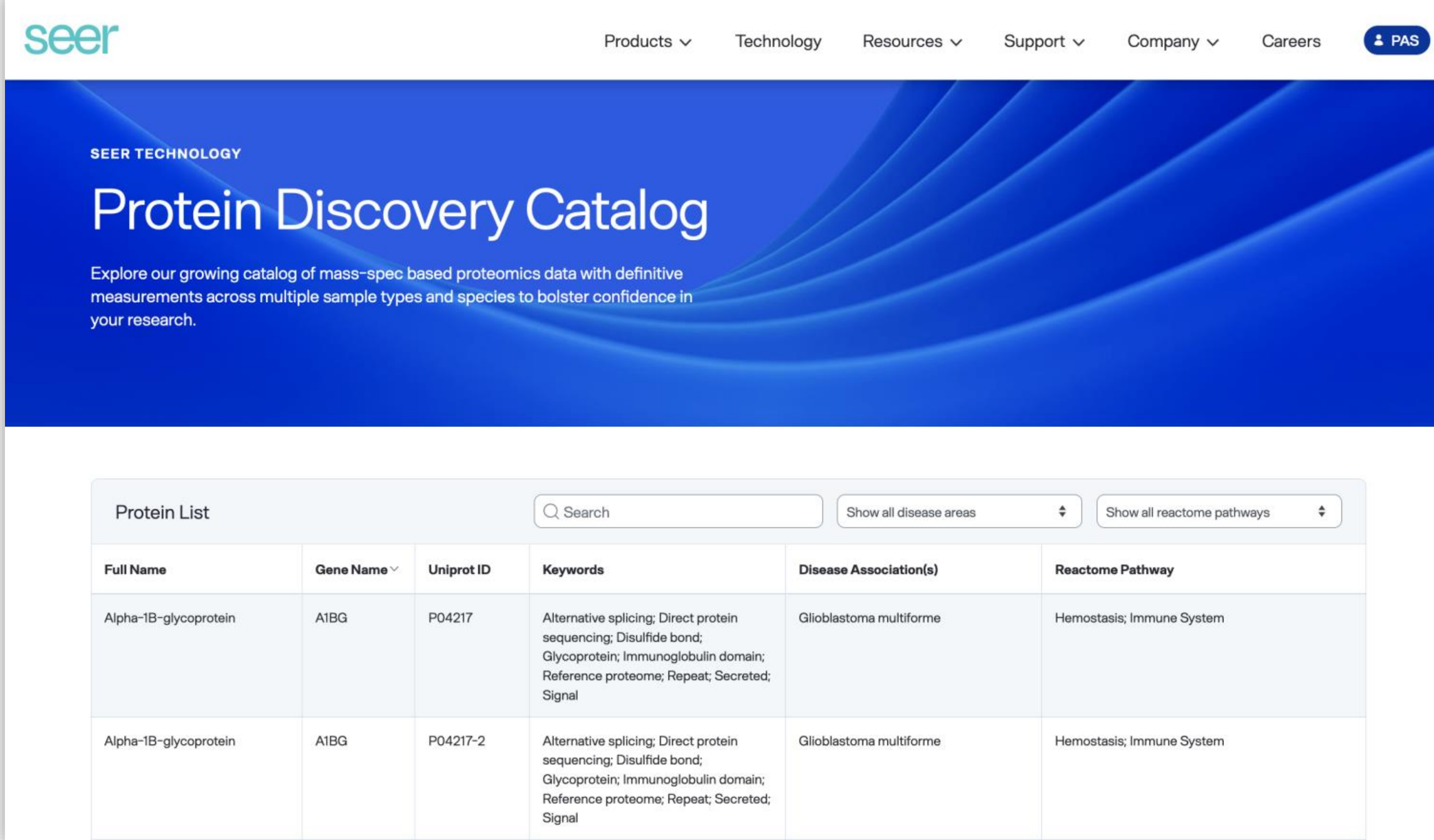
**150,000+ peptides, 10,000+ human proteins, >1,900 biological pathways**



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

# Seer’s Protein Discovery Catalog enables the discovery of biological value

- Growing catalog of 36,000+ proteins across multiple species
- Enables discovery of proteins associated with 100,000+ possible biomarkers
- Includes proteins not yet associated with diseases
- Adds precision, insights, and opportunities for biomarker discovery to genomics and proteomics studies



SEER TECHNOLOGY

Protein Discovery Catalog

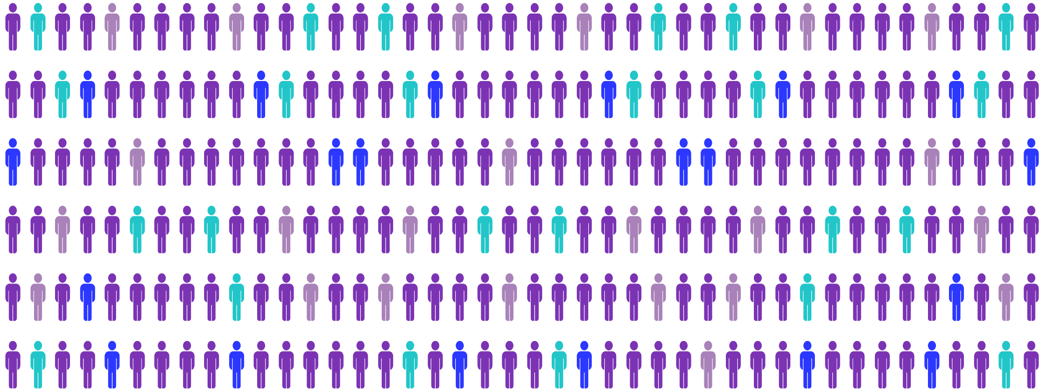
Explore our growing catalog of mass-spec based proteomics data with definitive measurements across multiple sample types and species to bolster confidence in your research.

