J.P. Morgan Healthcare Conference

January 2024

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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.

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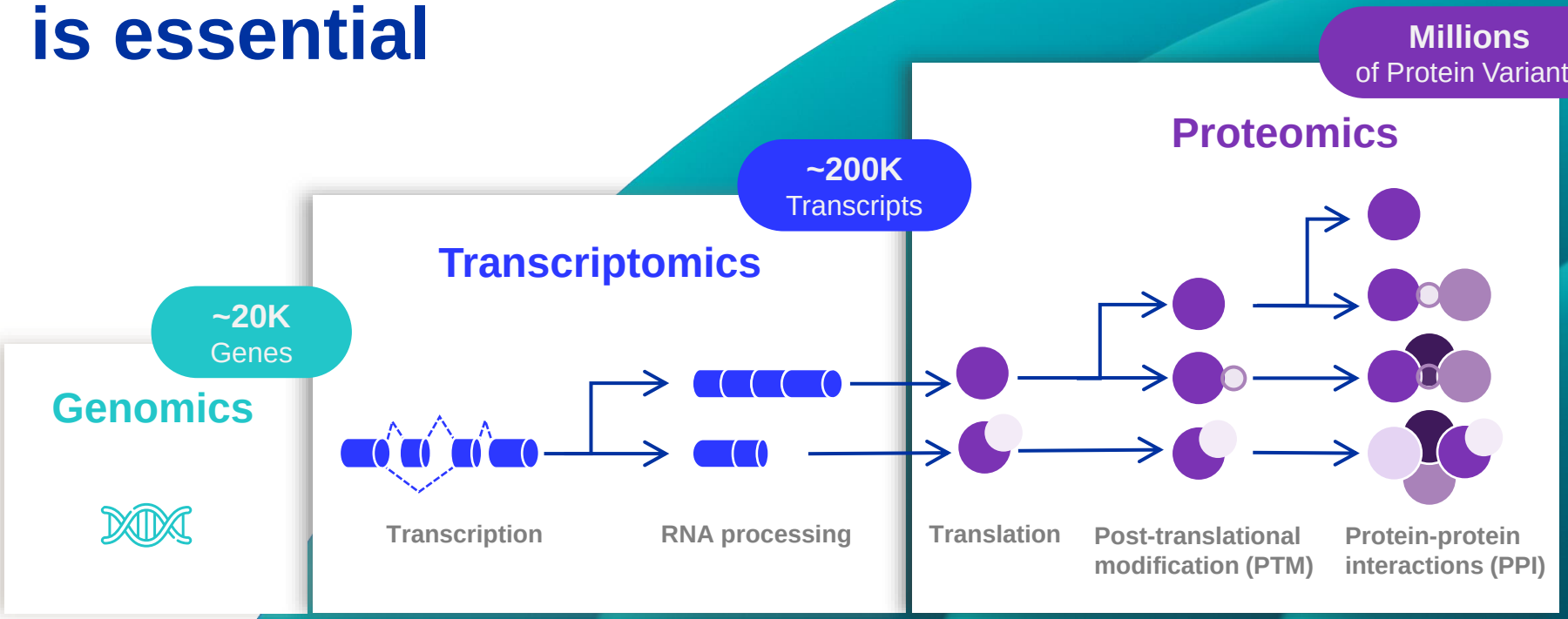
We imagine and
pioneer new ways to

decode the biology of the proteome

to improve human health

seer

Full characterization of the proteome is essential

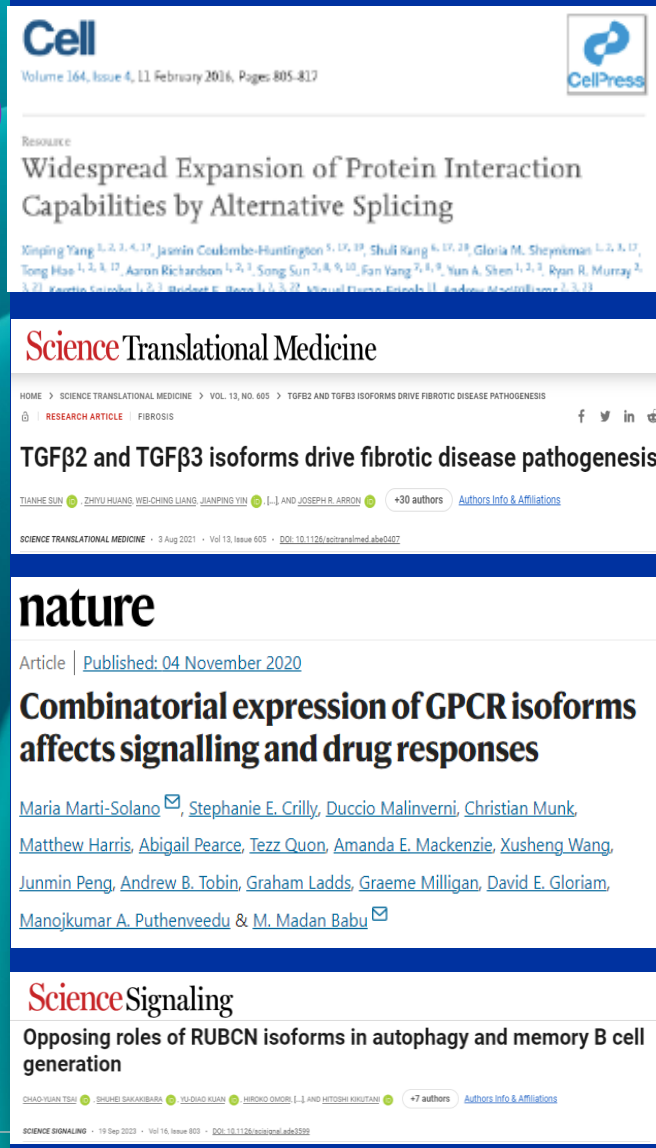


Static → Dynamic

>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



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 study 15,000 begins
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

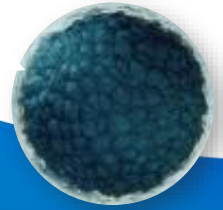
Able to analyze 10,000+ samples per year

