seer

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.

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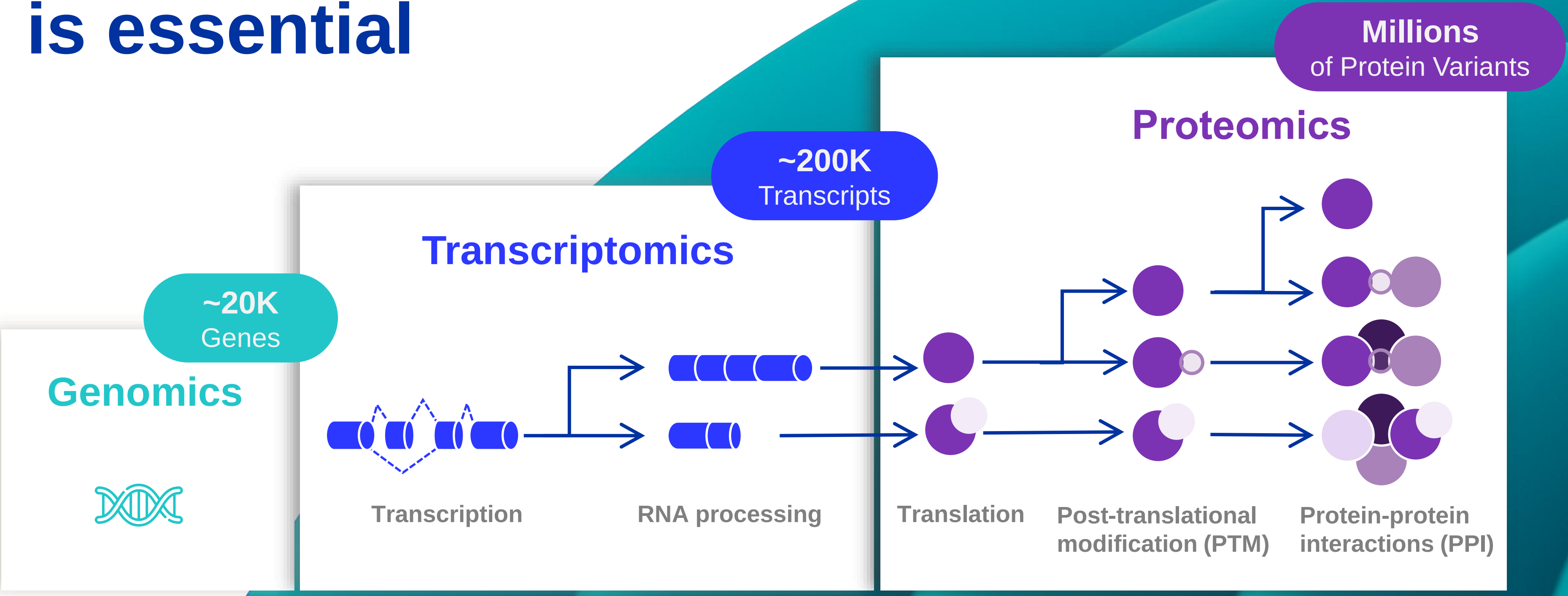
In light of the foregoing, investors are urged not to rely on any forward-looking statement in reaching any conclusion or making any investment decision about any securities of the Company.

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

Transcription

RNA processing

Millions
of Protein Variants

Proteomics

Translation

Post-translational modification (PTM)

Protein-protein interactions (PPI)

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

CellPress

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, 20], 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

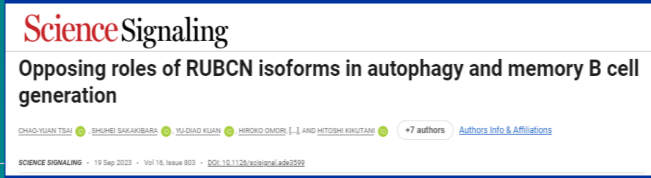
SCIENCE TRANSLATIONAL MEDICINE • 3 Aug 2021 • Vol 13, Issue 605 • DOI: 10.1126/scitranslmed.abe0407

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

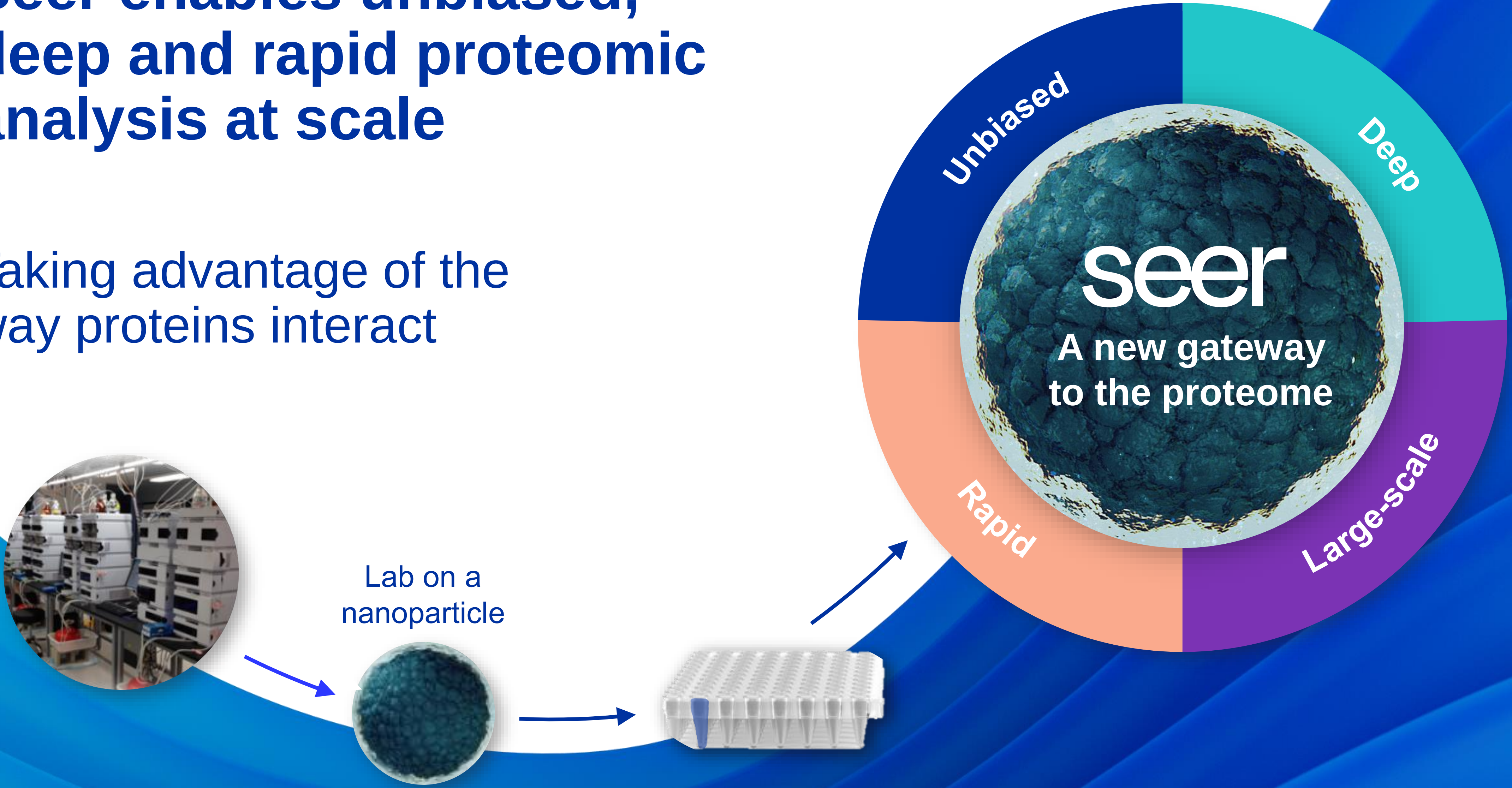
Seer is positioned to lead the proteomics revolution