Protein List

| Full Name | Gene Name | Uniprot ID | Keywords | Disease Association(s) | Reactome Pathway |
|---|---|---|---|---|---|
| Alpha-1B-glycoprotein | A1BG | P04217 | Alternative splicing; Direct protein sequencing; Disulfide bond; Glycoprotein; Immunoglobulin domain; Reference proteome; Repeat; Secreted; Signal | Glioblastoma multiforme | Hemostasis; Immune System |
| Alpha-1B-glycoprotein | A1BG | P04217-2 | Alternative splicing; Direct protein sequencing; Disulfide bond; Glycoprotein; Immunoglobulin domain; Reference proteome; Repeat; Secreted; Signal | Glioblastoma multiforme | Hemostasis; Immune System |

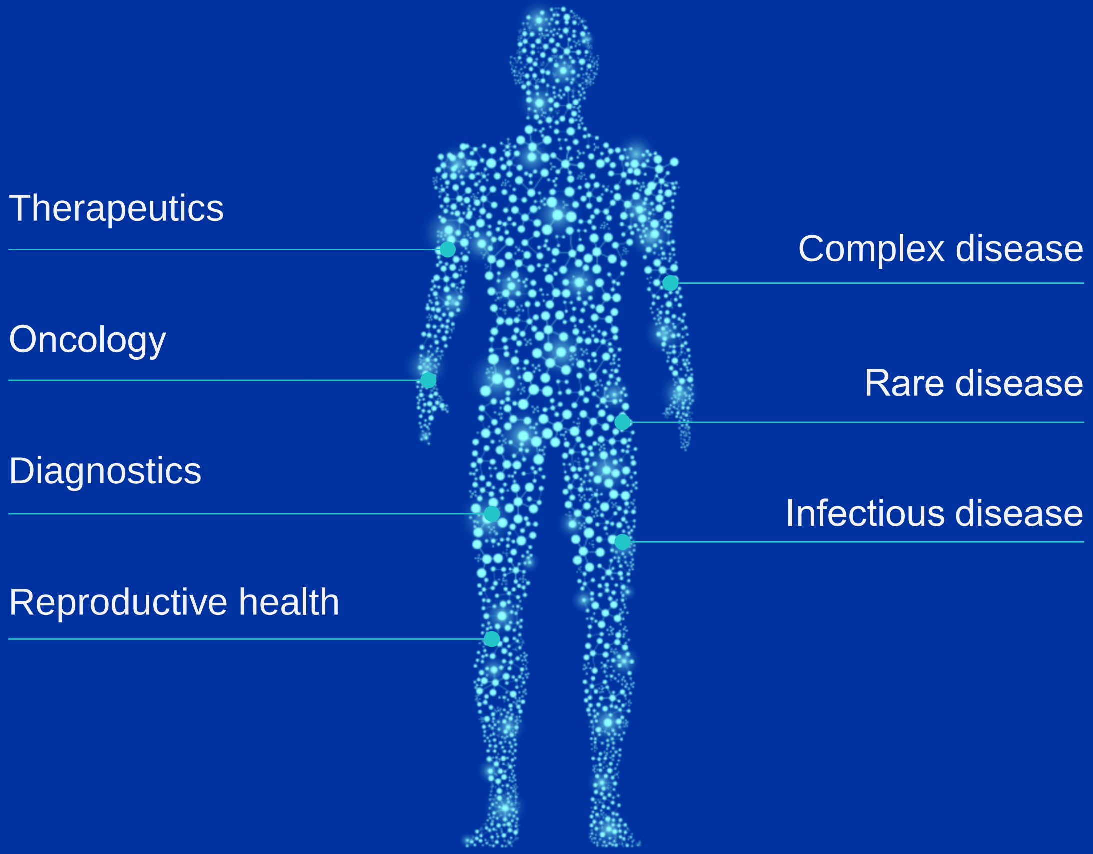
# Functional implication of protein variants across the population is massive

## Population (~455,000 individuals)



| **All protein genetic variants** | **8,868,971** |
|---|---|
| Potential deleterious variants | 6,345,457 |
| Protein loss of function | 915,289 |
| Change protein structure/binding | > 3 million |

