



J.P. Morgan Healthcare Conference

January 2024

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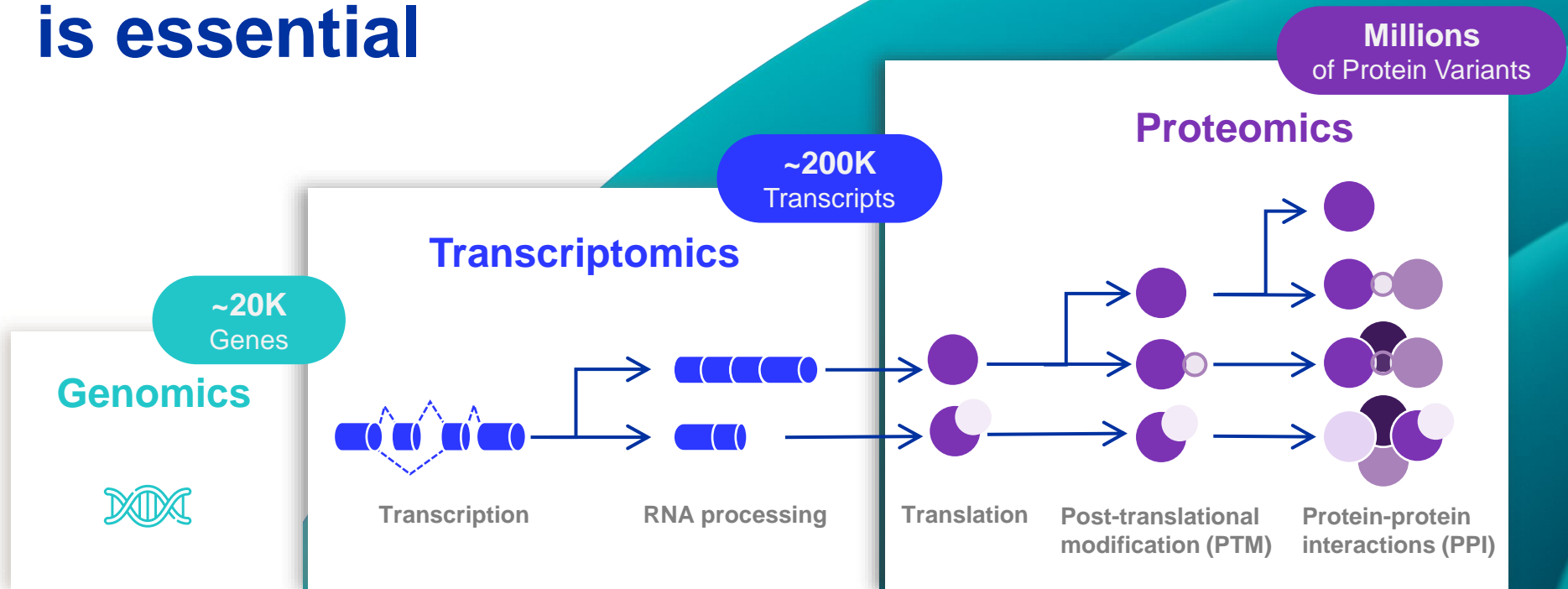
We imagine and
pioneer new ways to

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



Widespread Expansion of Protein Interaction Capabilities by Alternative Splicing

Xiping Yang^{1,2,3,4,17}, Jasmin Coulombe-Huntington^{5,18,19}, Shuli Kang^{6,17,20}, Gloria M. Sheynkin^{1,2,3,17}, Tong Hae^{1,2,3,17}, Aaron Richardson^{1,2,3}, Song Sun^{2,4,9,10}, Fan Yang^{2,4,9,10}, Yun A. Shen^{1,2,3}, Ryan R. Murray^{2,3,21}, Kerstin Szobos^{1,2,3}, Robert E. Brown^{1,2,3,22}, Michael Hasan-Friedl¹¹, Andrew M. Lesch^{12,3,23}

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 SUN¹, ZHUYU HUANG¹, WELCHING LIANG¹, JIANPING YIN^{1,11} AND JOSEPH R. ARRON¹ +30 authors | Authors Info & Affiliations

SCIENCE TRANSLATIONAL MEDICINE • 3 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[✉], 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

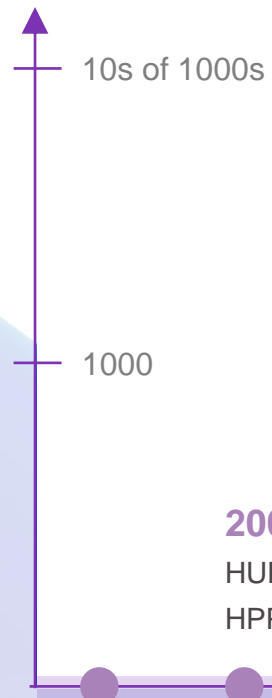
Opposing roles of RUBCN isoforms in autophagy and memory B cell generation

CHAO-YUAN TSAI¹, SHUHEI SAKAKIBARA², YUJIRO KUBO³, HIROKO ONOBE¹⁻³ AND HITOSHI KUNITANI¹ +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

1st 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 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

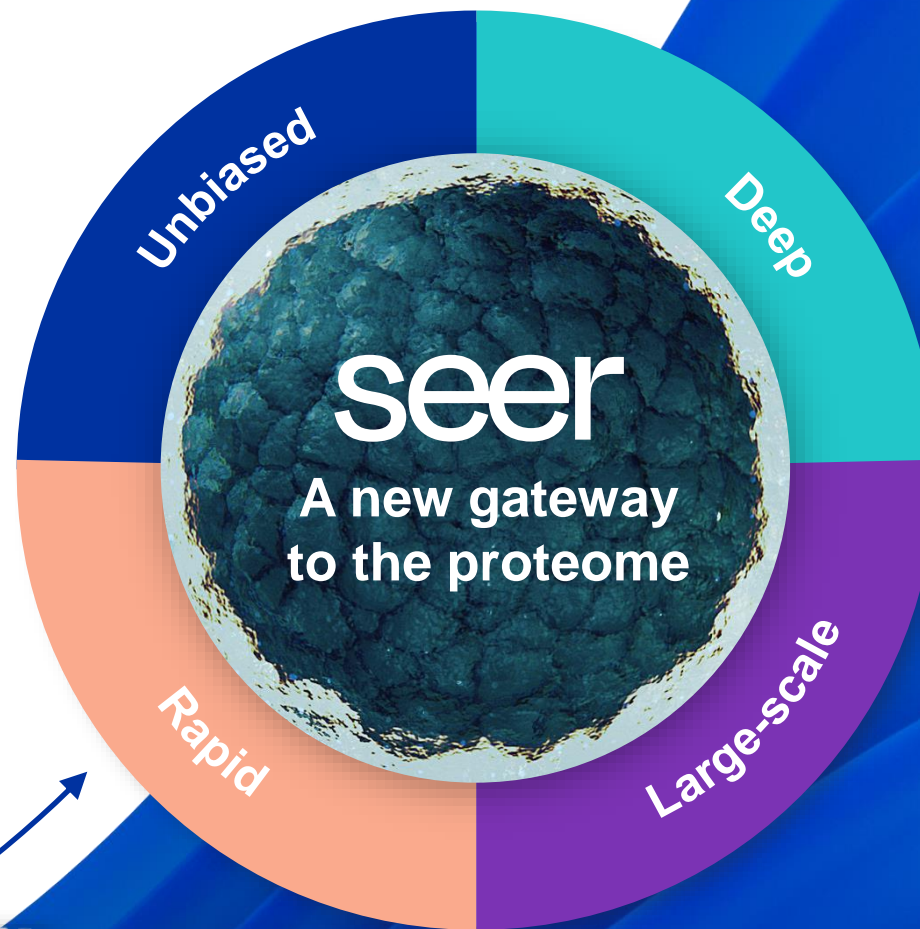
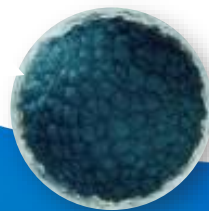