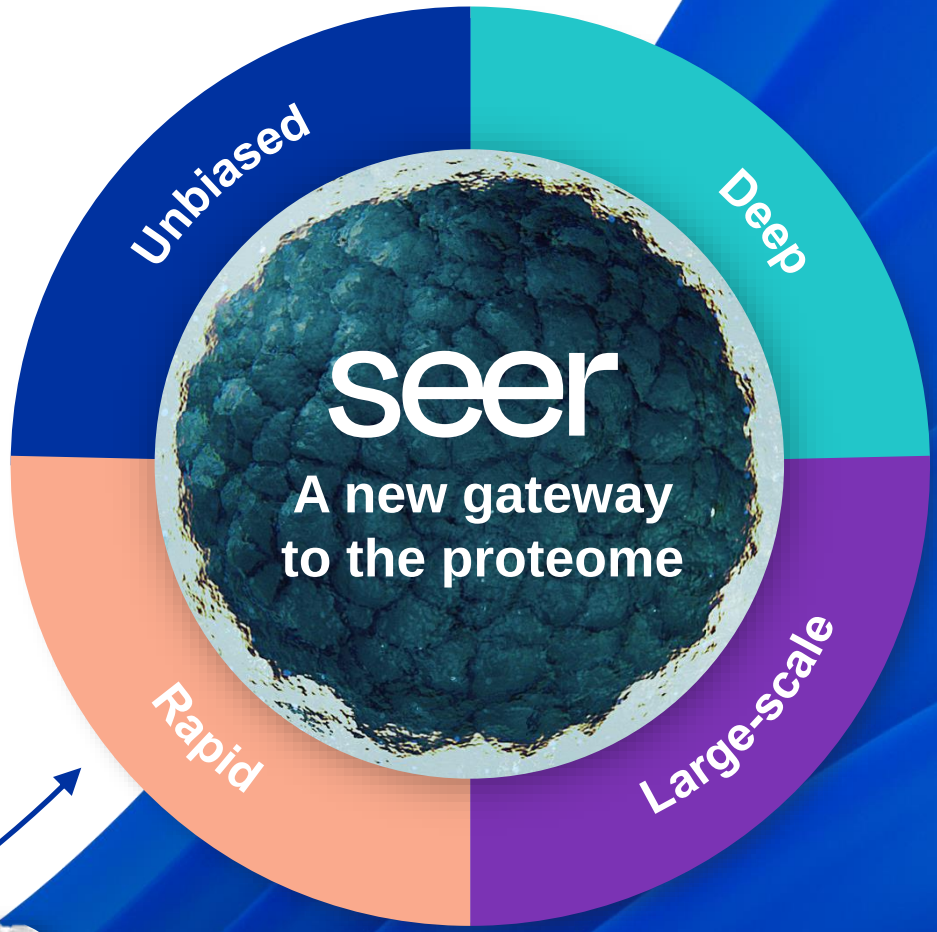
seer

Seer enables unbiased, deep and rapid proteomic analysis at scale

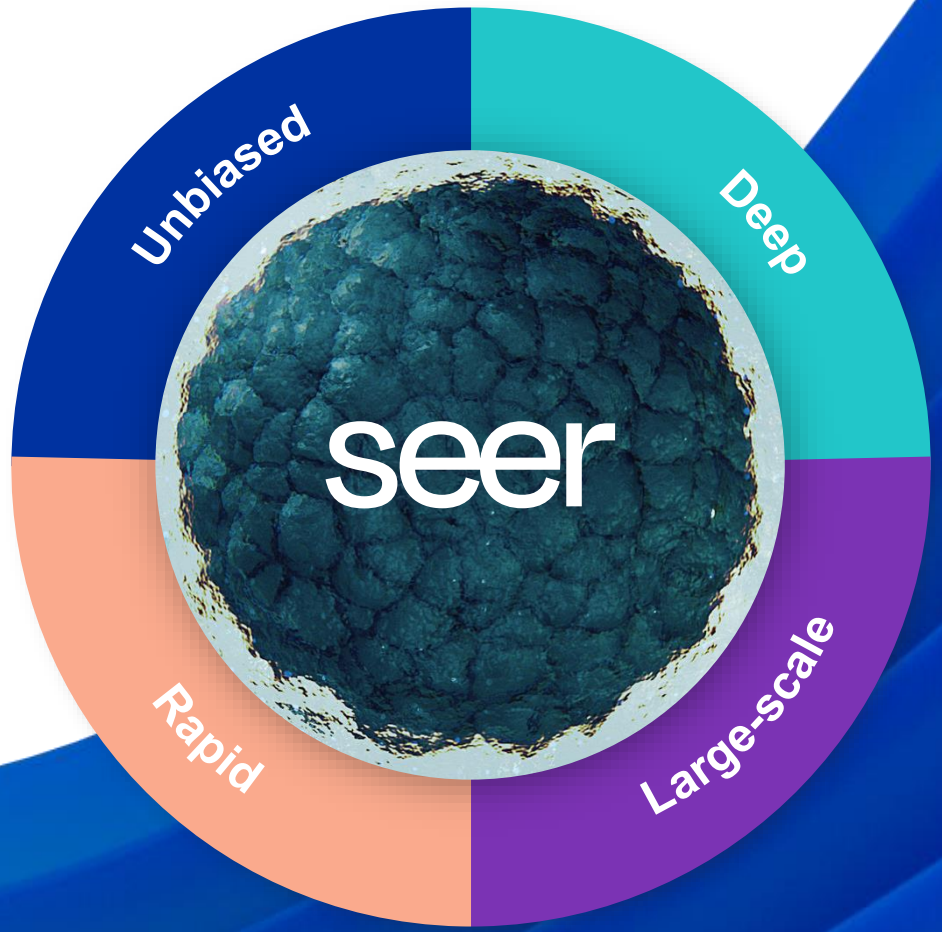
Taking advantage of the way proteins interact

Lab on a nanoparticle





seer

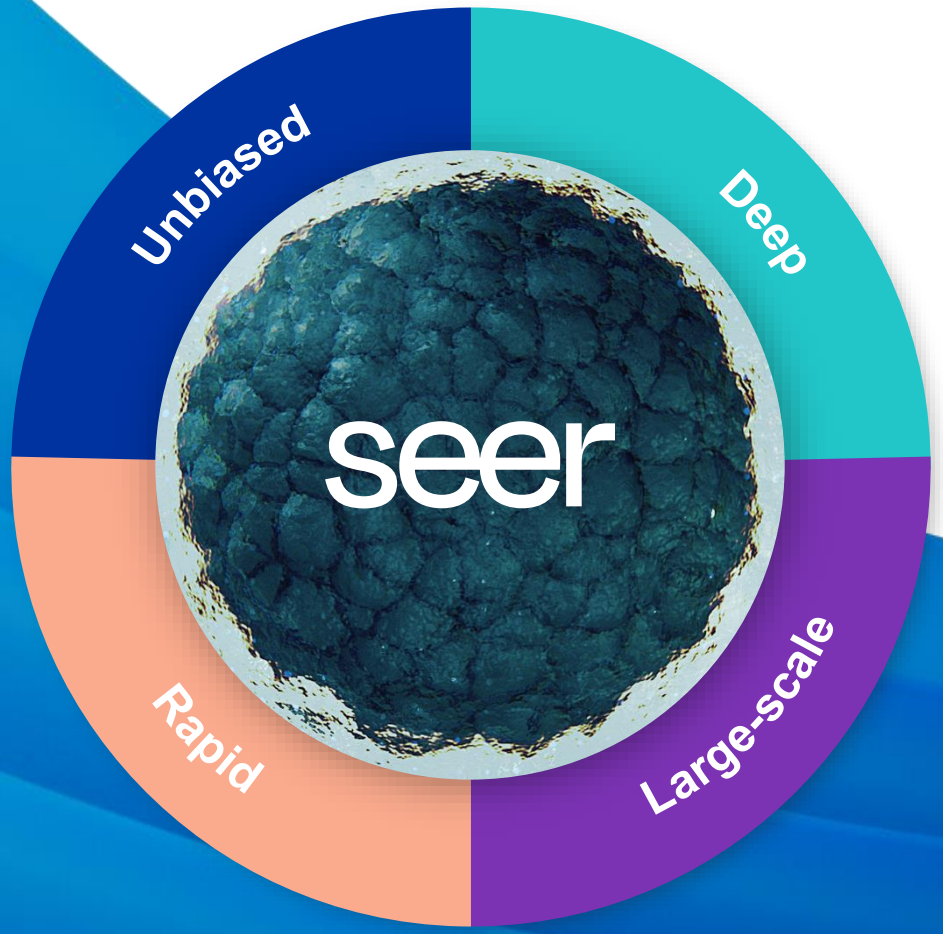


Exceptional performance and flexibility

- 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

Strong execution across 2023

1

Developed / enhanced technology

- ✓ Launched Proteograph XT
- ✓ Updates to Proteograph Analysis Suite (PAS)

2

Removed barriers to enhance access

- ✓ Launched Seer Technology Access Center (STAC)
- ✓ Launched Strategic Instrument Placement Program (SIPP)
- ✓ Expanded Centers of Excellence (COE) program