## Proteogenomics



Therapeutics

Oncology

Diagnostics

Reproductive health

Complex disease

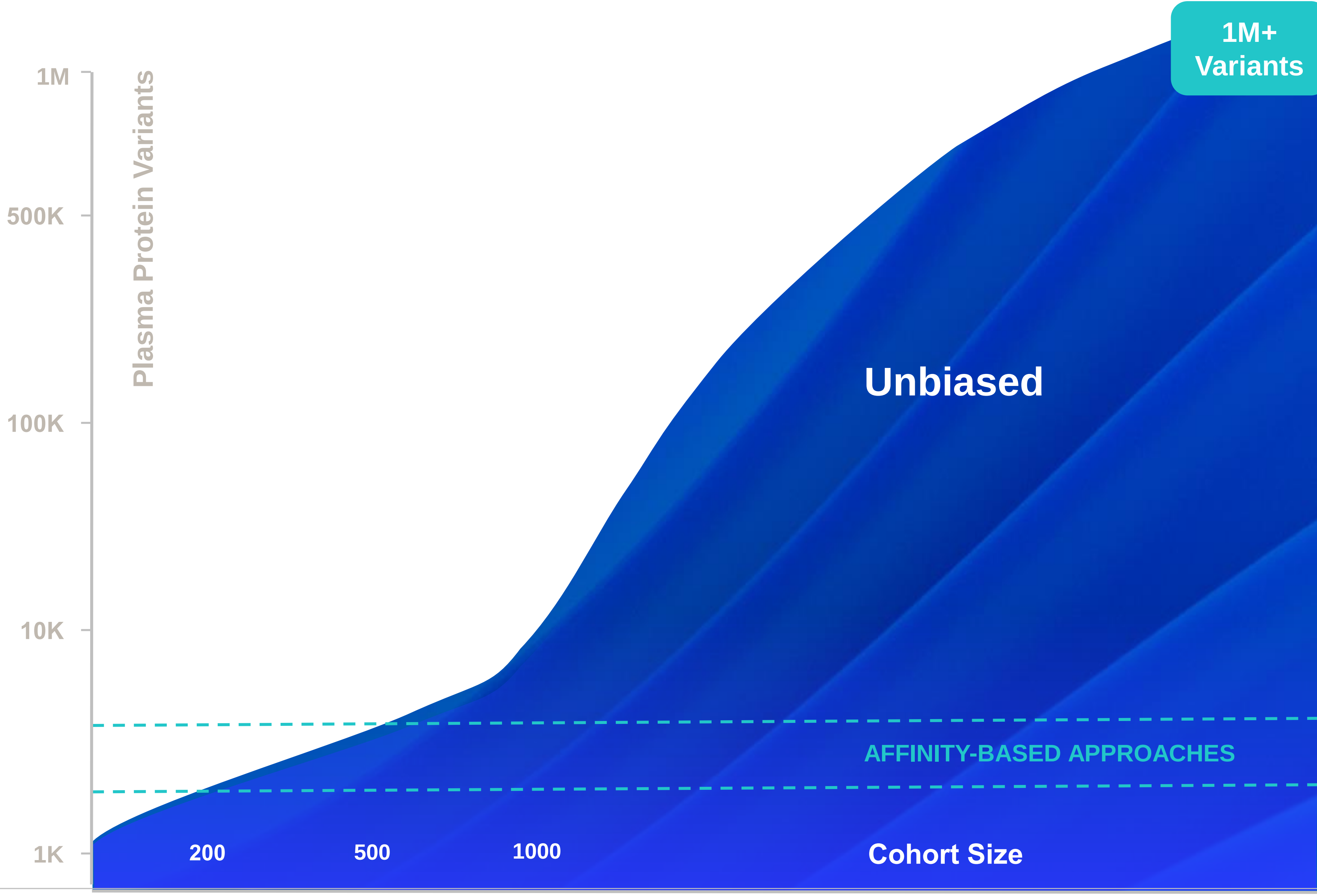
Rare disease

Infectious disease

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

# Proteograph enables proteomic content discovery

**To date, we have seen 10,000+ human proteins and 150,000+ peptides and the numbers are growing**



# 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**

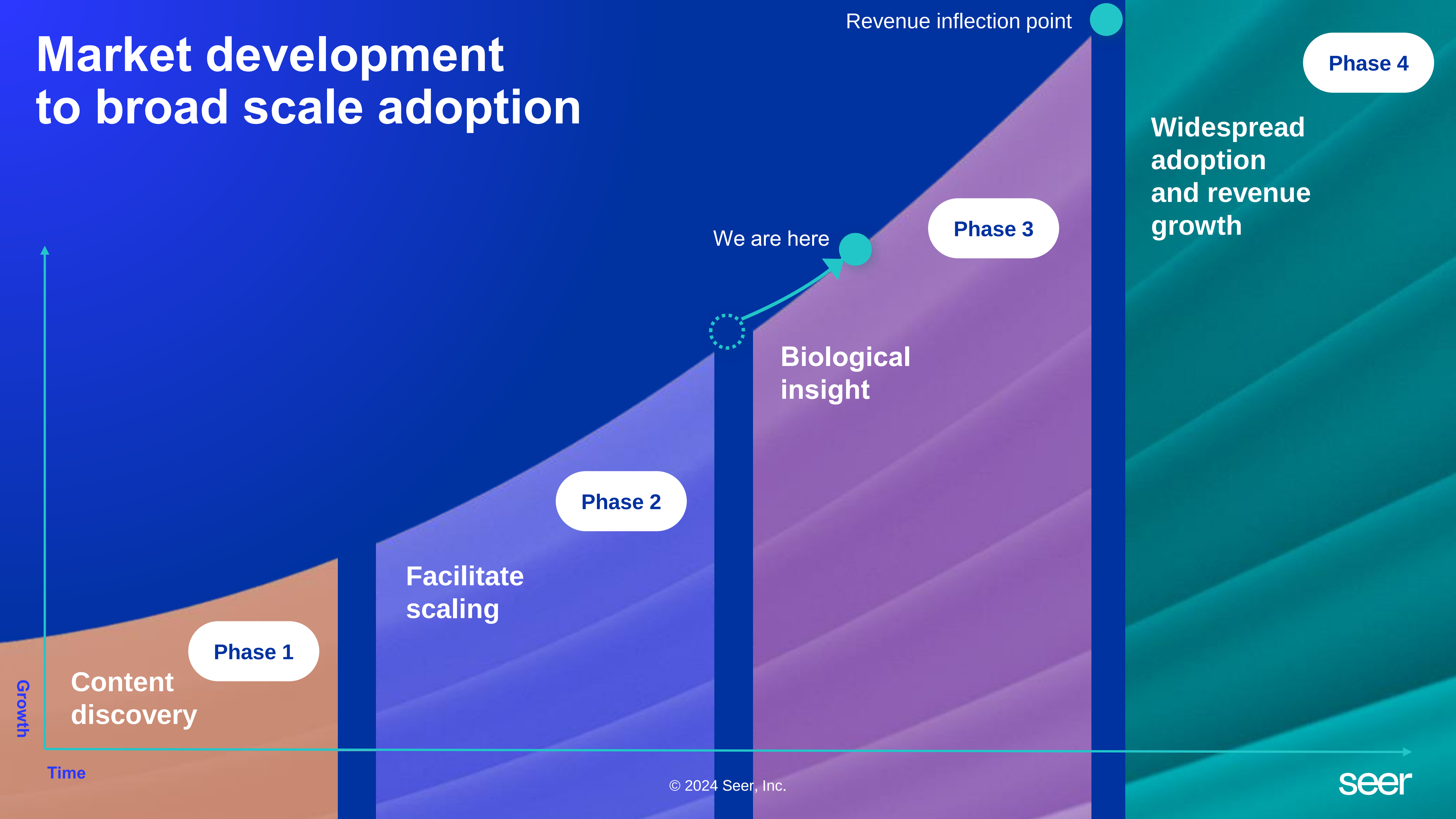