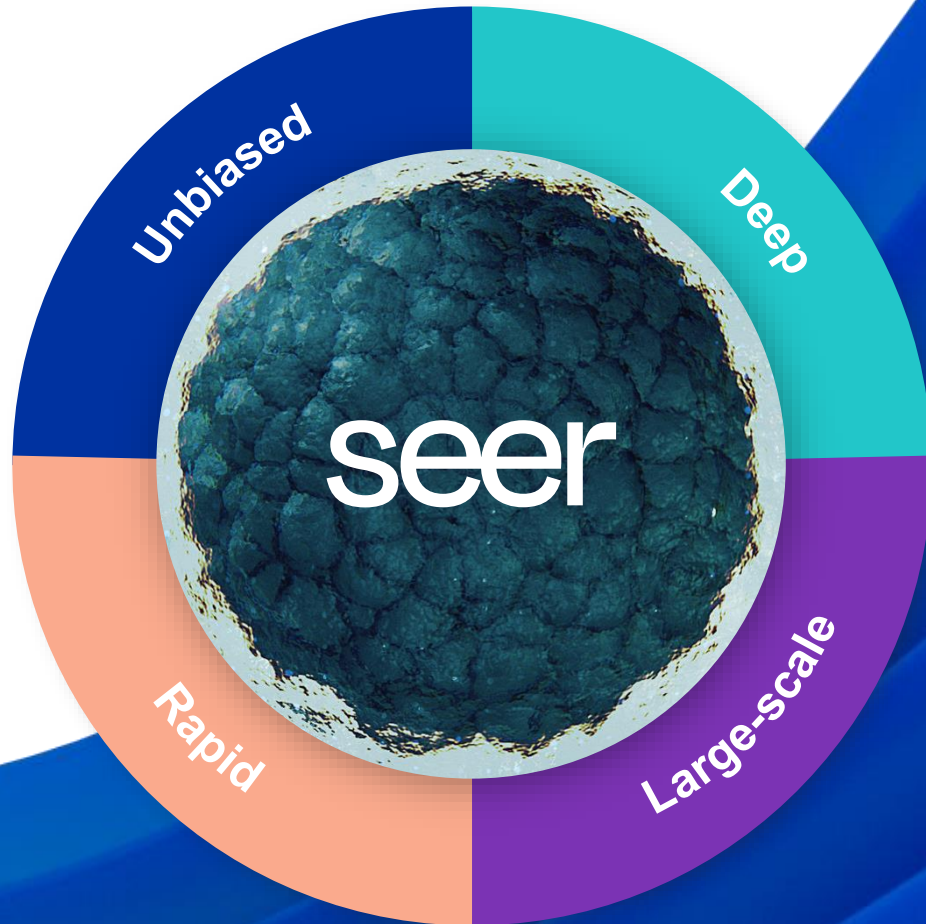
Seer enables unbiased, deep and rapid proteomic analysis at scale