3

Expanded commercial reach and validation

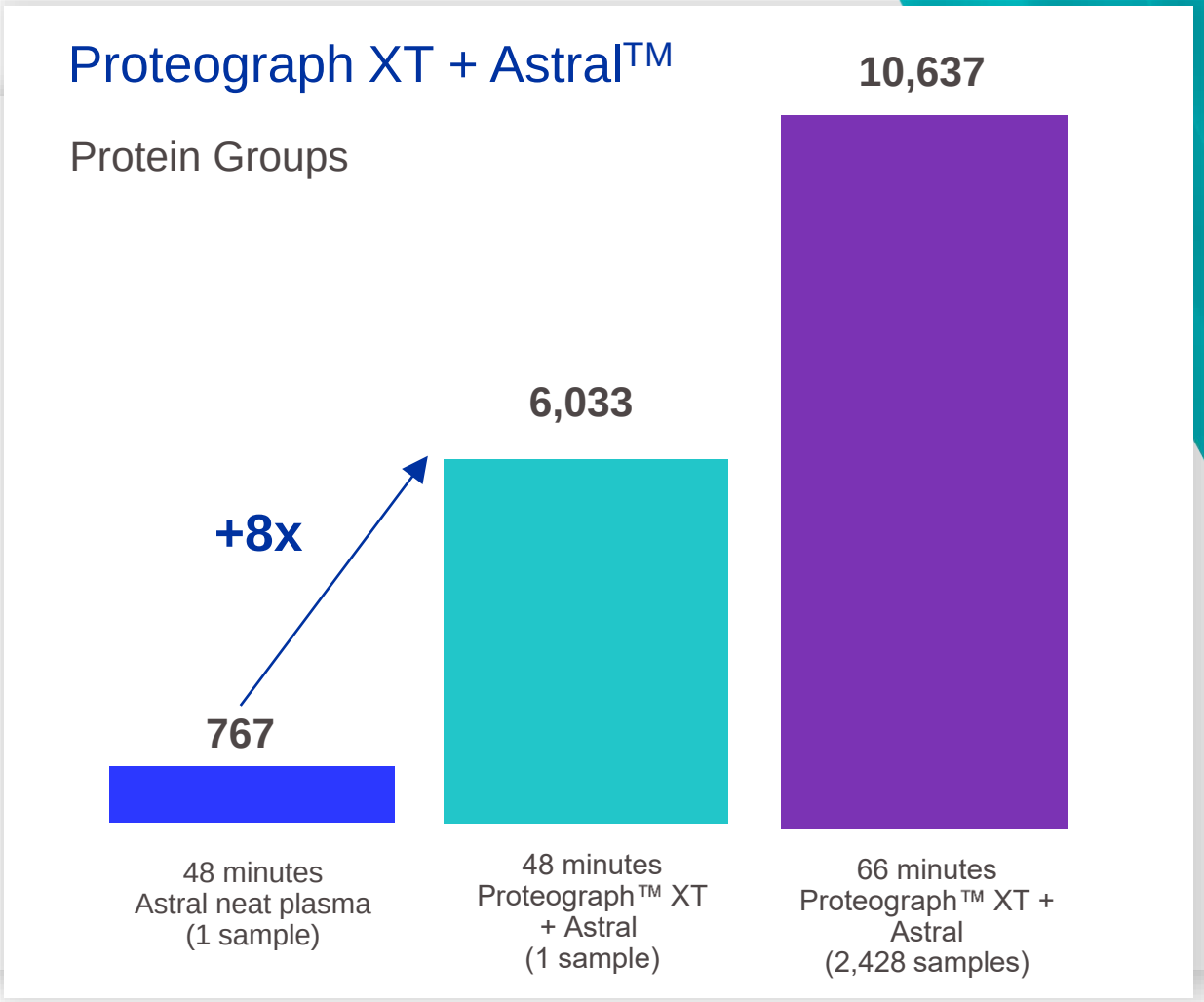
- ✓ Added four new distributors
- ✓ Added publications & pre-prints
- ✓ Received ISO 13485 & 27001 certifications

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

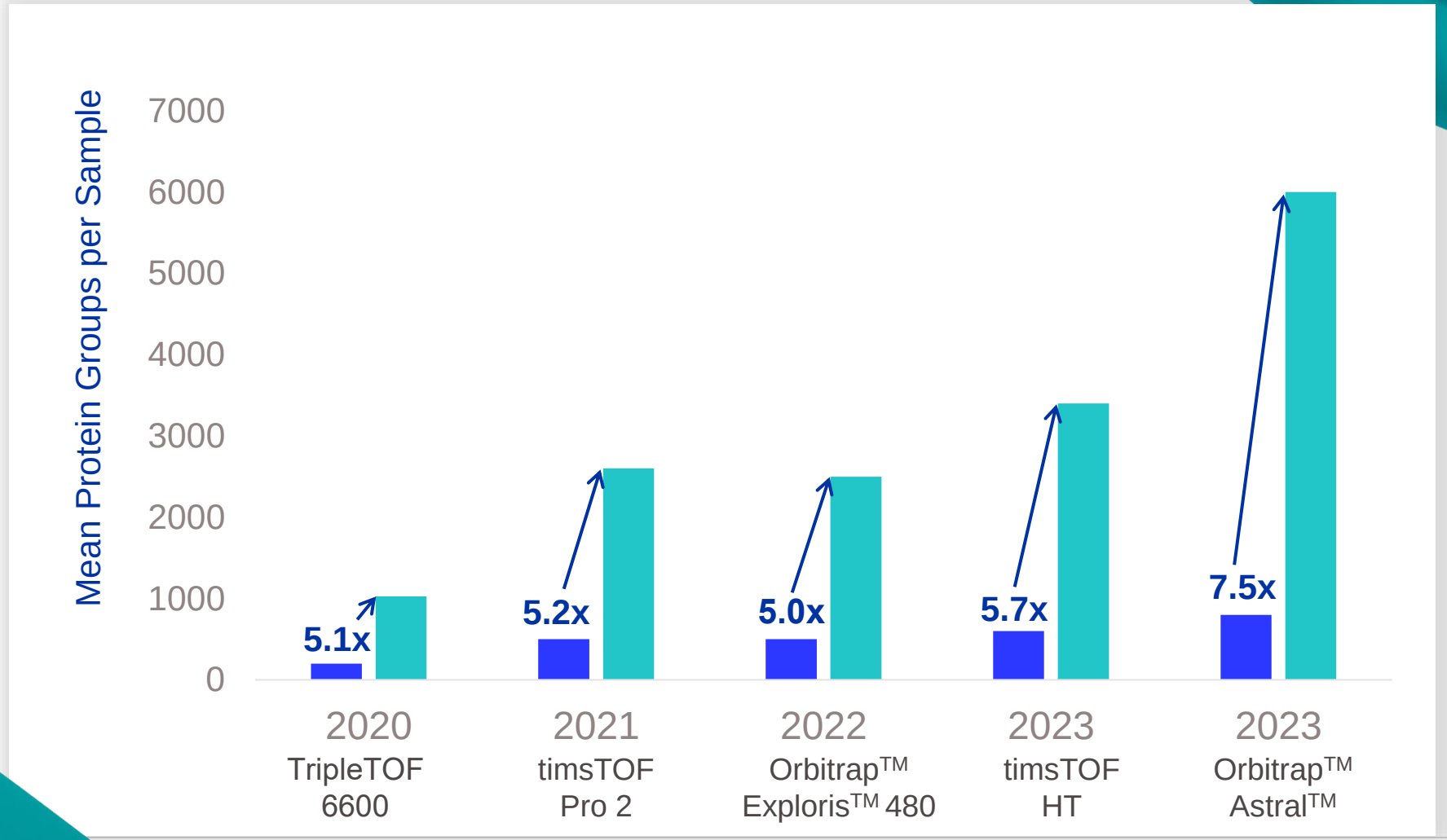
2.5x sample throughput without sacrificing depth