**66** **Organizations served**

**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



seer

# Growing validation of Seer technology


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

**9**

Manuscripts in bioRxiv

**18**

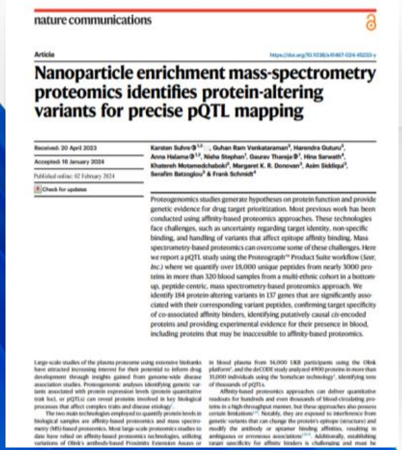
Peer-reviewed articles


Journal of proteome research

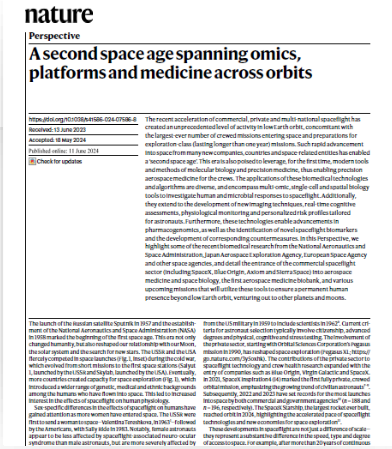
timsTOF HT Improves Protein Identification and Quantitative Reproducibility for Deep Unbiased Plasma Protein Biomarker Discovery