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

seer

A new gateway to the proteome

Unbiased

Deep

Large-scale

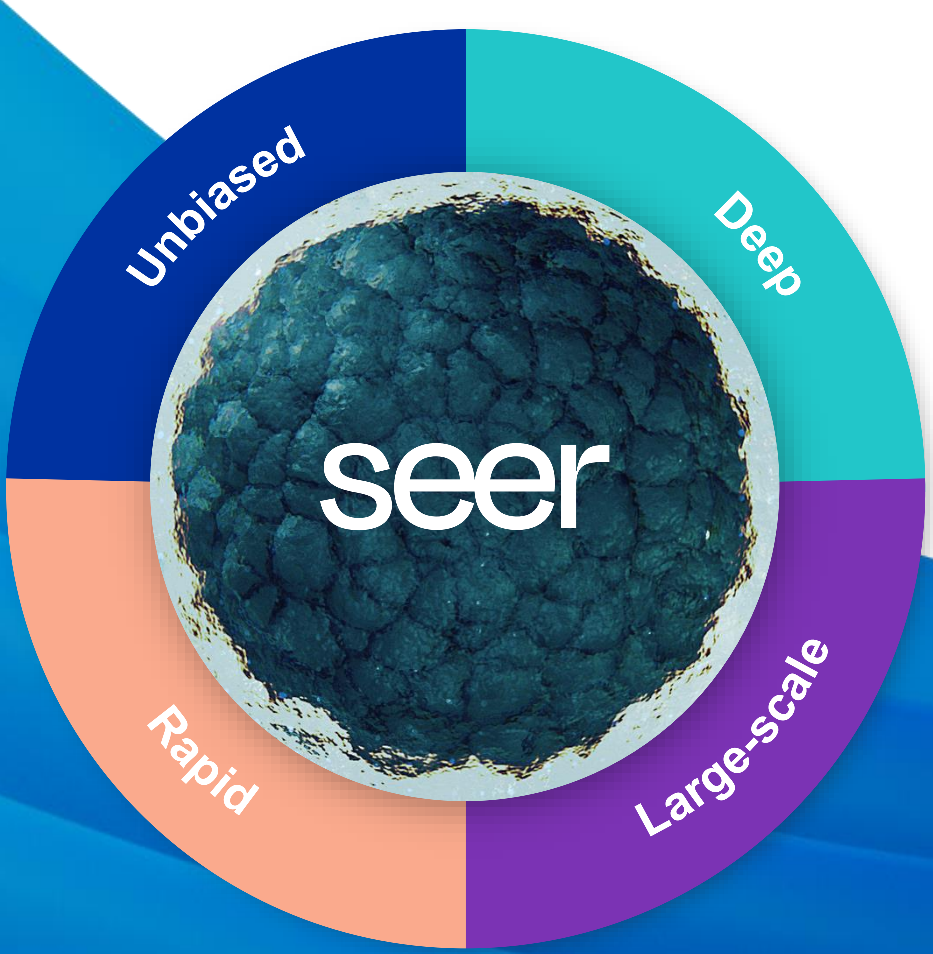
Rapid

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

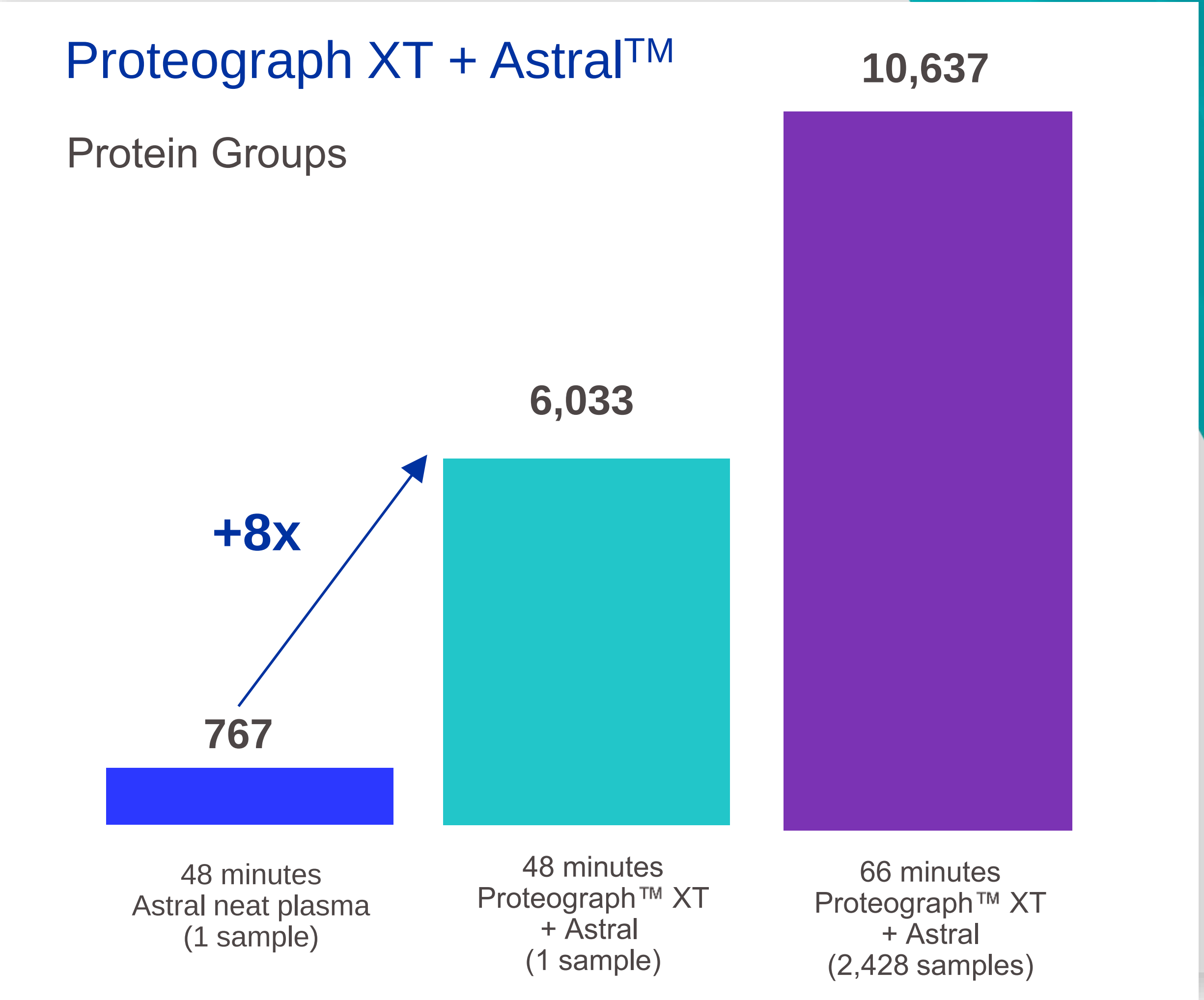
Sources: Allied Market Research, Technavio estimates for 2022