Significantly more proteins detected by mass spec with Seer technology

Now ~50% of installed base **upgraded to XT**



Seer’s Proteograph consistently improves mass spec performance

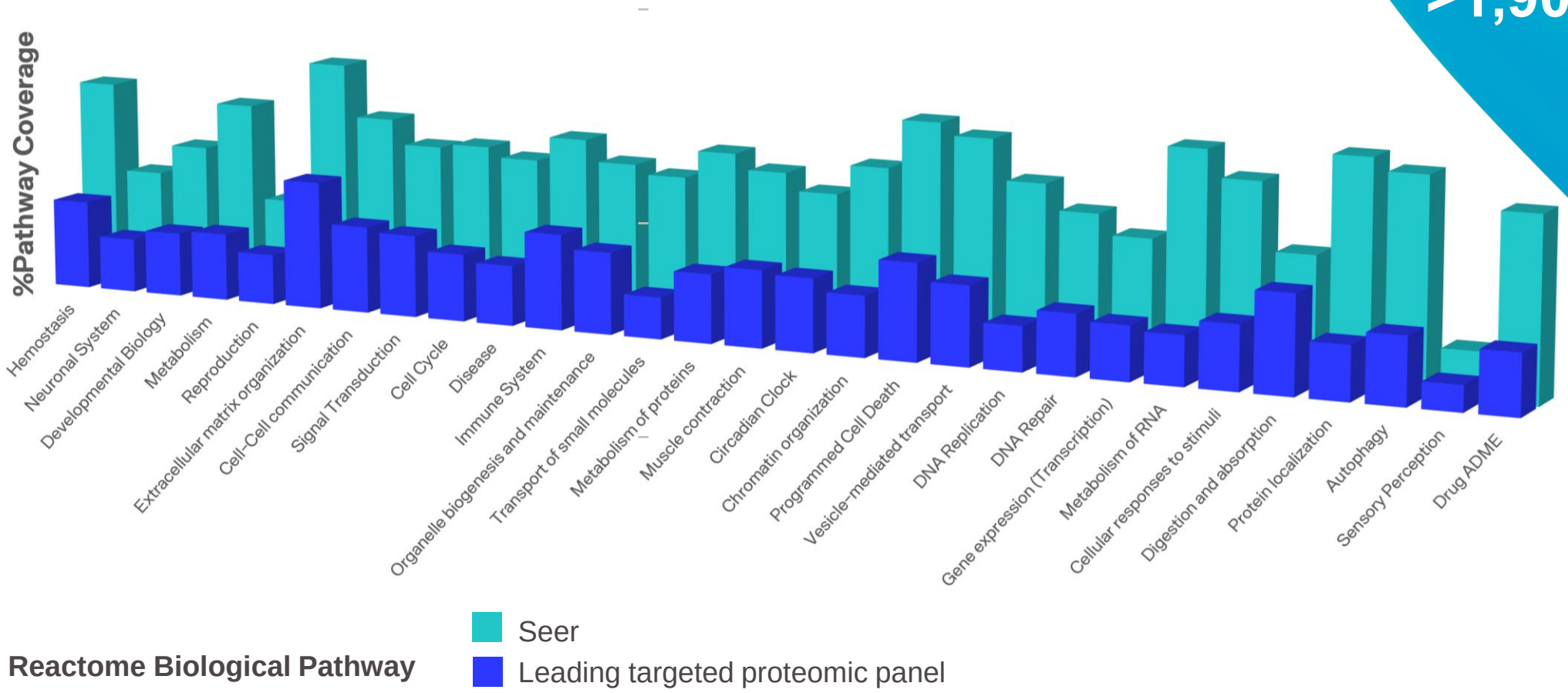


These are representative numbers achieved on these platforms in these years. This is not a direct head-to-head evaluation

Proteograph XT provides industry-leading measurement depth

2

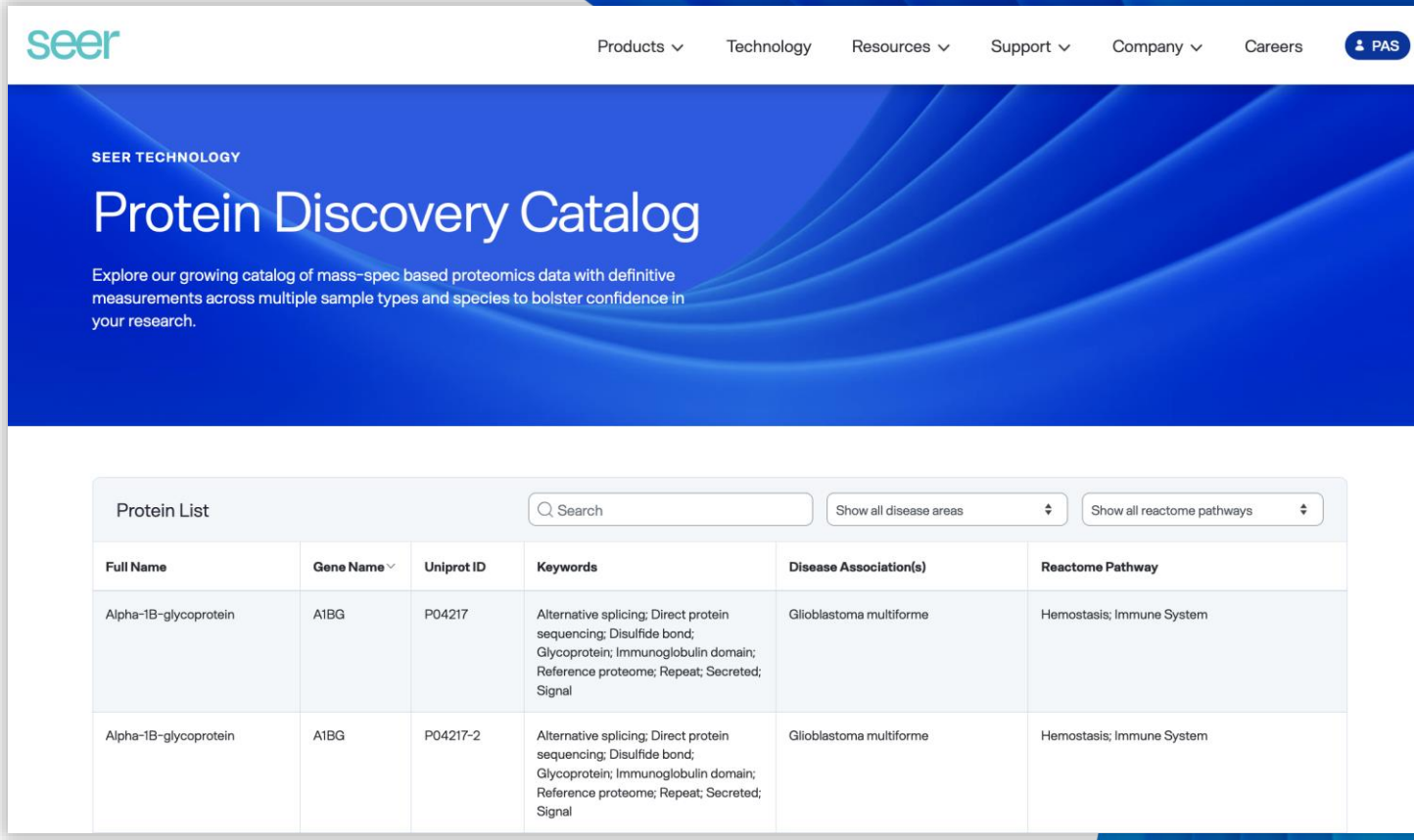
150,000+ peptides, 10,000+ proteins, >1,900 biological pathways



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

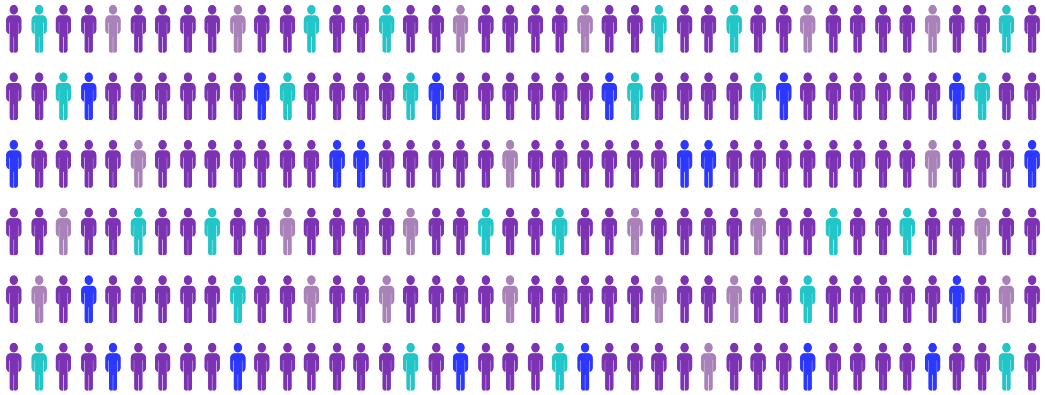
Introducing Seer's Protein Discovery Catalog for discovering biological value

- Growing catalog of 10,000+ proteins across 1,900+ pathways
- Discover proteins associated with 100,000+ possible biomarkers
- Includes proteins not yet associated with diseases
- Add precision, insights, and opportunities for biomarker discovery to genomics and proteomics studies