nature COMMUNICATIONS

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


nature communications

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


nature

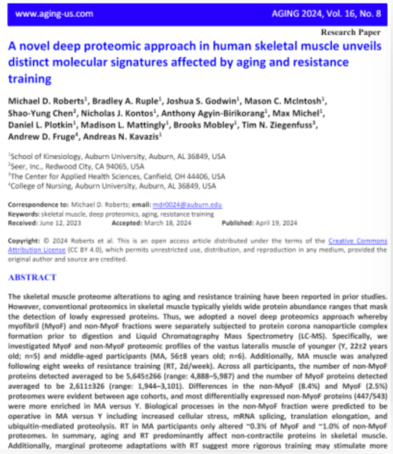
Perspective

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


FASEB Journal

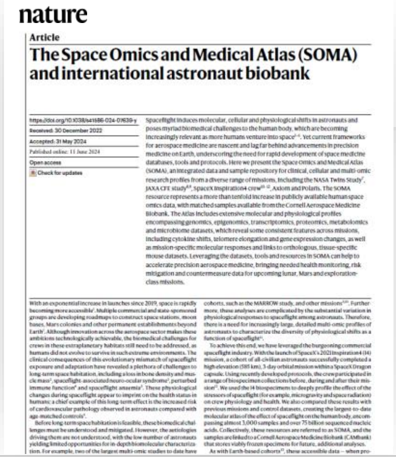
RESEARCH ARTICLE

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

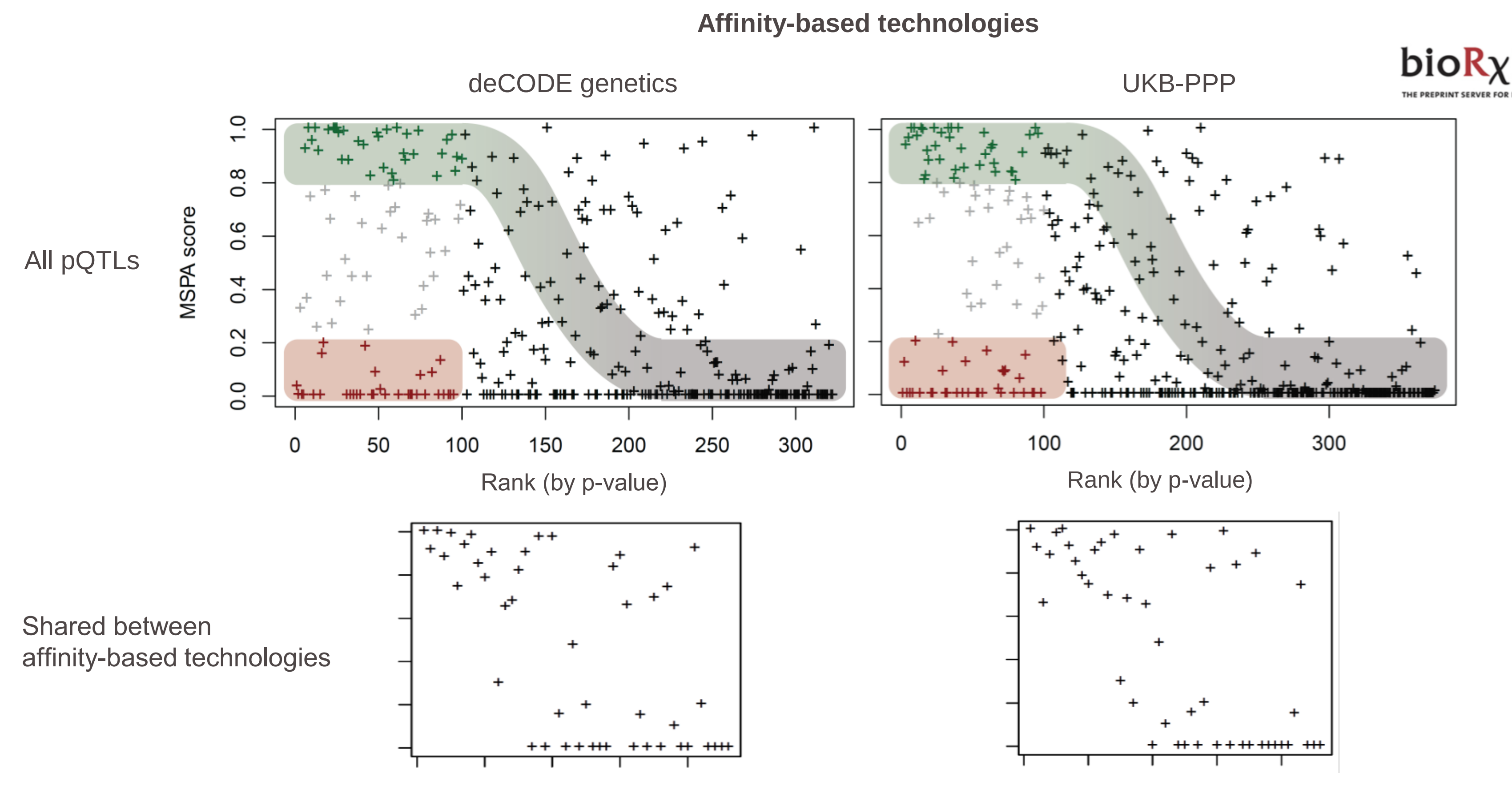

nature communications

Article

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

# Proteograph distinguishes between true pQTLs and false positives

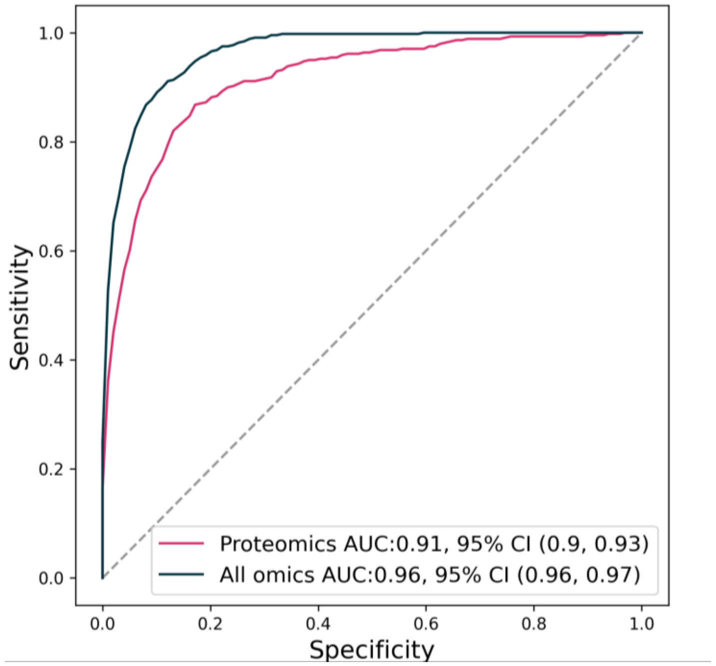
- **First large-scale pQTL study** using Proteograph for deep, unbiased proteomics with mass spec