Taking advantage of the way proteins interact



Lab on a nanoparticle



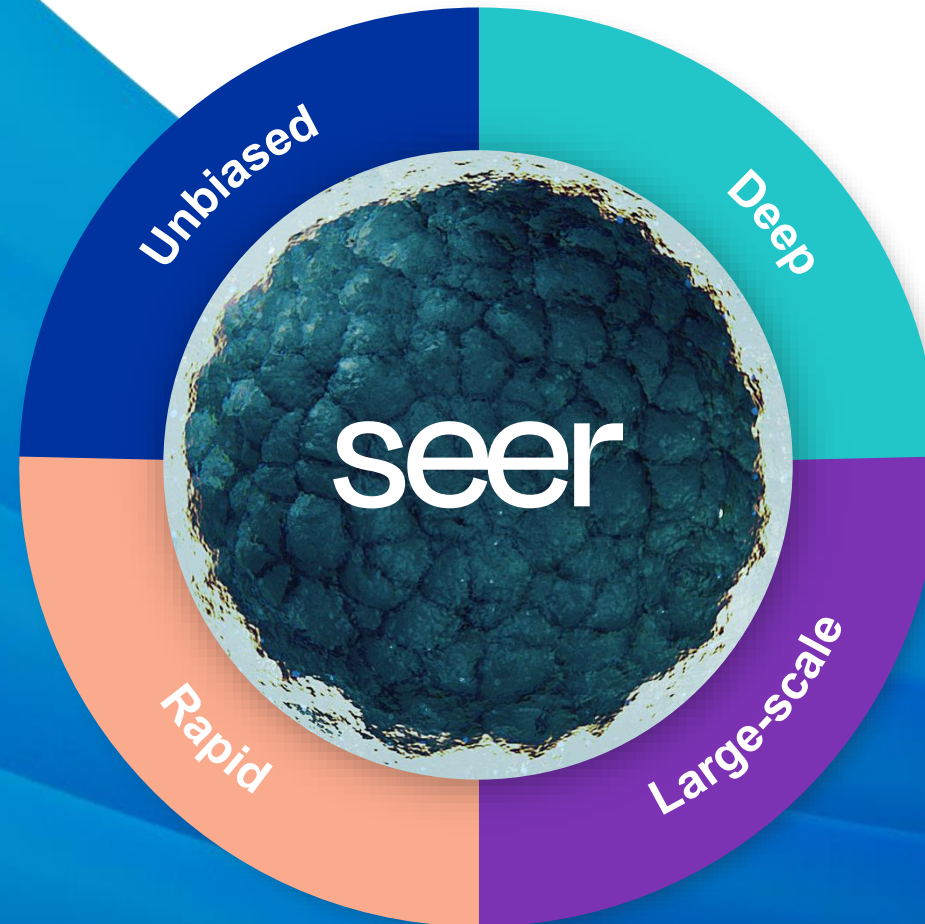


Exceptional performance and flexibility

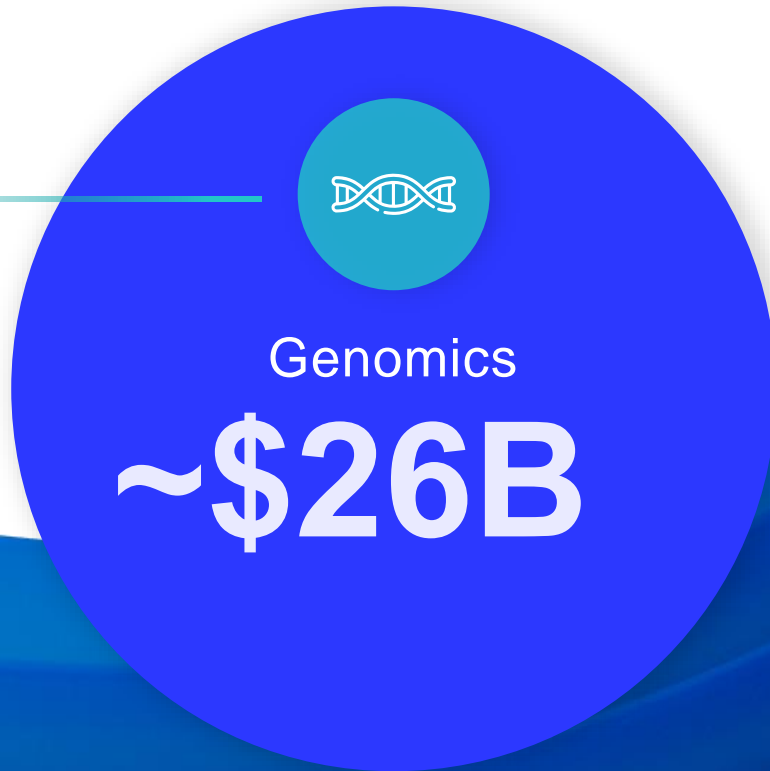
- High accuracy and reproducibility
- Quantitative measurement
- Broad dynamic range
- 1% false discovery rate (FDR)
- Wide range of sample types
- Species agnostic

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

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

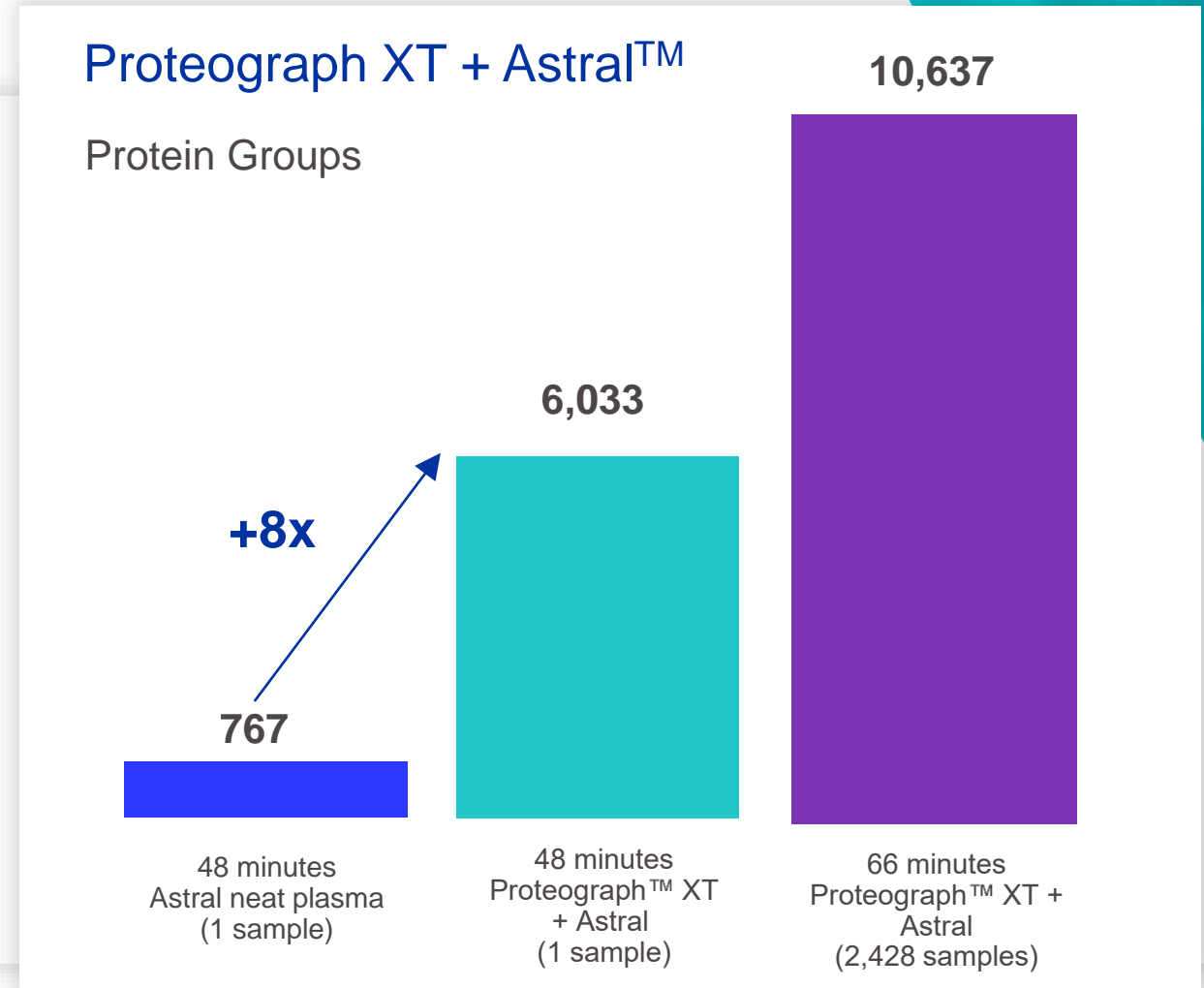
- ✓ Added four new distributors
- ✓ Added publications & pre-prints
- ✓ Received ISO 13485 & 27001 certifications