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

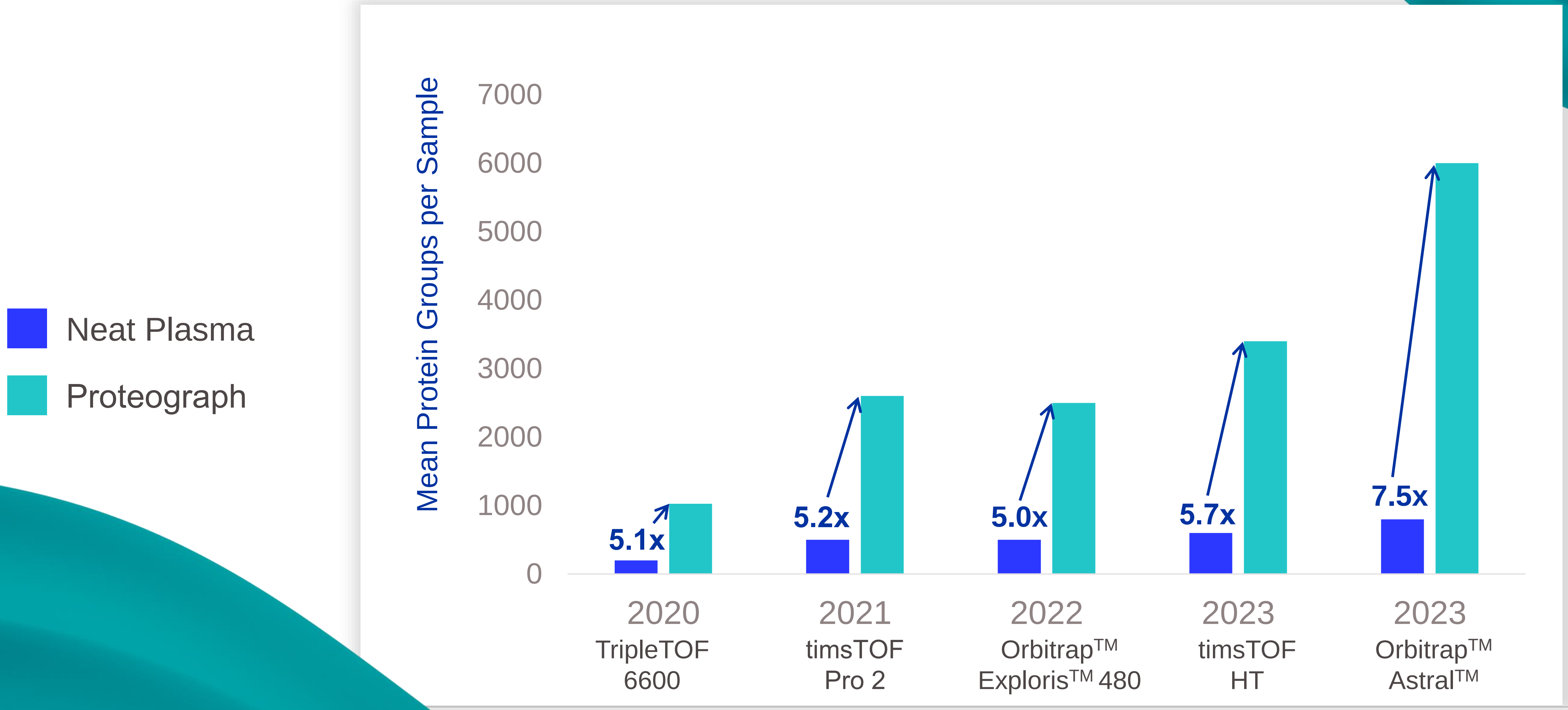
2.5x sample throughput
without sacrificing depth

Significantly more proteins detected by mass spec with Seer technology

~80% of installed base
using Proteograph XT



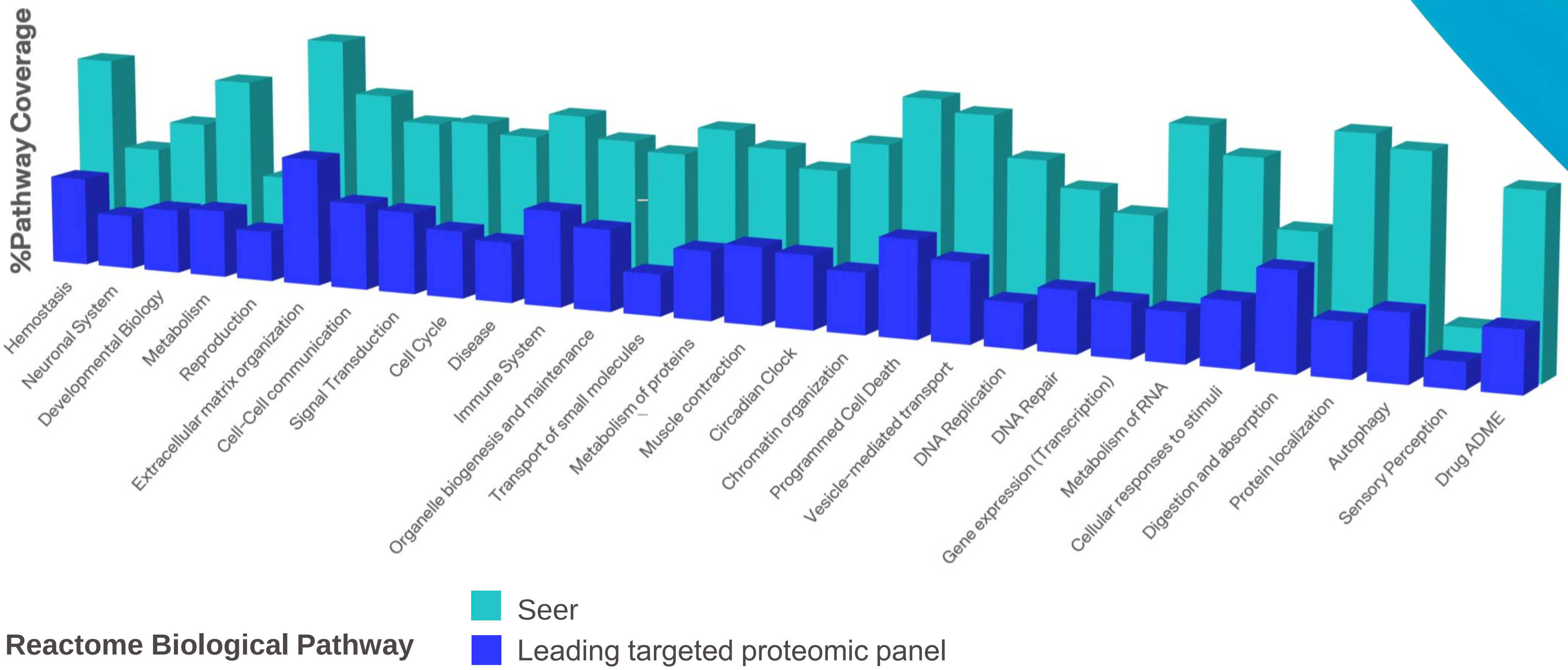
Seer's Proteograph consistently improves mass spec performance