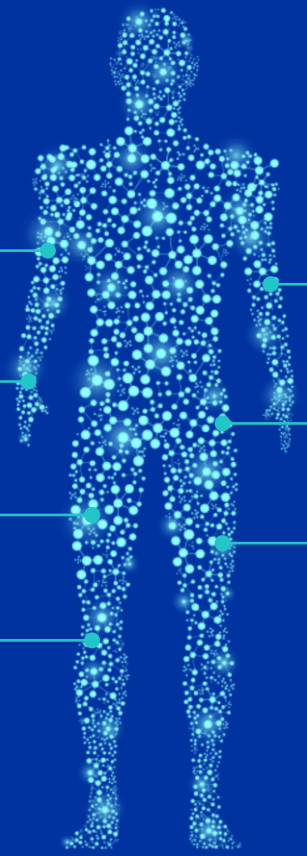
Functional implication of protein variants across the population is massive

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



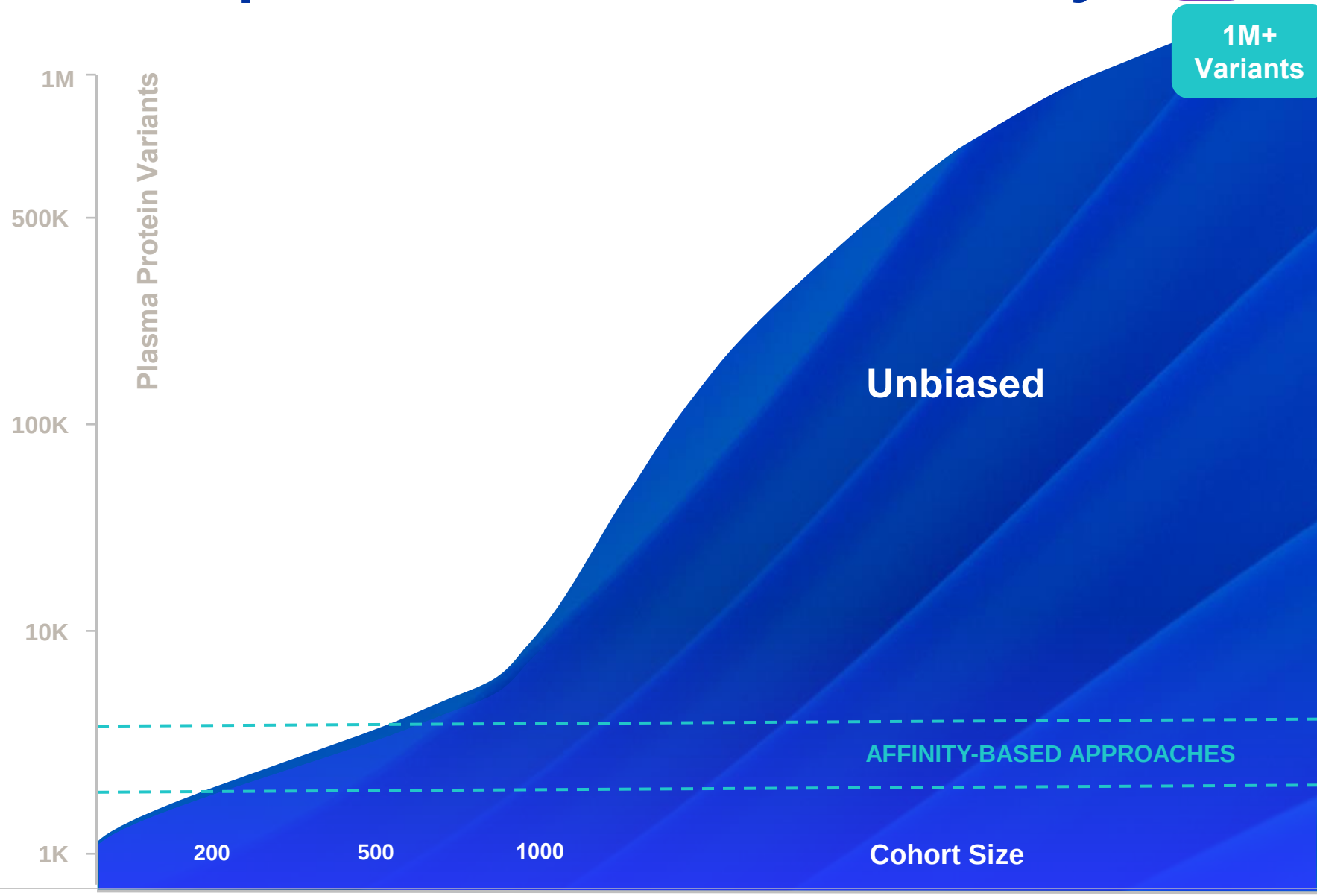
- Therapeutics
- Oncology
- Diagnostics
- Reproductive health
- Complex disease
- Rare disease
- Infectious disease

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

1

To date, we have seen 10,000+ 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**

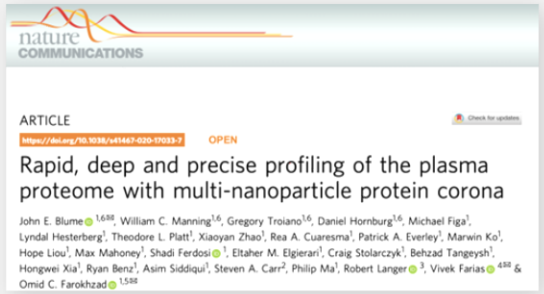
48 Organizations served

6 Large pharma customers

7,410 Average protein groups per plasma study

6.8x Average fold improvement over neat plasma

Growing validation of Seer technology


nature COMMUNICATIONS

ARTICLE

OPEN

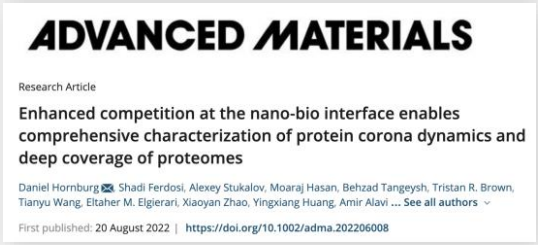
Rapid, deep and precise profiling of the plasma proteome with multi-nanoparticle protein corona


PNAS

RESEARCH ARTICLE | APPLIED BIOLOGICAL SCIENCES ENGINEERING

OPEN ACCESS

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


ADVANCED MATERIALS

Research Article

Enhanced competition at the nano-bio interface enables comprehensive characterization of protein corona dynamics and deep coverage of proteomes

Daniel Hornburg, Shadi Ferdosi, Alexey Stukalov, Moaraj Hasan, Behzad Tangeysh, Tristan R. Brown, Tianyu Wang, Eltaher M. Elgierari, Xiaoyan Zhao, Yingxiang Huang, Amir Alavi ... See all authors

First published: 20 August 2022 | https://doi.org/10.1002/adma.202206008


PLOS ONE

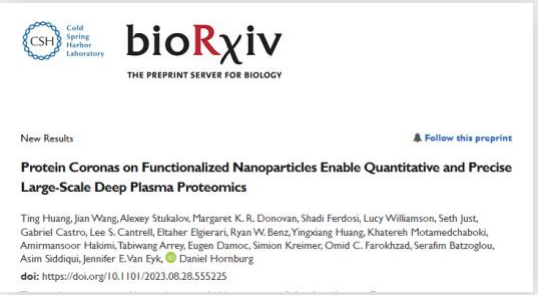
OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Functionally distinct BMP1 isoforms show an opposite pattern of abundance in plasma from non-small cell lung cancer subjects and controls

Margaret K. R. Donovan, Yingxiang Huang, John E. Blume, Jian Wang, Daniel Hornburg, Shadi Ferdosi, Iman Mohtashemi, Sangtae Kim, Marwin Ko, Ryan W. Benz, Theodore L. Platt, Serafim Batzoglou, Luis A. Diaz, Omid C. Farokhzad, Asim Siddiqui

Published: March 29, 2023 • https://doi.org/10.1371/journal.pone.0282821


Cold Spring Harbor Laboratory

bioRxiv

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New Results

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Protein Coronas on Functionalized Nanoparticles Enable Quantitative and Precise Large-Scale Deep Plasma Proteomics