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

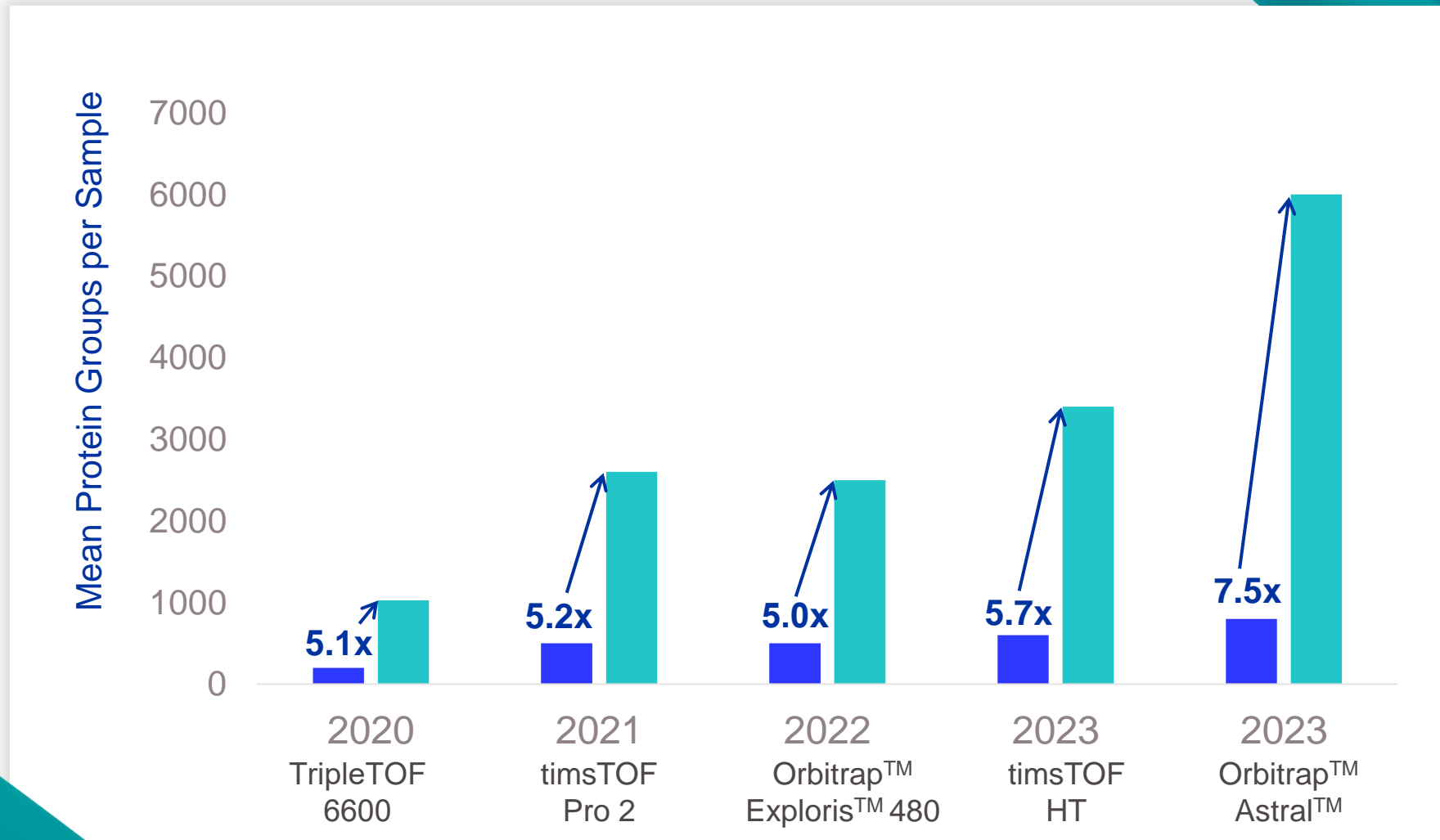
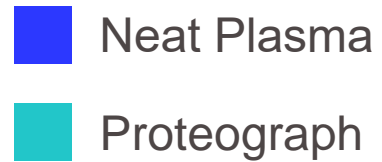
2.5x sample throughput
without sacrificing depth

Significantly more proteins detected by mass spec with Seer technology

Now ~50% of installed base upgraded to XT



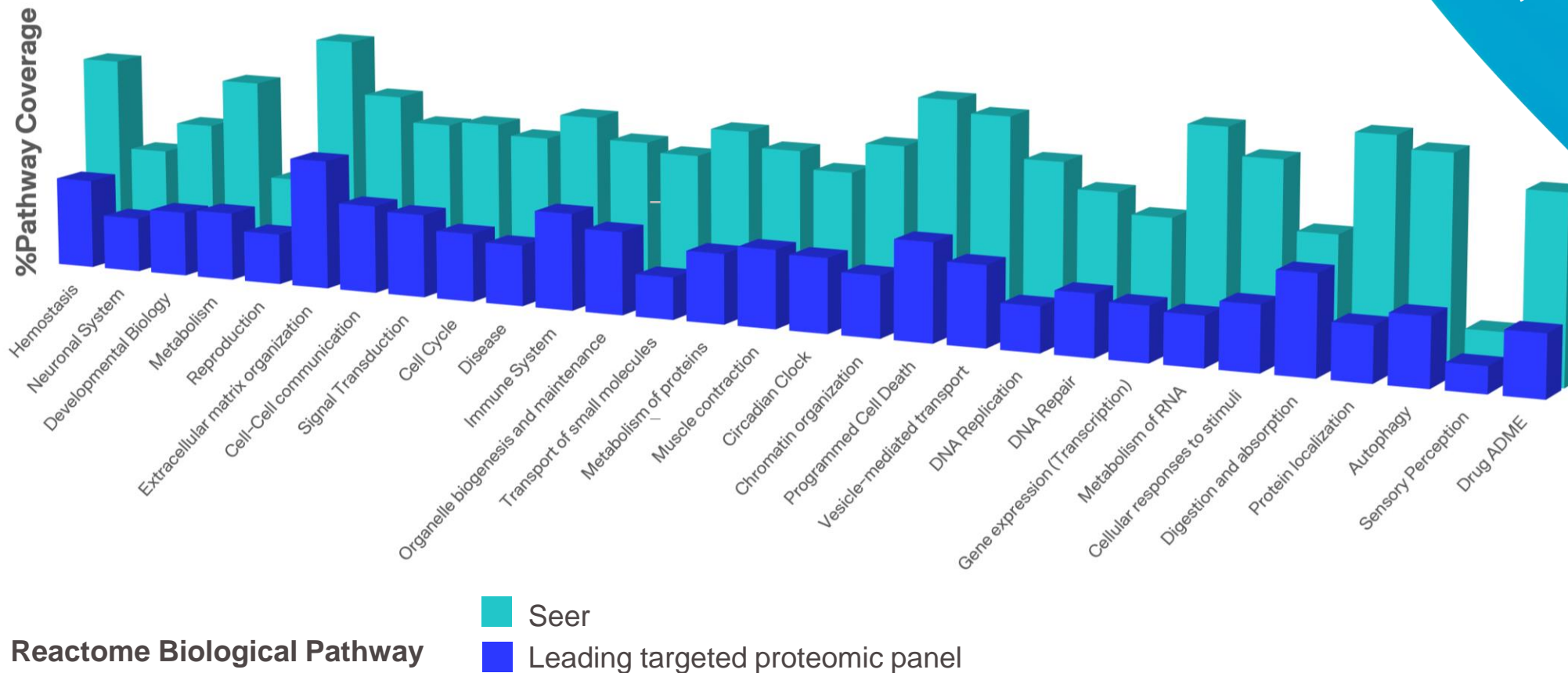
Seer's Proteograph consistently improves mass spec performance



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

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



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

The screenshot shows the Seer Protein Discovery Catalog website. The header includes the Seer logo and navigation links for Products, Technology, Resources, Support, Company, and Careers, along with a user profile icon labeled 'PAS'. The main heading is 'SEER TECHNOLOGY Protein Discovery Catalog'. Below the heading is a descriptive paragraph: '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.' The main content area features a 'Protein List' table with a search bar and two filter buttons: 'Show all disease areas' and 'Show all reactome pathways'. The table displays two entries for Alpha-1B-glycoprotein.