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

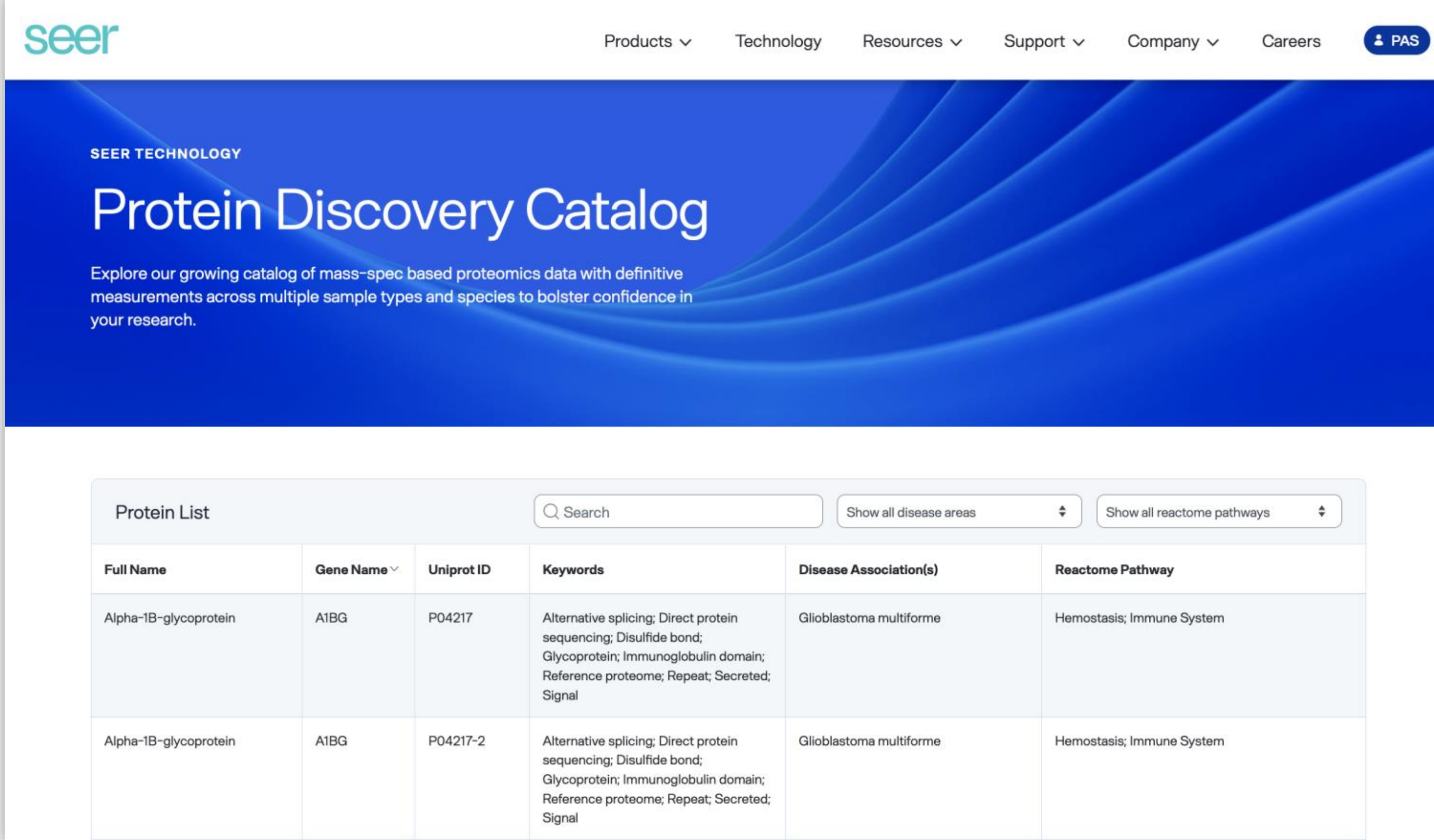
150,000+ peptides, 10,000+ human proteins, >1,900 biological pathways



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

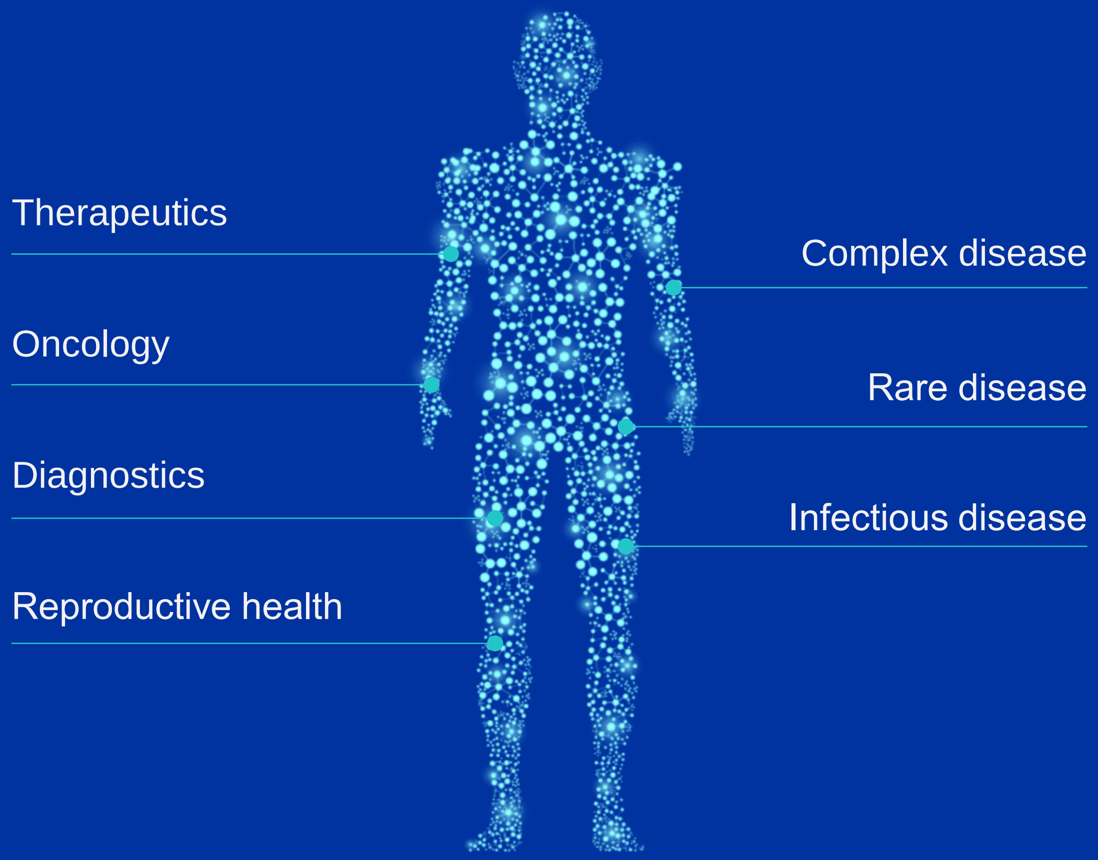
Full Name	Gene Name	Uniprot ID	Keywords	Disease Association(s)	Reactome Pathway
Alpha-1B-glycoprotein	A1BG	P04217	Alternative splicing; Direct protein sequencing; Disulfide bond; Glycoprotein; Immunoglobulin domain; Reference proteome; Repeat; Secreted; Signal	Glioblastoma multiforme	Hemostasis; Immune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