Ting Huang, Jian Wang, Alexey Stukalov, Margaret K. R. Donovan, Shadi Ferdosi, Lucy Williamson, Seth Just, Gabriel Castro, Lee S. Cantrell, Eltaher Elgierari, Ryan W. Benz, Yingxiang Huang, Khatereh Motamedchaboki, Amirmansoor Hakimi, Tabiwang Arrey, Eugen Damoc, Simion Kreimer, Omid C. Farokhzad, Serafim Batzoglou, Asim Siddiqui, Jennifer E.Van Eyk, Daniel Hornburg

doi: https://doi.org/10.1101/2023.08.28.555225

180

Public presentations to date

48

Posters and presentations by customers

8

Manuscripts in bioRxiv

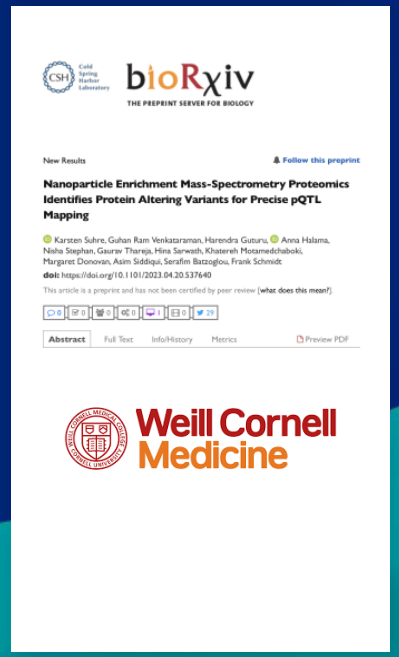
4

Peer-reviewed articles

Emergence of Third-Party Customer Publications

>10 publications submitted by customers

April

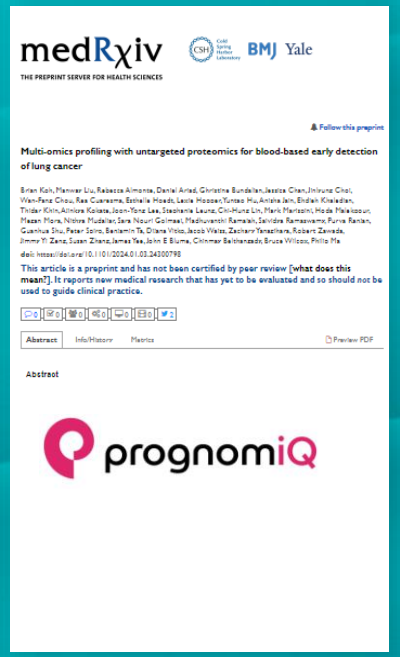


June

September

October

January



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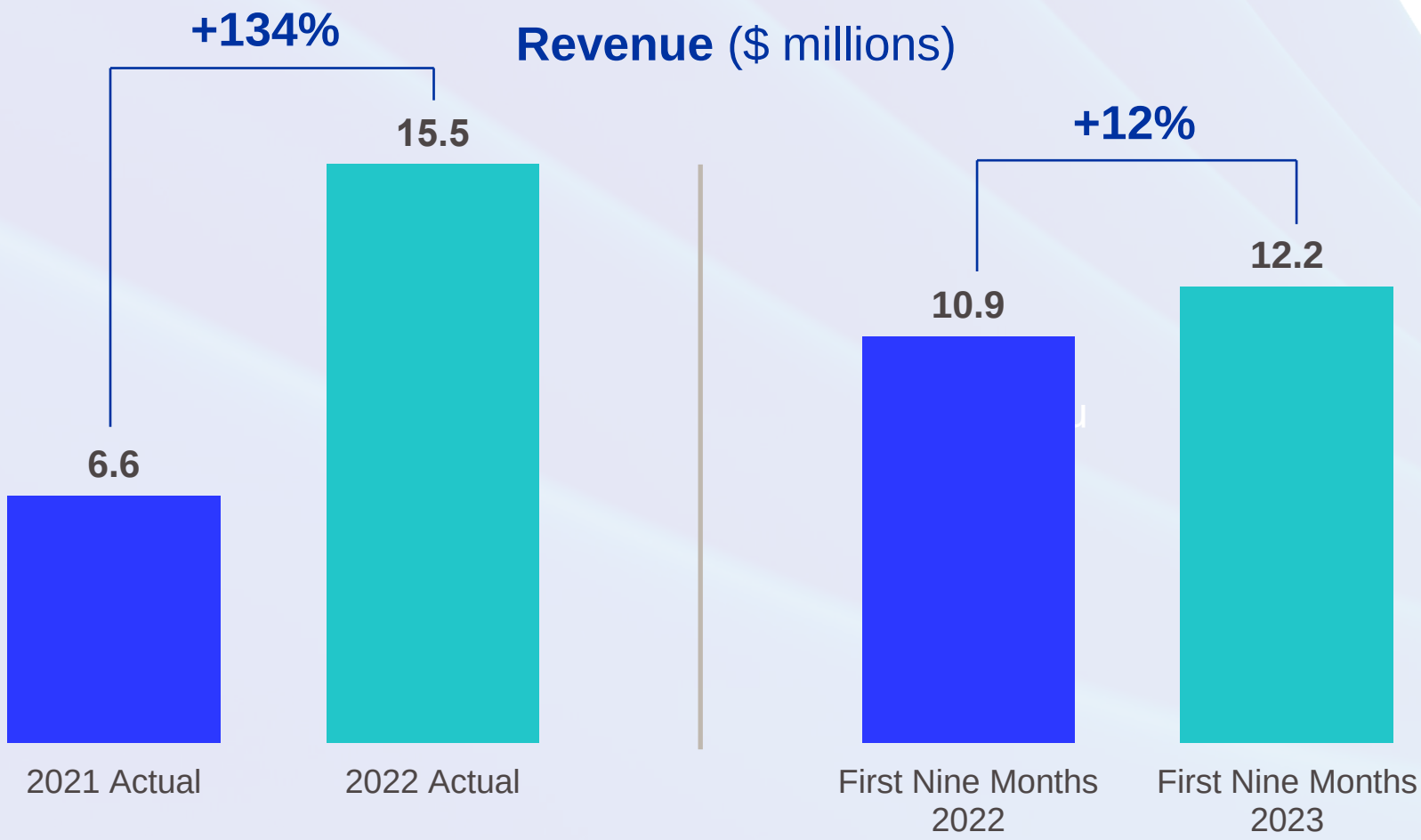
Growing revenue and strong balance sheet



1. As of September 30, 2023

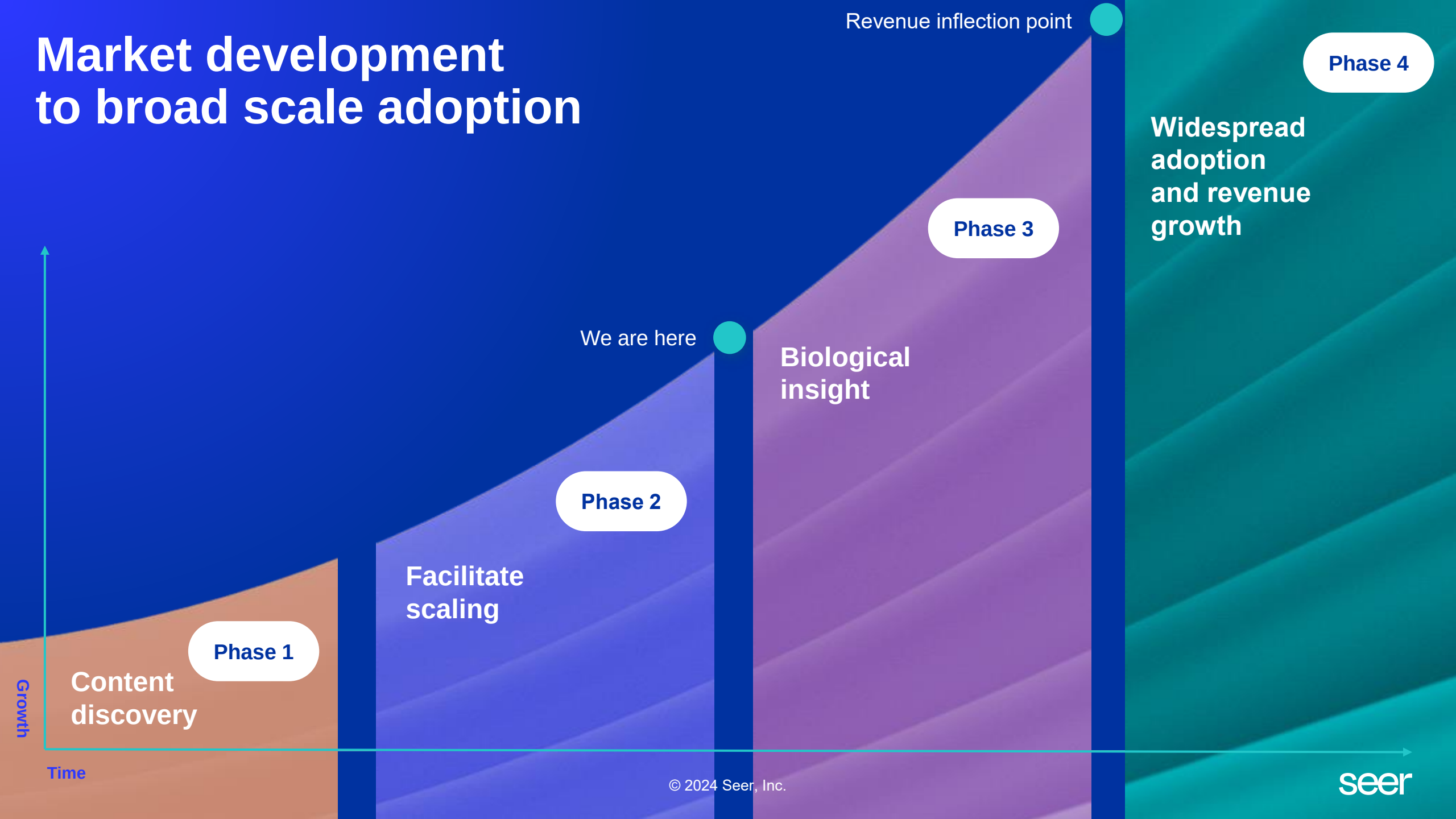
Strong Balance Sheet[1]