Protein List	Search		Show all disease areas	Show all reactome pathways	
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

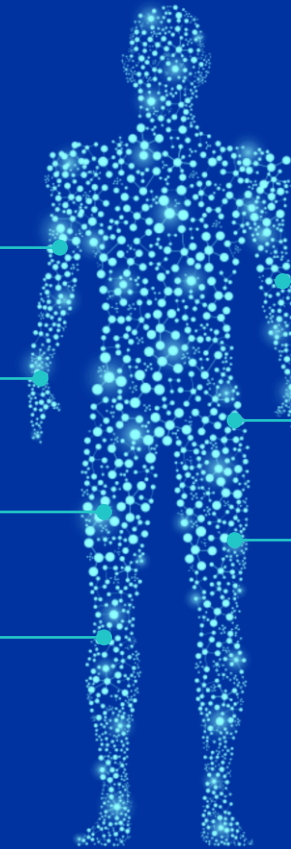
Diagnostics

Reproductive health

Complex disease

Rare disease

Infectious disease

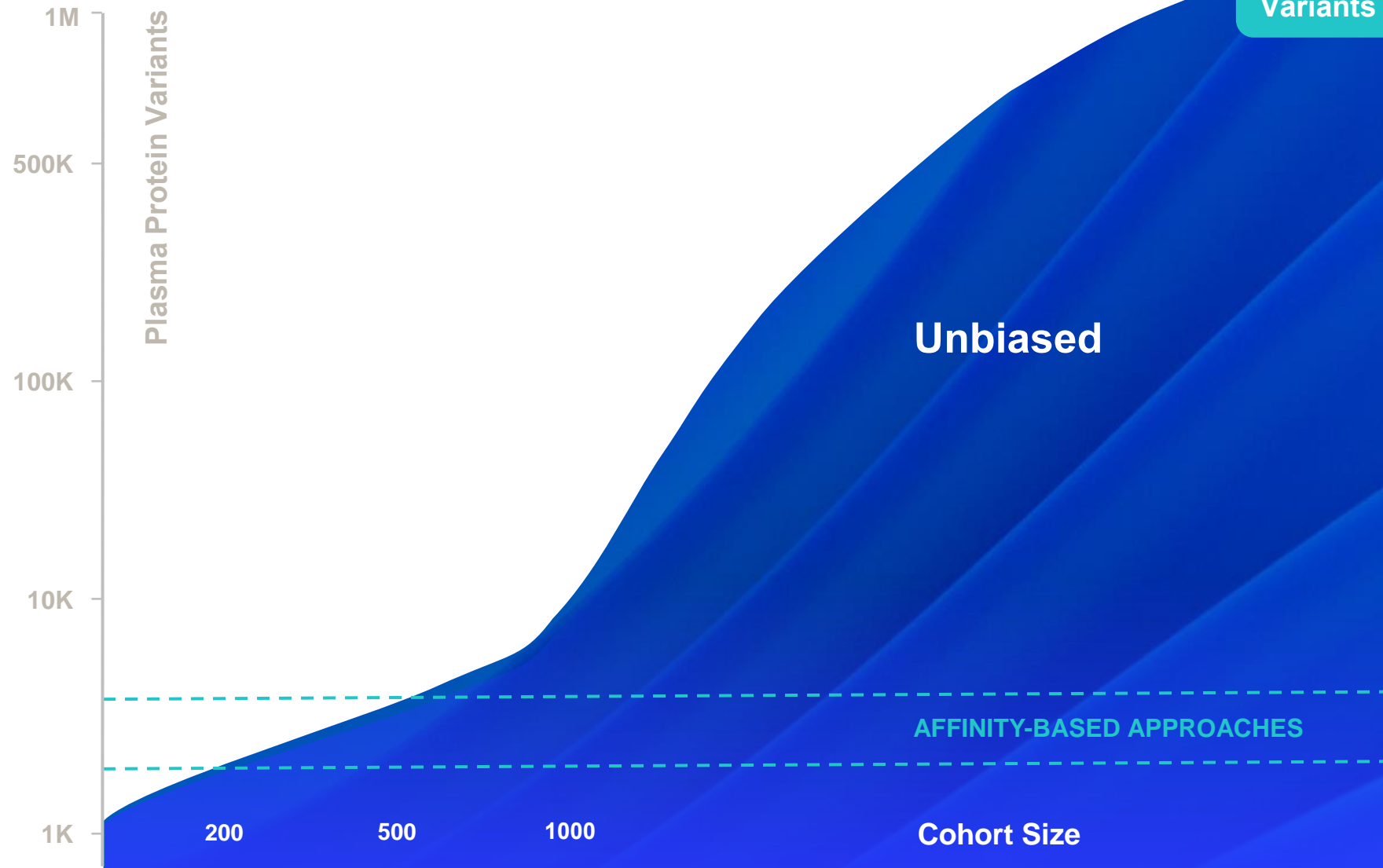


Proteograph enables proteomic content discovery

1

1M+
Variants

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

180

Public presentations to date

48

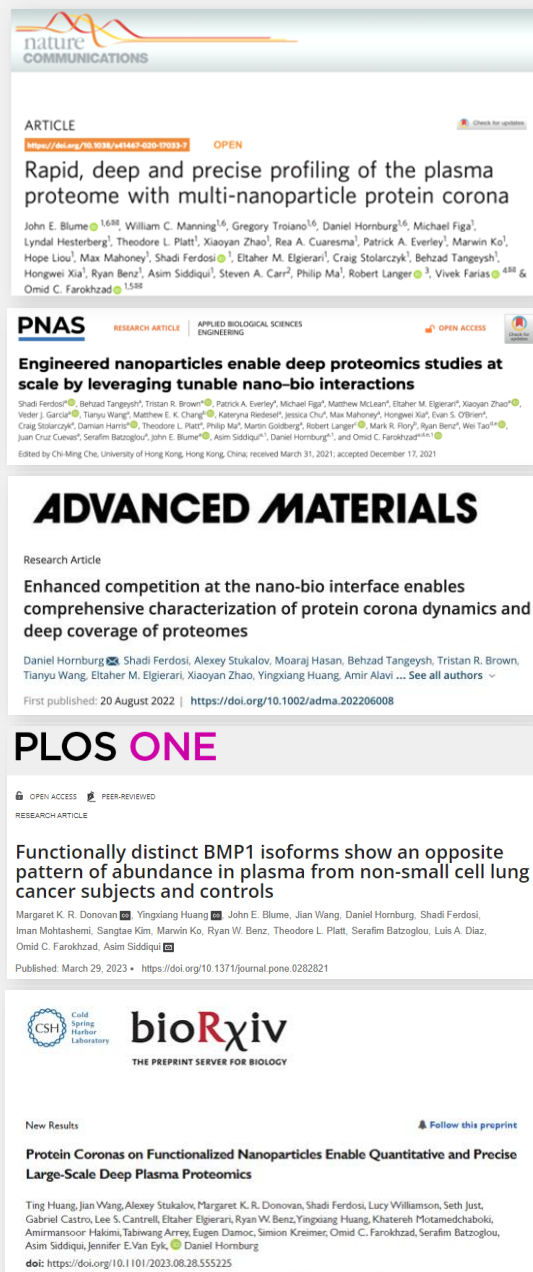
Posters and presentations by customers

8

Manuscripts in bioRxiv

4

Peer-reviewed articles



Emergence of Third-Party Customer Publications

3

>10 publications submitted by customers

April

June

September

October

January

bioRxiv
THE PREPRINT SERVER FOR BIOLOGY

New Results [Follow this preprint](#)

Nanoparticle Enrichment Mass-Spectrometry Proteomics Identifies Protein Altering Variants for Precise pQTL Mapping

Karsten Suhre, Guhan Ram Venkateshram, Harendra Gurusu, Anna Halama, Naiba Sheehan, Gurav Thangaj, Hira Sarwath, Khaterah Mozamedchaboki, Margarete Donovan, Asim Siddiqui, Serafini Battagelou, Frank Schmidt
doi: <https://doi.org/10.1101/2023.04.20.537640>
This article is a preprint and has not been certified by peer review [what does this mean?]