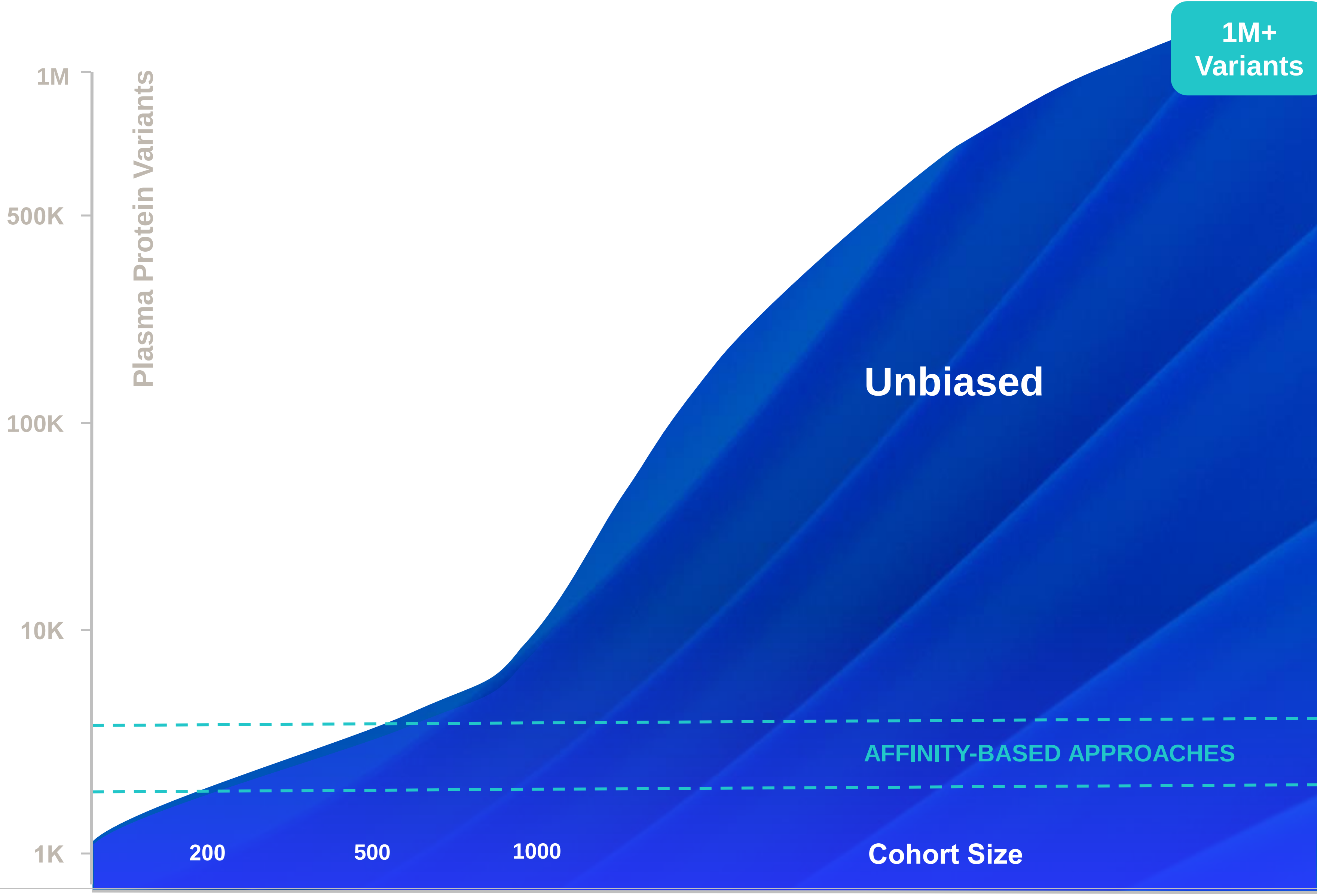
Rare disease

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

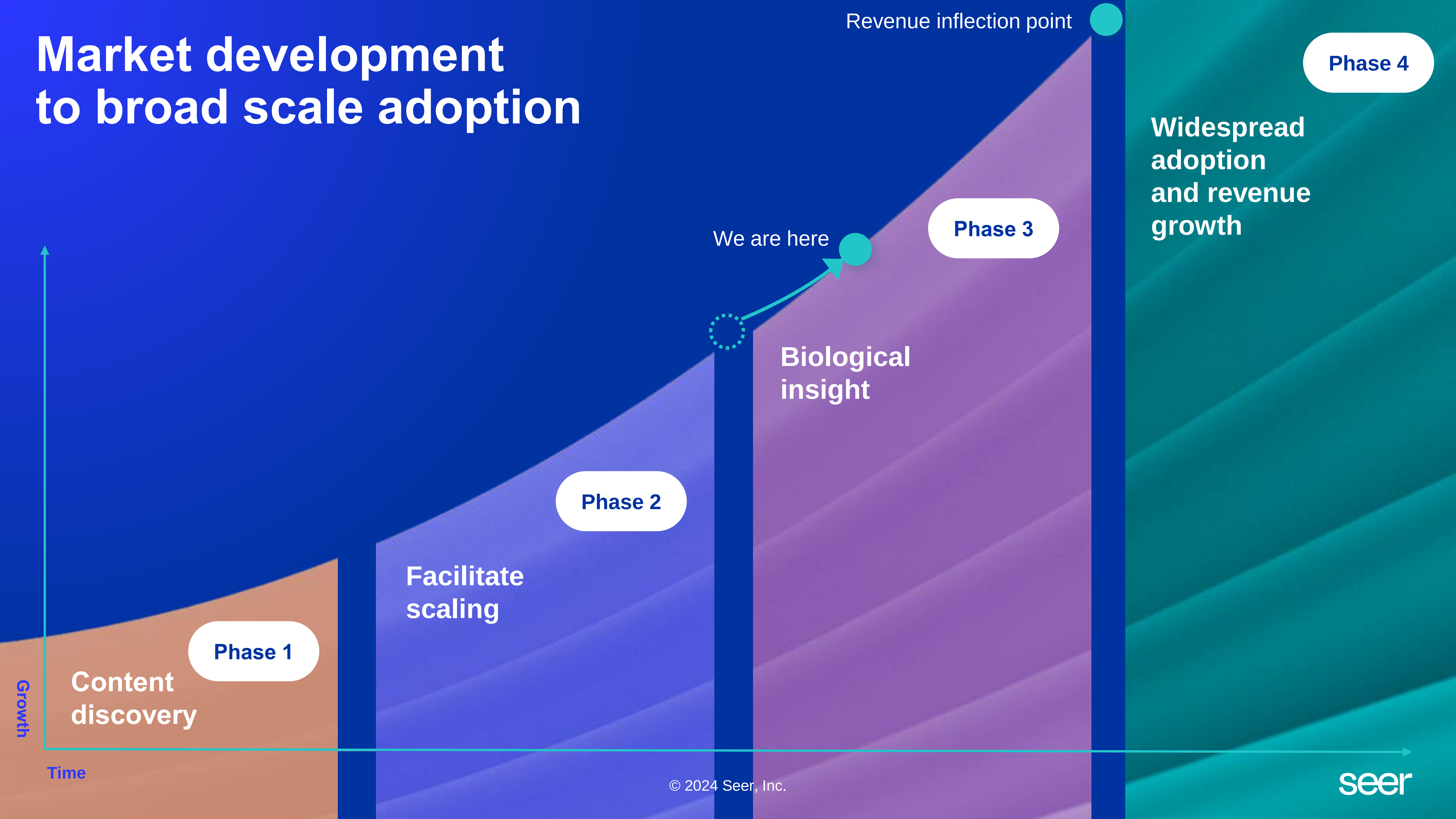
66 **Organizations served**

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



Phase 1

Content discovery

Phase 2

Facilitate scaling

We are here

Phase 3

Biological insight

Revenue inflection point

Phase 4

Widespread adoption and revenue growth

Growing validation of Seer technology

PNAS

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

Significance

Journal of proteome research

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

10

Manuscripts in bioRxiv

19

Peer-reviewed articles

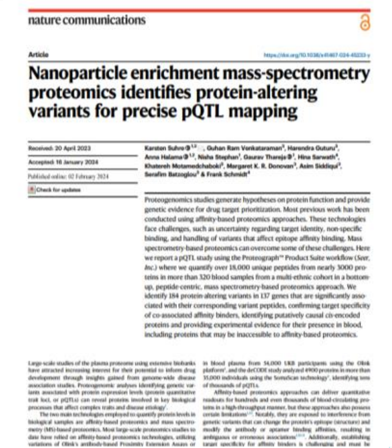
Journal of proteome research

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

nature COMMUNICATIONS

ARTICLE

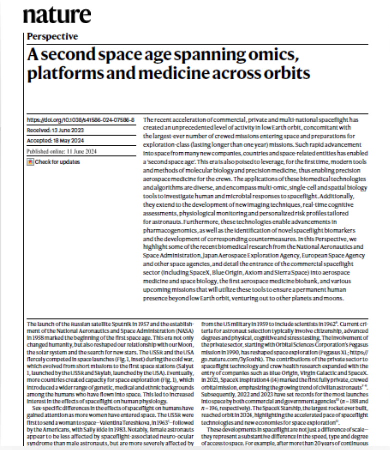
Rapid, deep and precise profiling of the plasma proteome with multi-nanoparticle protein corona



nature communications

Article

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



nature

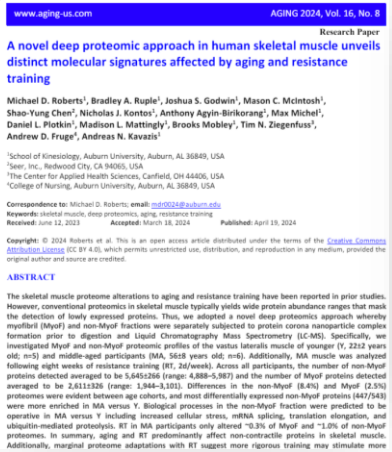
Perspective

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

RESEARCH ARTICLE

FASEB Journal

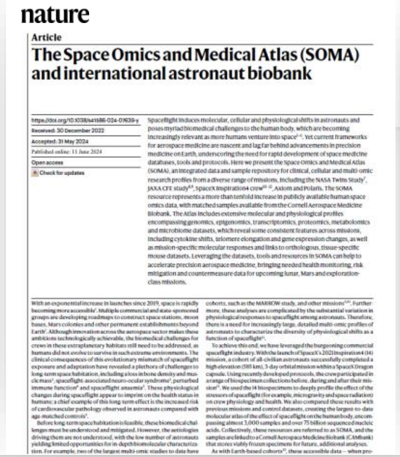
Resistance training rejuvenates the mitochondrial methylome in aged human skeletal muscle



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

Research Paper

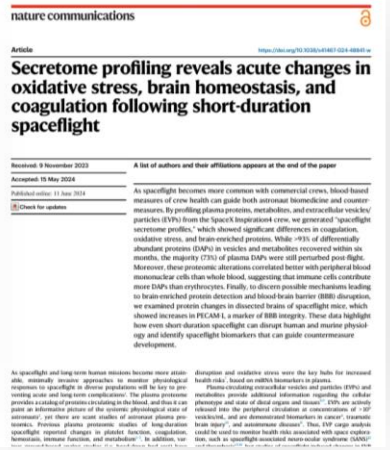
A novel deep proteomic approach in human skeletal muscle unveils distinct molecular signatures affected by aging and resistance training