- **Up to one third** of strongest pQTLs identified with affinity-based proteomics technologies in two cohorts are **likely false** due to epitope effects
- Follows *Nature Communications* publication demonstrating the ability of the Proteograph to **properly account for variant peptides**



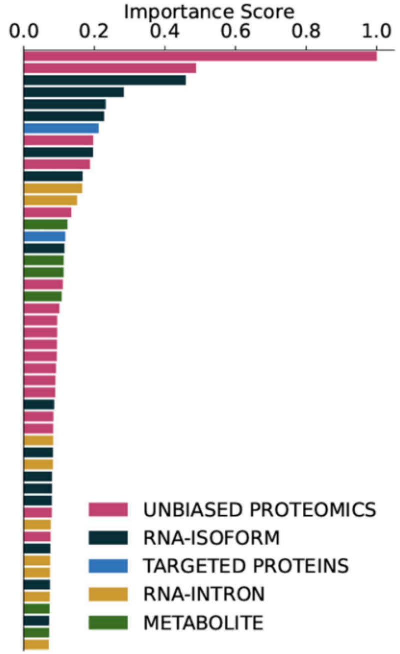
Suhre, K., et al. A genome-wide association study of mass spectrometry proteomics using the Seer Proteograph platform. BioRxiv

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

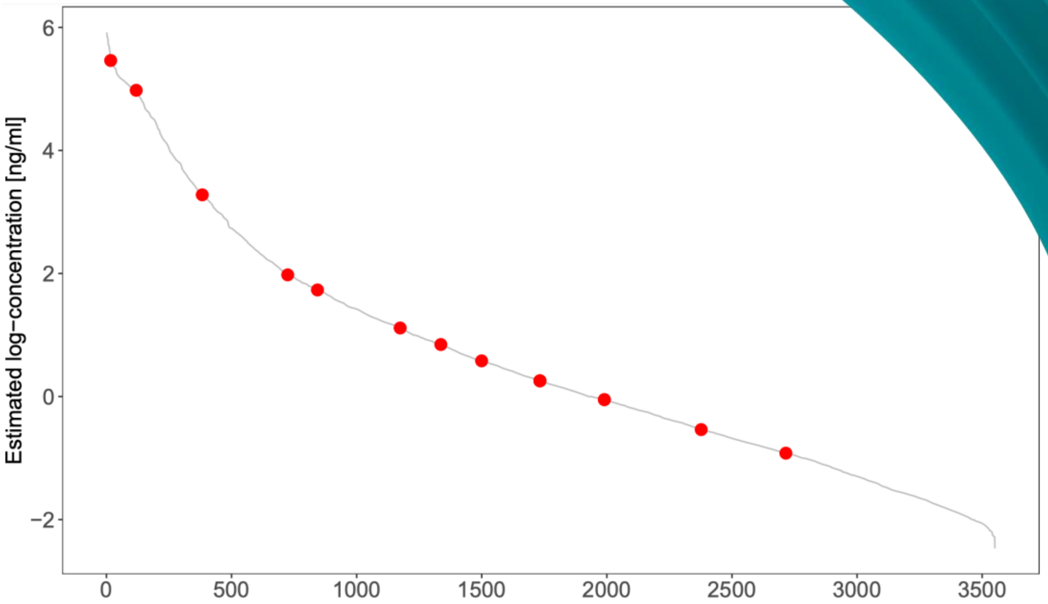
Multi-omics profiling detected >13,000 proteins groups, >200,000 RNA transcripts, and >1,000 metabolites