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New Results [Follow this preprint](#)

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

Michael D. Roberts, Bradley A. Ruple, Joshua S. Grodin, Mason C. McIntosh, Shao-Tung Chen, Nicholas J. Kontos, Anthony Agin-Birukoraj, Max Michel, Daniel L. Prodan, Madison L. Mattingly, C. Brooks Mobley, Tim N. Ziegenfuss, Andrew D. Fregie, Andreas N. Kavazis
doi: <https://doi.org/10.1101/2023.06.02.543459>
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Longitudinal Deep Multi-Omics Profiling in a *CLN3^{del7/8}* Minipig Model Reveals Novel Biomarker Signatures for Batten Disease

Mitchell J. Reckziegel, Brittany Lee, Christine Nevills, Ting Huang, Alex Rosa Campos, Khaterah Mozamedchaboki, Daniel Hornburg, Tyler B Johnson, Vicki J Swier, Jill M Wiemer, Jon J Bruening
doi: <https://doi.org/10.1101/2023.09.20.558629>
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OMICnAge: An integrative multi-omics approach to quantify biological age with electronic medical records

Qingwen Chen, Veronik Dvorakova, Naikola Camargo-Galvis, Kevin Hendrix, Yulu Chen, Sofia Begum, Pysybhakshi Karthikeyan, Nikita Prasad, Harshil Wani, Tavis Hendrix, Arjun Liu, Logan Turner, Patrick Hoyle, Scott H. Chu, Richard S. Kelly, Scott T. Weiss, Nicholas J.W. Hoang, Victor H. Galanter, Elizabeth Karhson, Craig W. Hoesly, Amy A. Pflieger, Amber Duhon, Huihua J. McGeehee, Ryan Smith, Jessica A. Lusty-Su
doi: <https://doi.org/10.1101/2023.10.16.562114>
This article is a preprint and has not been certified by peer review [what does this mean?]

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ABSTRACT
Biological aging is a multifactorial process involving complex interactions of cellular and biochemical processes that is reflected in omic profiles. Using common clinical laboratory measures in ~30,000 individuals from the MGB-BioBank, we developed a robust, predictive biological aging phenotype, EMICnAge, that balances clinical biomarkers with overall mortality risk and can be broadly implemented across EMRs. We first validated EMICnAge in

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New Results [Follow this preprint](#)

The effects of resistance training on denervated myofibers, senescent cells, and associated protein markers in middle-aged adults

Bradley A. Ruple, Madison L. Mattingly, Joshua S. Grodin, Mason C. McIntosh, Nicholas J. Kontos, Anthony Agin-Birukoraj, Max Michel, Daniel L. Prodan, Shao-Tung Chen, Tim N. Ziegenfuss, Andrew D. Fregie, L. Bruce Gladden, Austin T. Robinson, C. Brooks Mobley, Arjun L. Hoyle, Michael D. Roberts
doi: <https://doi.org/10.1101/2023.10.04.560958>
This article is a preprint and has not been certified by peer review [what does this mean?]

[Abstract](#) [Full Text](#) [Info/History](#) [Metrics](#) [Preview PDF](#)

ABSTRACT
Denervated myofibers and senescent cells are hallmarks of skeletal muscle aging. However, sparse research has examined how resistance training affects these outcomes. We investigated the effects of unilateral leg extension resistance training on denervated myofibers, senescent cells, and associated protein markers in middle-aged participants (MA, 55-61 years old, 17 females, 9 males). We obtained vastus lateralis (VL) muscle cross-sectional area

medRxiv
THE PREPRINT SERVER FOR HEALTH SCIENCES

New Results [Follow this preprint](#)

Multi-omics profiling with untargeted proteomics for blood-based early detection of lung cancer

Brian Koh, Hanwei Liu, Rebecca Almona, Daniel Arad, Christina Bundhara, Jessica Chen, Jinhua Chen, Yan-Pan Chou, Rex Coimbra, Estelita Hoad, Lavinia Hoad, Tanya Pli, Anisha Jhu, Endah Kuswandi, Yitong Kuo, Anshu Kishore, Jason-Steve Lee, Stephanie Lewis, Chih-Hung Lin, Mark Maragani, Heide Theodorou, Haseem Pata, Nitona Poddar, Lara Nouri, Guizhen, Mahavandhi Ramani, Javeda Ramamama, Purva Ramesh, Guanghui Shi, Peter Sato, Benjamin N. Diano, Vitaliia Shteyn, Zachary Tashiro, Robert Zaretski, Jeremy Y. Zeng, Susan Zivak, Janna Yekimov, E. Bruce, Glenora Balharadea, Bruce Wilson, Prita Ma
doi: <https://doi.org/10.1101/2024.01.03.24300798>
This article is a preprint and has not been certified by peer review [what does this mean?]. It reports new medical research that has yet to be evaluated and so should not be used to guide clinical practice.

[Abstract](#) [Info/History](#) [Metrics](#) [Preview PDF](#)

Abstract

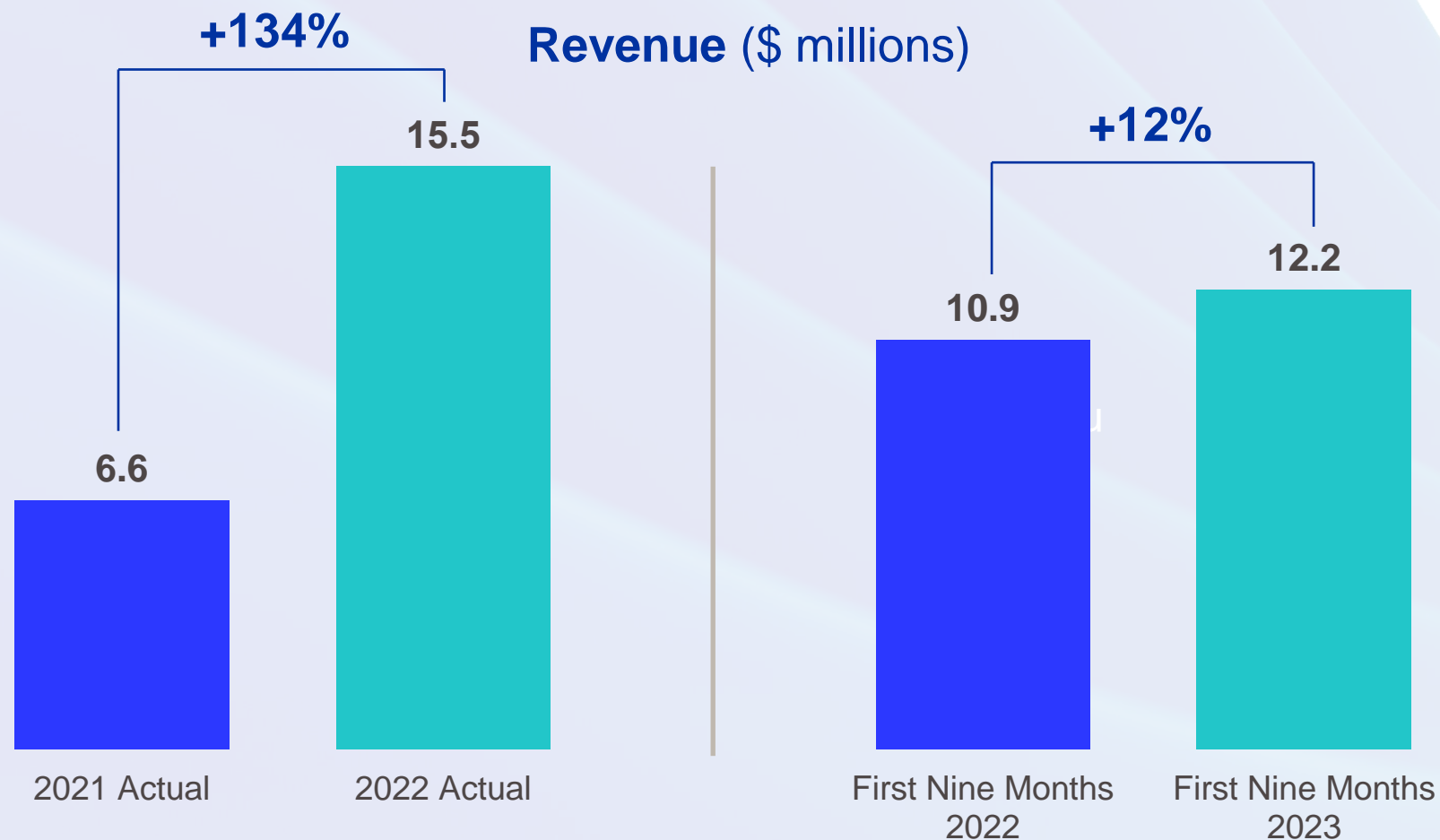
Growing revenue and strong balance sheet