nature

Article

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



nature communications

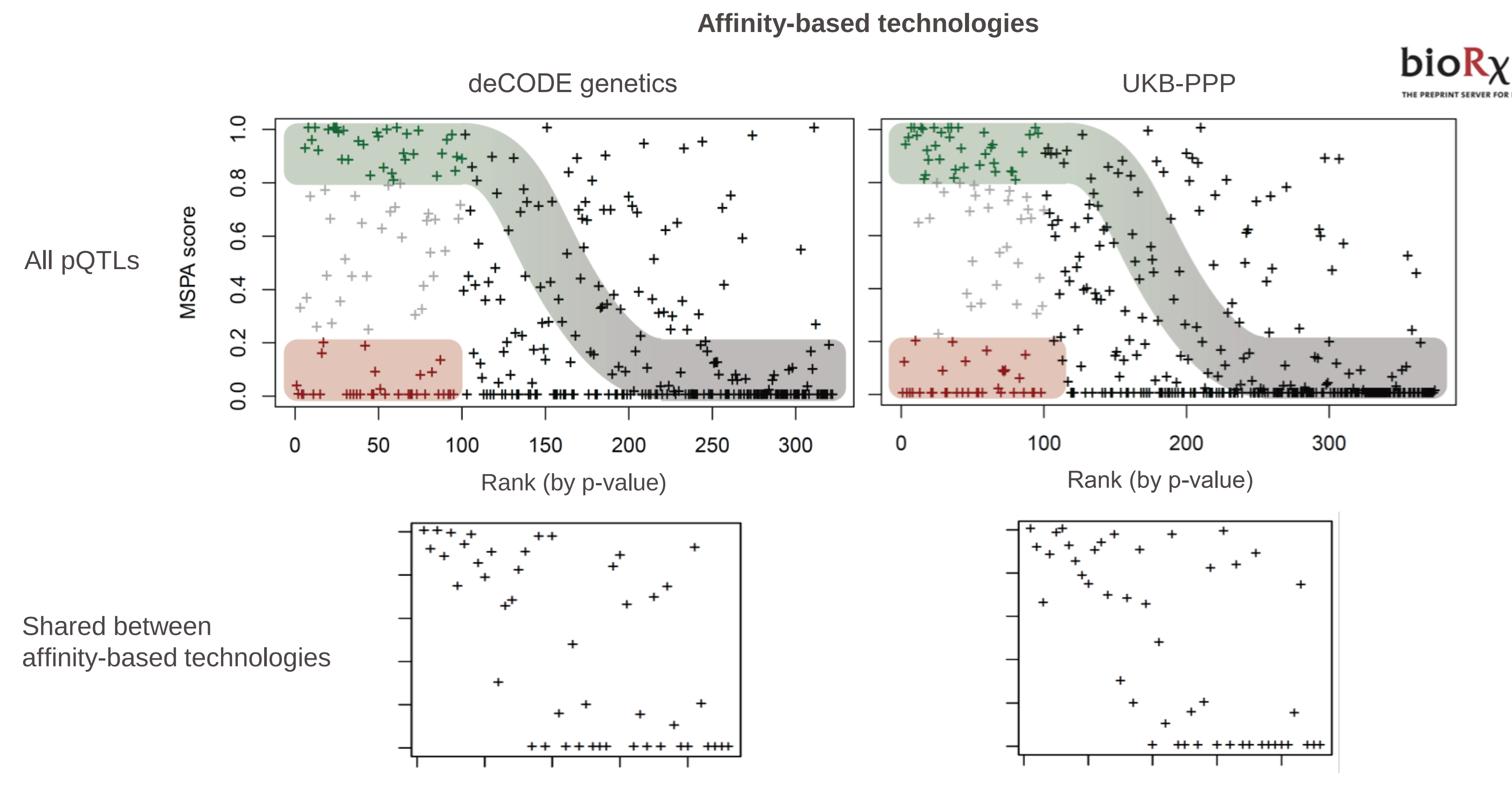
Article

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

seer

Proteograph distinguishes between true pQTLs and false positives

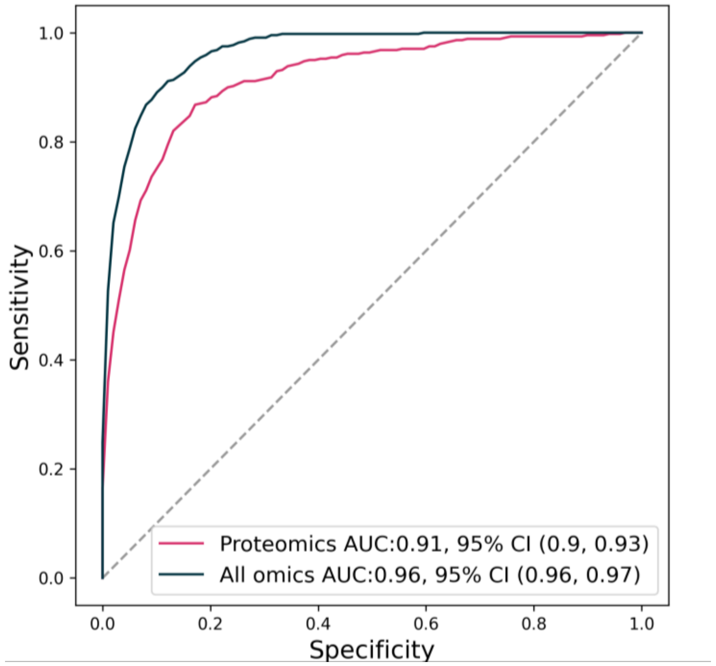
- **First large-scale pQTL study** using Proteograph for deep, unbiased proteomics with mass spec
- **Up to one third** of strongest pQTLs identified with affinity-based proteomics technologies in two cohorts are **likely false** due to epitope effects