$381 Million

Cash, Cash Equivalents and Investments

No Debt

Market development to broad scale adoption



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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 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

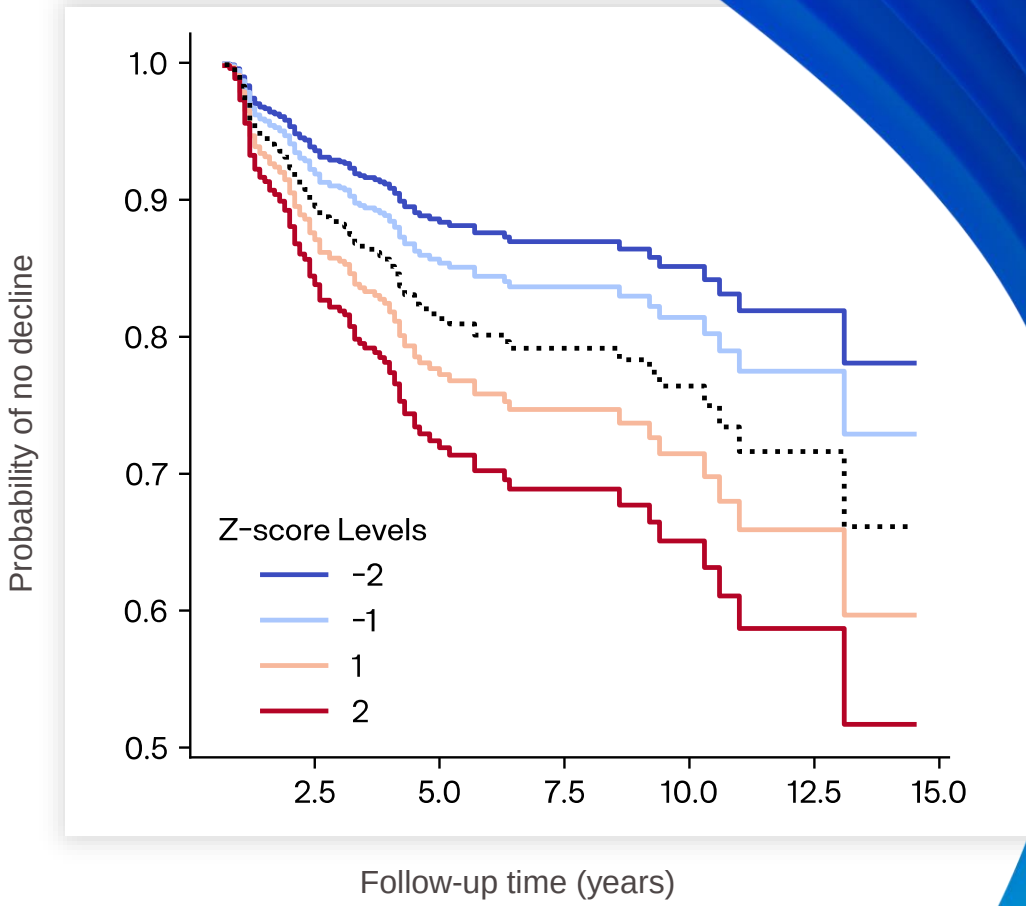
Putative novel Alzheimer's disease biomarkers

8

identified markers distinguishing fast and slow progressors of cognitive decline

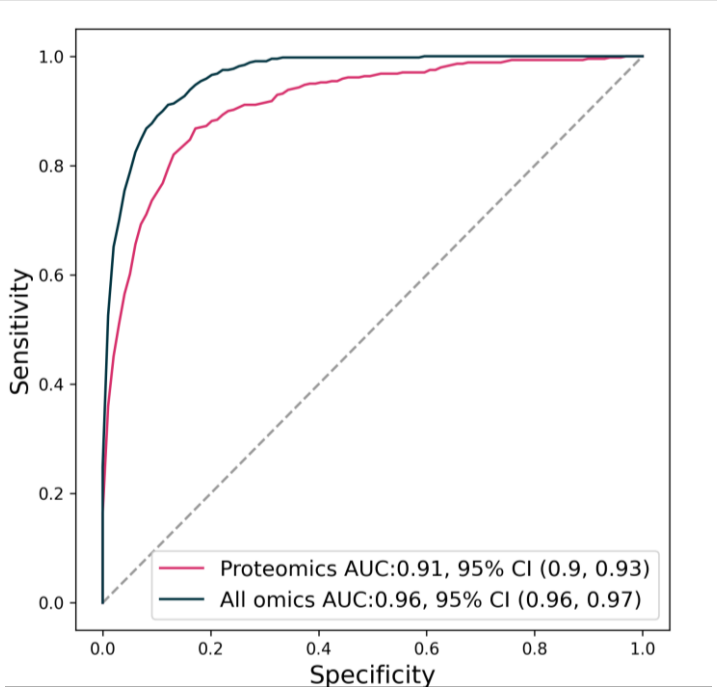
75%

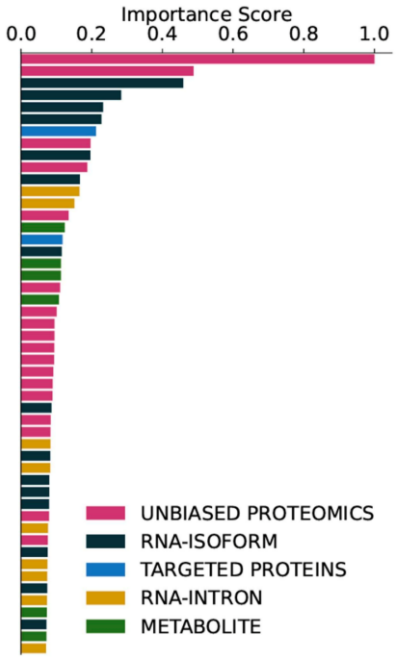
are not present on high-plex affinity panel