Strong Balance Sheet¹

\$381 Million

Cash, Cash Equivalents
and Investments

No Debt



1. As of September 30, 2023

Market development to broad scale adoption

Revenue inflection point

Phase 4

Widespread adoption and revenue growth

Phase 3

Biological insight

We are here

Phase 2

Facilitate scaling

Phase 1

Content discovery

Growth

Time

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

~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

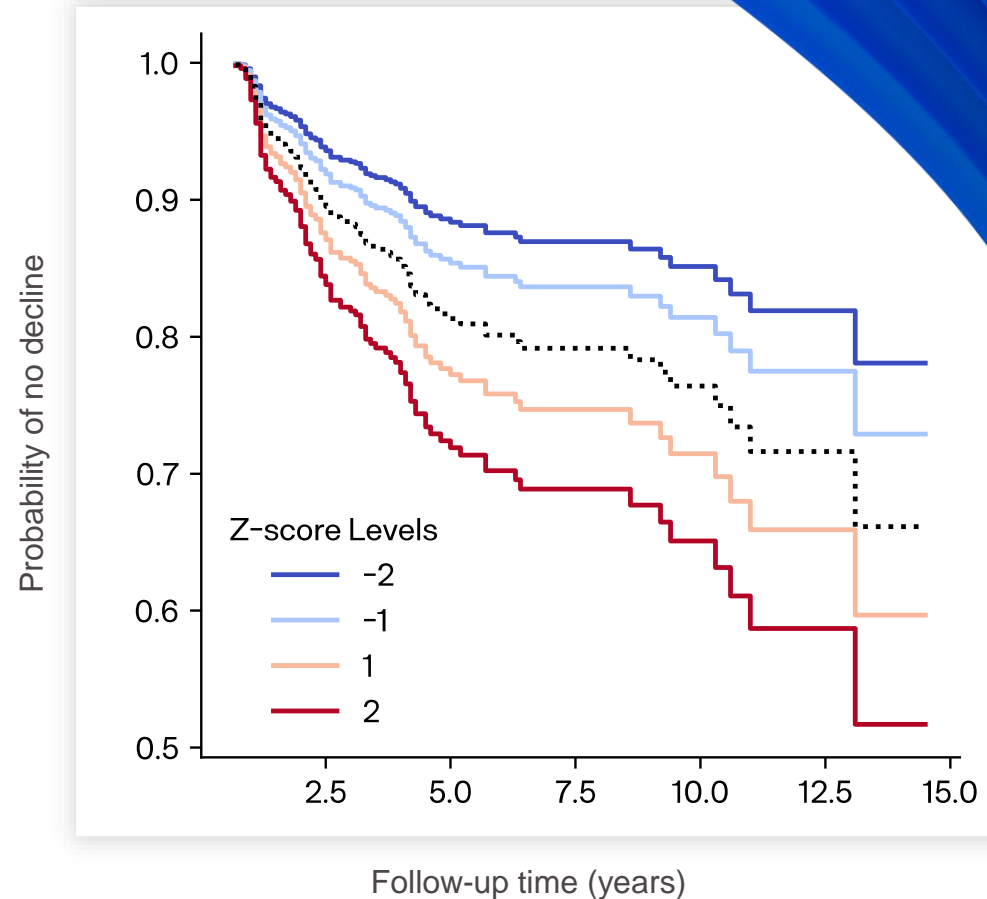
Putative novel Alzheimer's disease biomarkers