- Follows *Nature Communications* publication demonstrating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

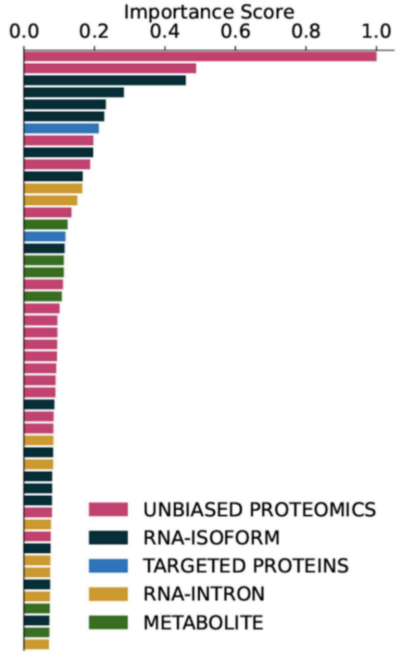


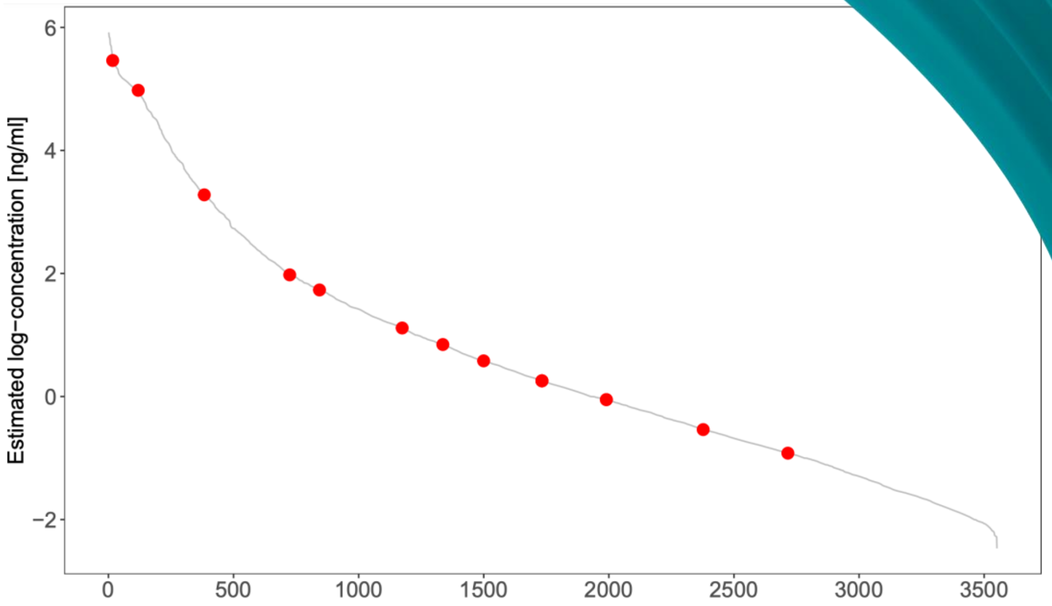
Suhre, K., et al. A genome-wide association study of mass spectrometry proteomics using the Seer Proteograph platform. BioRxiv

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

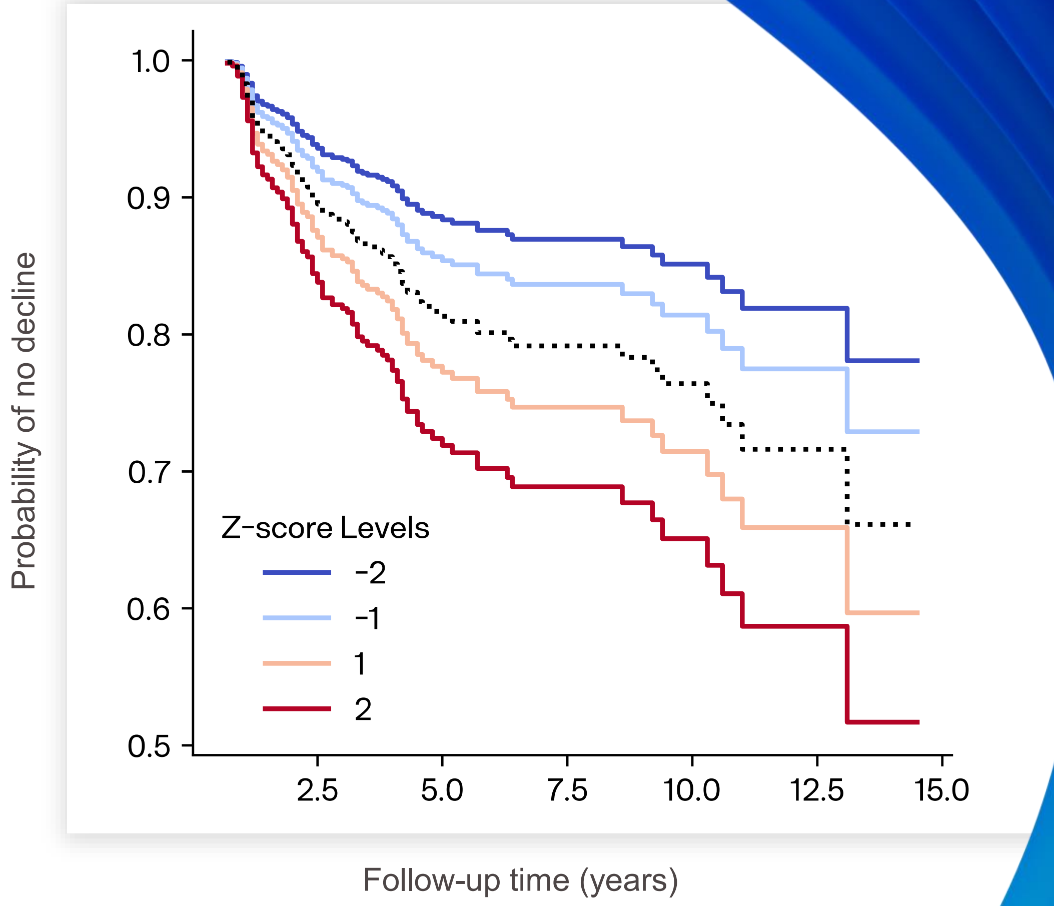
putative novel Alzheimer’s disease biomarkers