- ✓ 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

MGH / SEER DATA

# ~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**

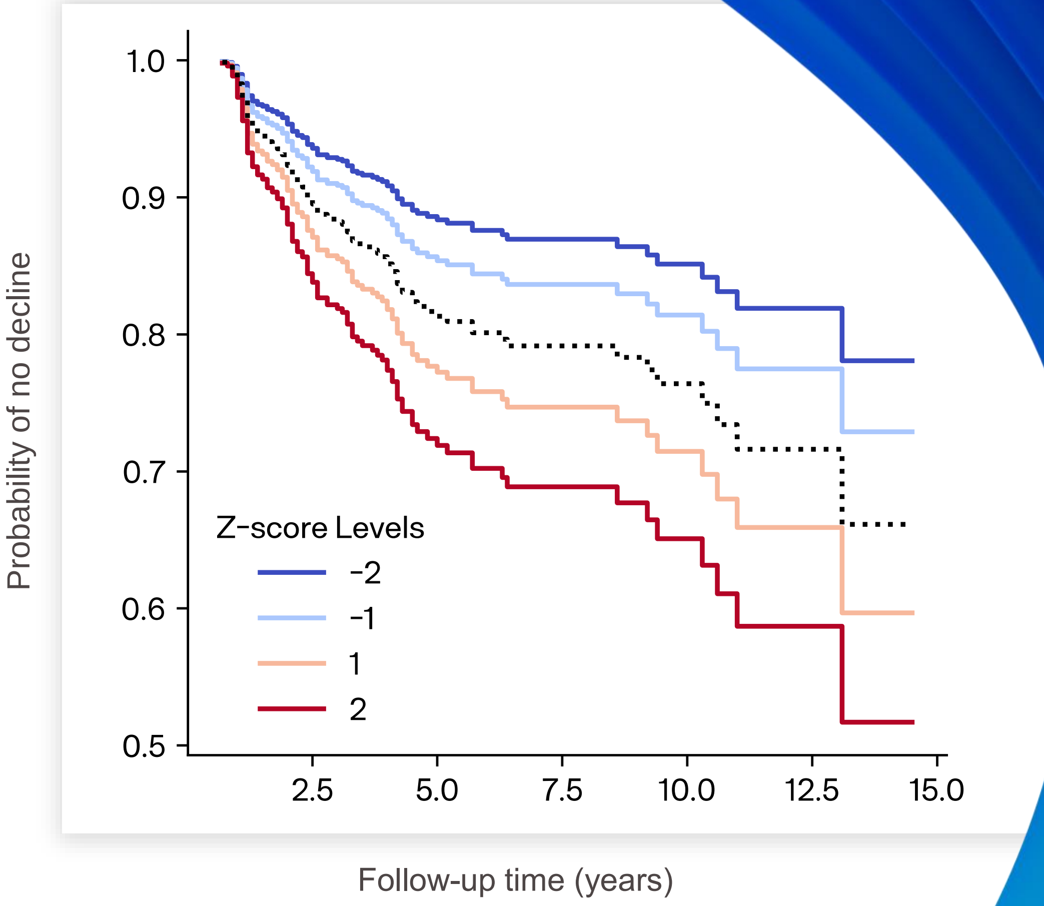
putative novel Alzheimer's disease biomarkers