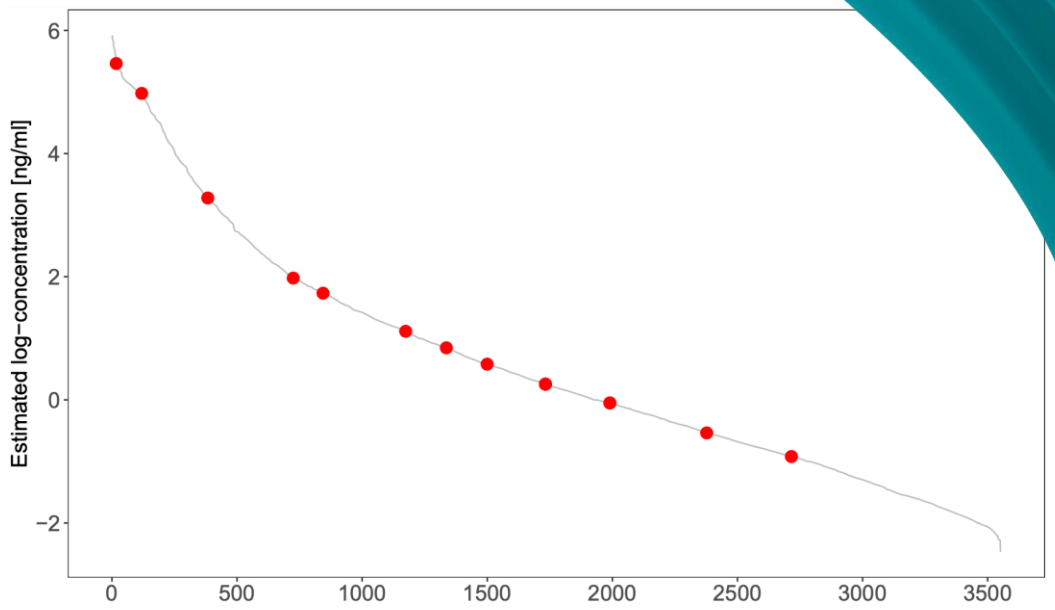


Deep, unbiased proteomics at scale powers a breakthrough advance in early lung cancer detection

Multi-omics profiling detected 8,385 proteins groups, >200,000 RNA transcripts, and >1,000 metabolites





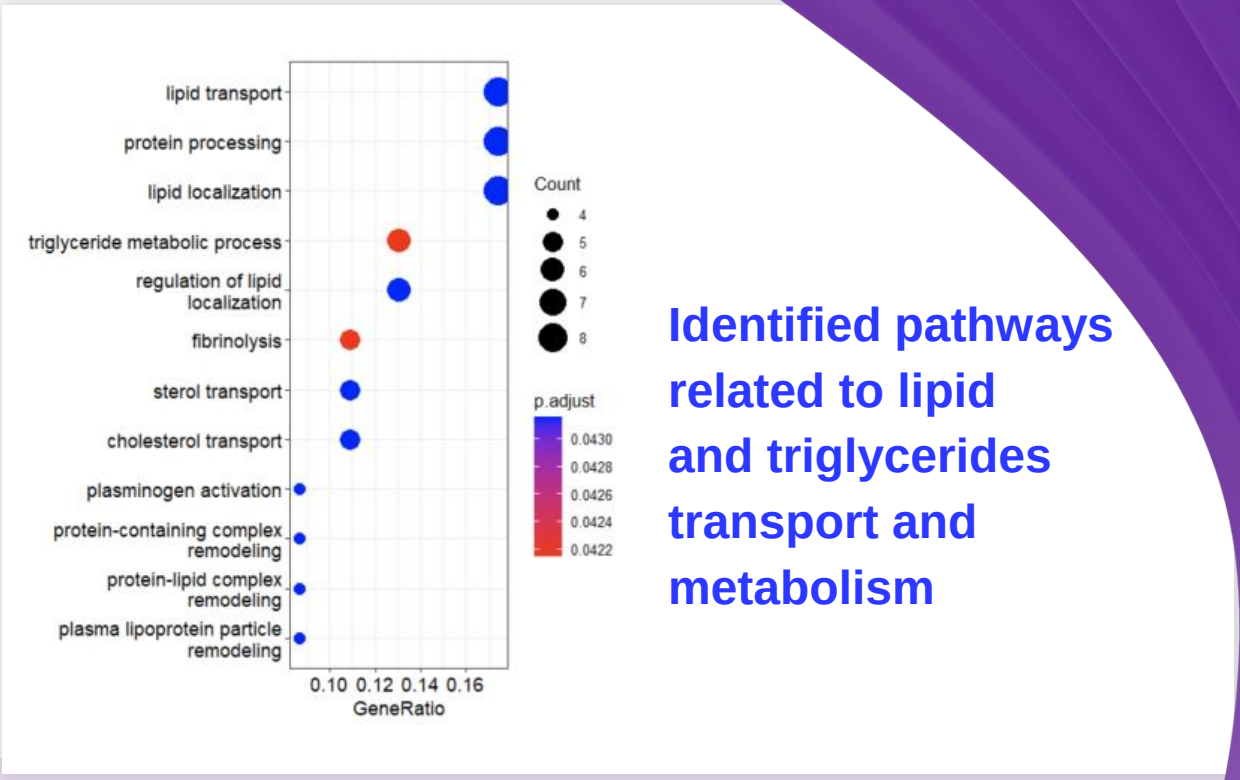


- Extremely strong performance
- Unbiased proteomics is the key driver
- Classifier proteins fall across the dynamic range

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

Unbiased discovery proteomics used to develop circulating aging signatures in mice

- 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



Identified pathways related to lipid and triglycerides transport and metabolism

"The **Proteograph platform has unlocked several new research directions that were previously hampered by technical challenges** in our lab. For the first time, we are able to look comprehensively at longitudinal age-related changes in low volumes of mouse blood and generate unprecedented biomarker signatures of aging-related outcomes…**enabling a more biologically relevant view of the secretome**.

Nate Basisty, PhD

NIH National Institute on Aging

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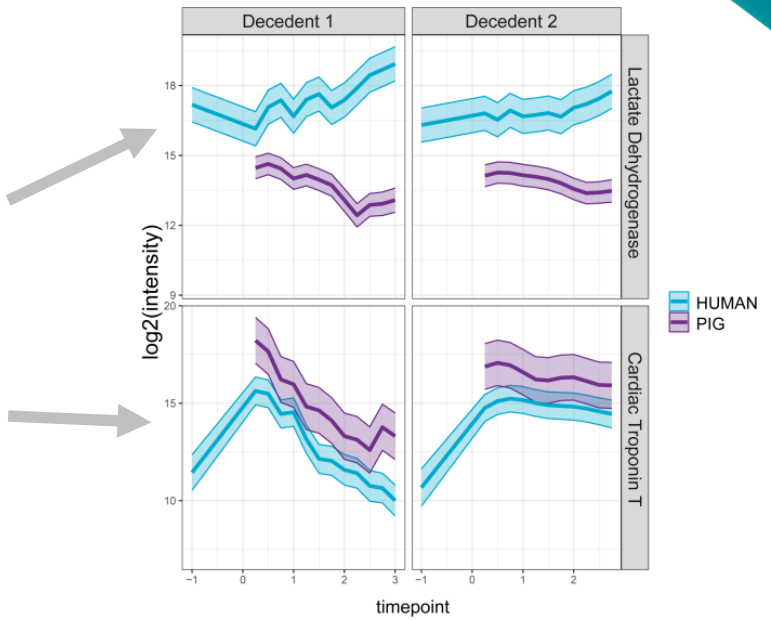
Deep protein profiling in xenotransplant enables simultaneous profiling of human and pig proteins

- 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



Transplant Operation at Timepoint 0

> Only 25-30% of individuals on the transplant waiting lists receive a life-saving organ. Gene-editing pig organs are a very promising avenue to address this need...**We have been able to detect over 8,000 pig and human proteins in the plasma of these human decedents and it has facilitated analyses we never thought possible.**

Brendan Keating, PhD
NYU Grossman School of Medicine
Department of Surgery

Apps Lab continues to expand protocols, sample types & applications

2024 catalysts

1

Drive evidence and publications

Increase publications and large-scale studies

- Deliver cohort studies and strategic collaborations to drive third-party evidence
- Invest in helping customers to accelerate publications
- Continue demonstrating how an unbiased approach accelerates discovery

2

Continue to enhance access

Increase use of STAC and SIPP

- Continue to drive market access
- Double down on efforts to reach genomics audience
- Make PAS more user-friendly for biologists
- Expand STAC capacity to accelerate more samples to data

3

Product innovation and application expansion

Increase product enhancements and applications from Apps Lab

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

Q&A