8

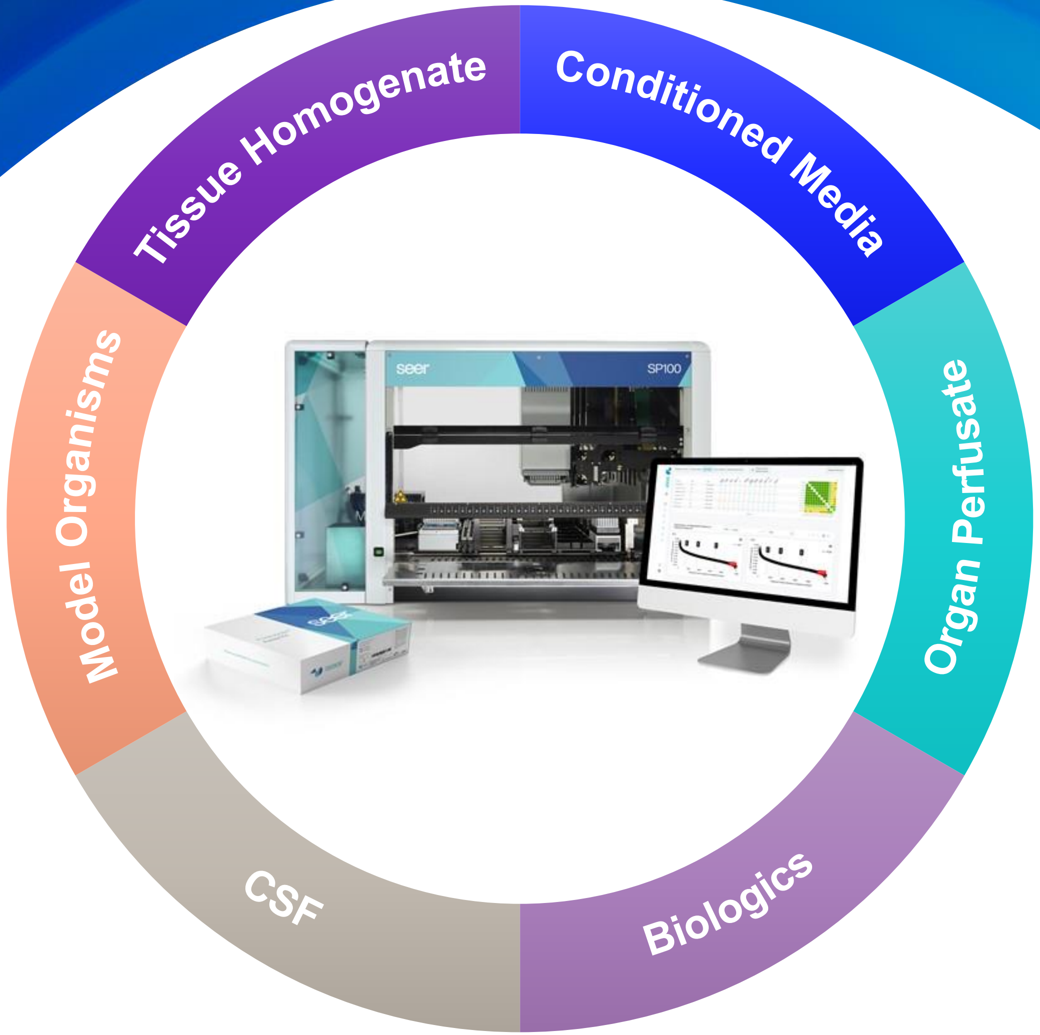
identified markers distinguishing fast and slow progressors of cognitive decline

75%

are not present on high-plex affinity panel



Apps Lab continues to expand protocols, sample types & applications



Tissue Homogenate

Conditioned Media

Organ Perfusate

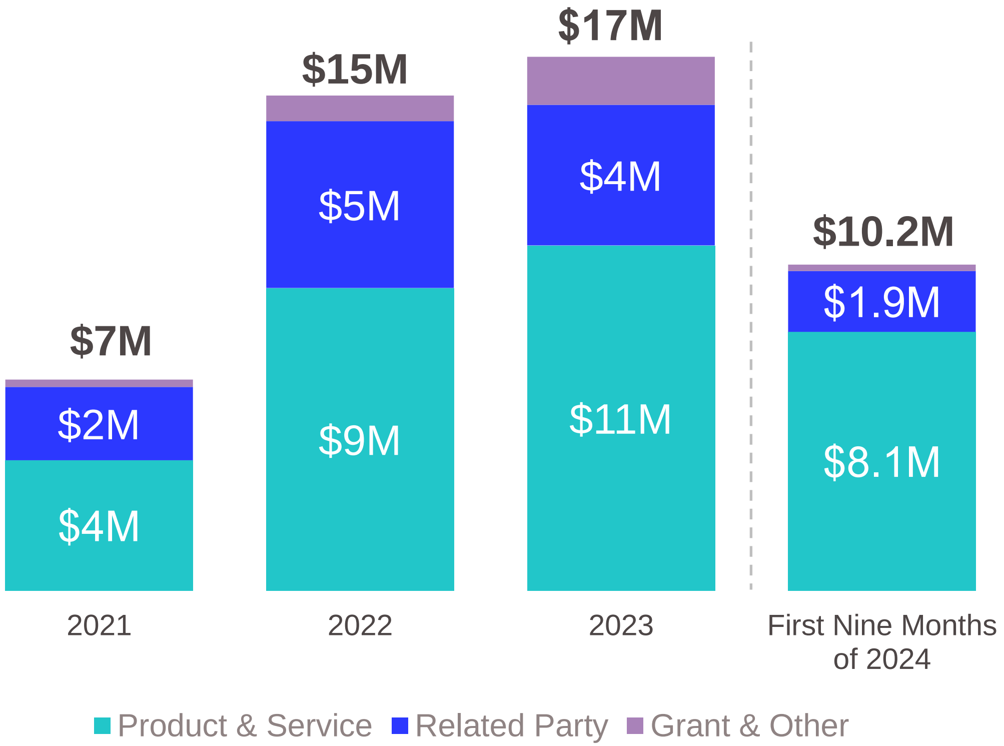
Biologics

CSF

Model Organisms

Enhancing access to Proteograph while preserving strong balance sheet

Revenue ($ million)



$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

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

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