8

identified markers distinguishing fast and slow progressors of cognitive decline

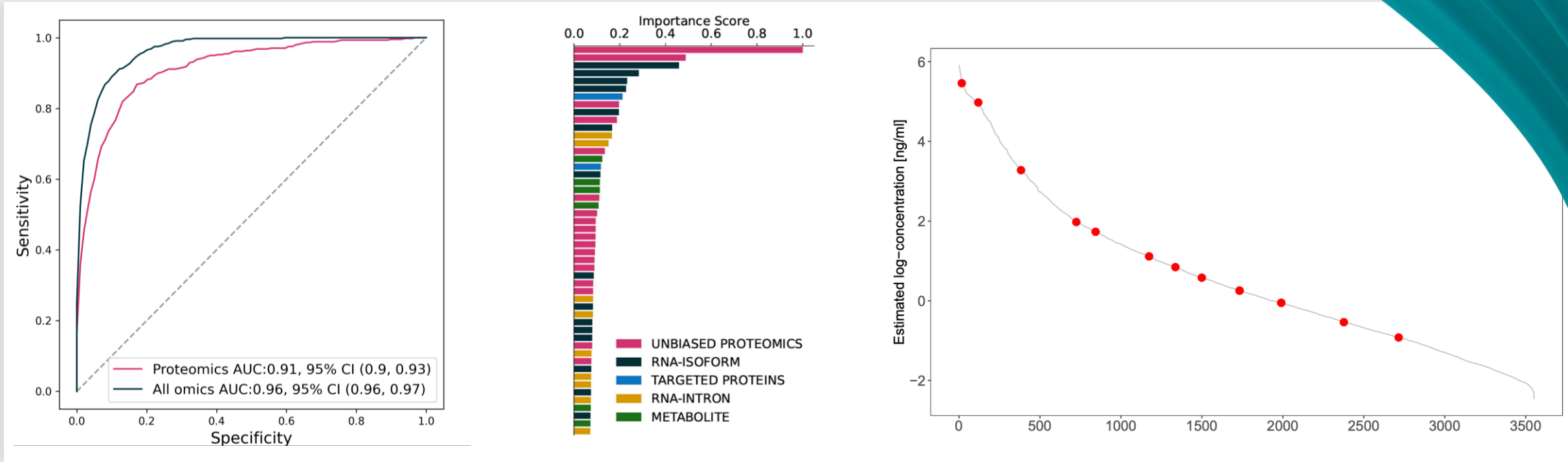
75%

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



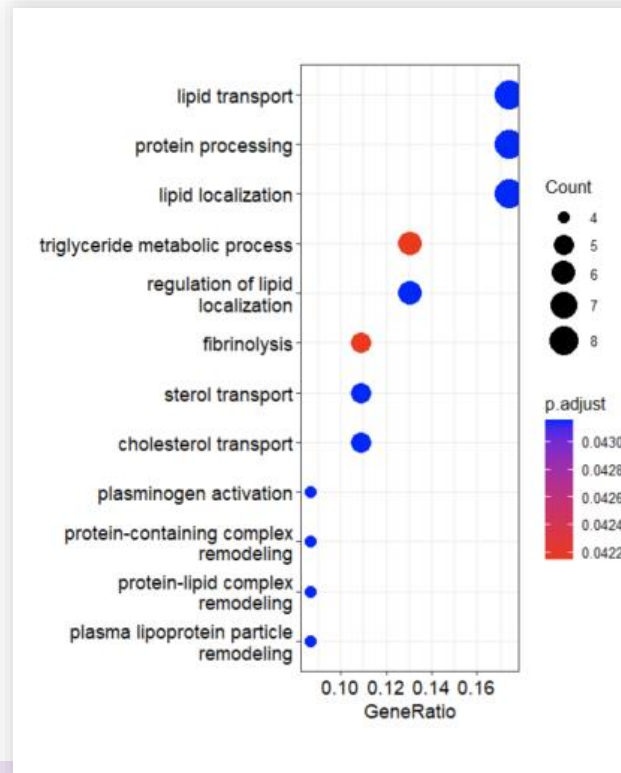
✓ Extremely strong performance

✓ Unbiased proteomics is the key driver

✓ Classifier proteins fall across the dynamic range

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



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

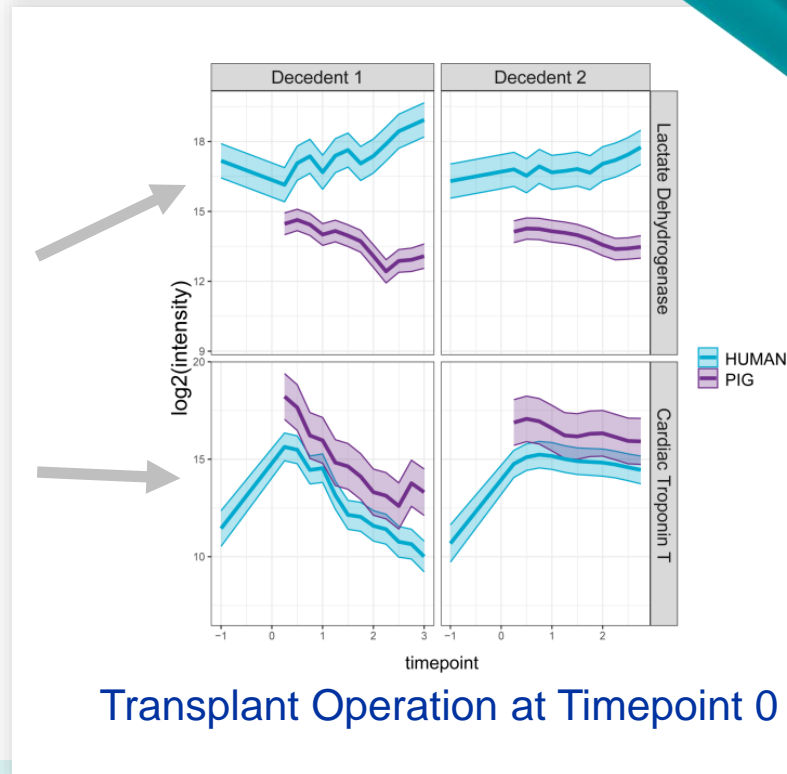
- 2 decedent humans received a pig heart transplant
- Levels of human proteins and their pig ortholog are separately monitored
- Proteograph delivers unique value even for the most complex and unusual sample types

>6,850
human proteins

>1,850
pig proteins



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.**

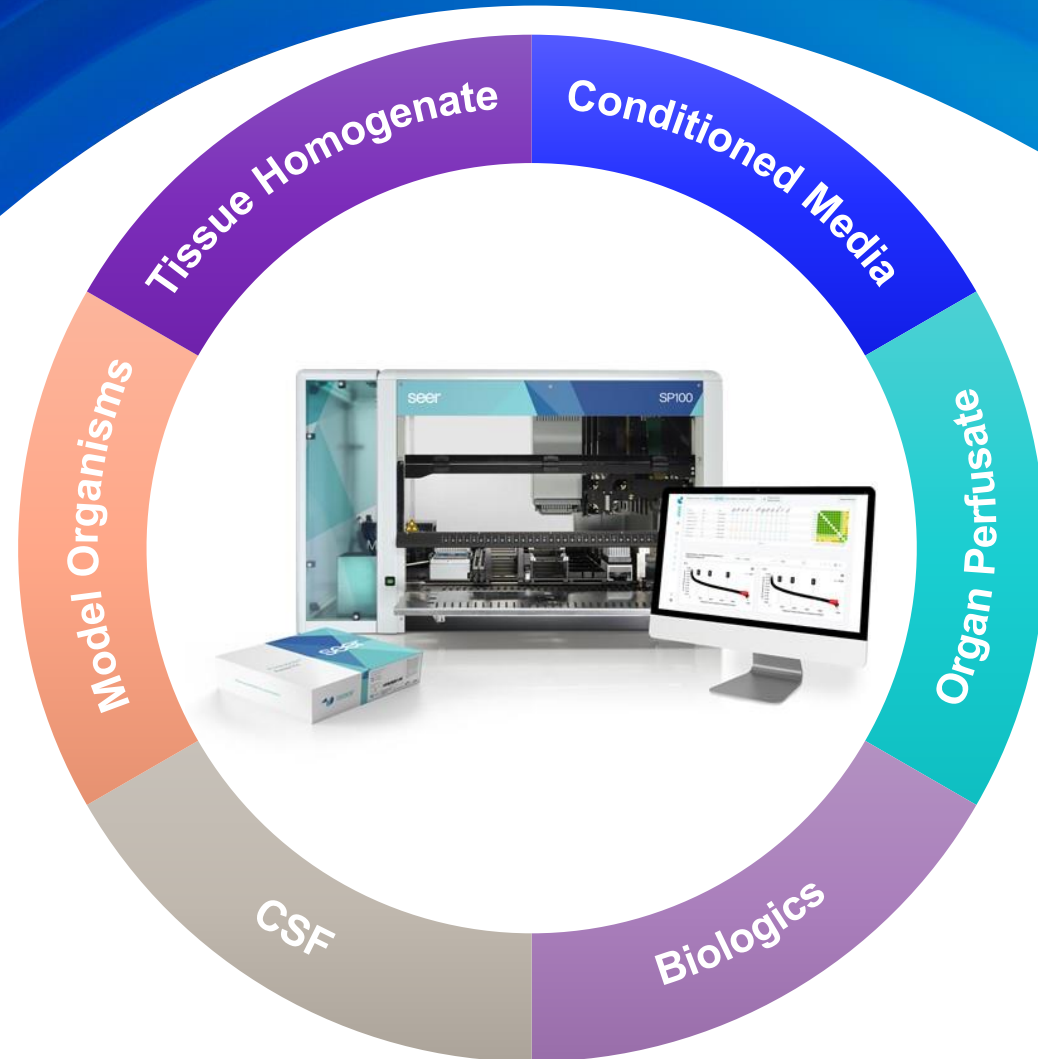


Brendan Keating, PhD

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