**8**

identified markers distinguishing fast and slow progressors of cognitive decline

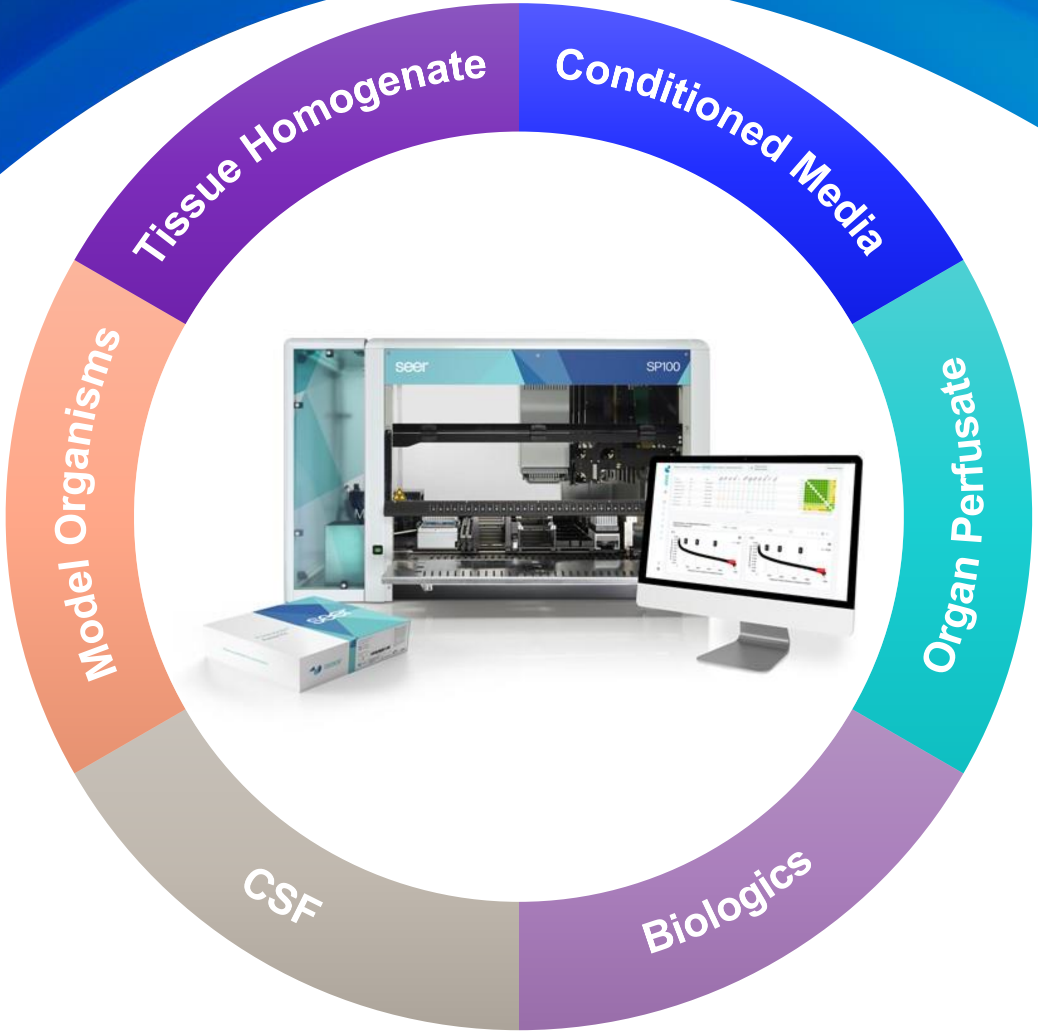
**75%**

are not present on high-plex affinity panel

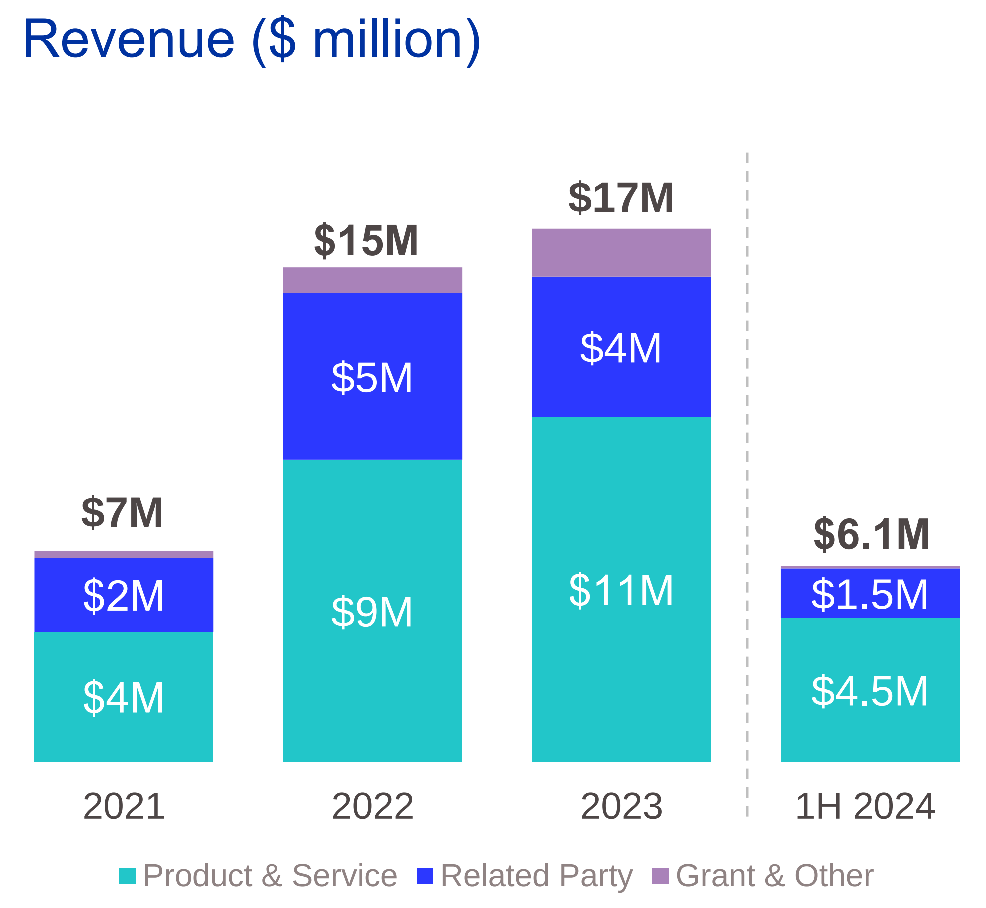


seer

# Apps Lab continues to expand protocols, sample types & applications



# Enhancing access to Proteograph while preserving strong balance sheet



**$344.6 million**
cash, cash equivalents and investments, no debt as of June 30, 2024

**50% gross margin** in 1H 2024

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

Authorized **$25 million**
open-market repurchase program in Q1 2024

# Focus areas for 2024

1

## Drive evidence and publications

Deliver cohort studies and strategic collaborations to drive third-party data and evidence

2

## Continue to enhance access

Continue to enhance market access and drive additional revenue through STAC

3

## Product innovation and application expansion

Address customer adoption barriers with new automation, assays, and software to improve performance, throughput, and lower cost

seer