

seer

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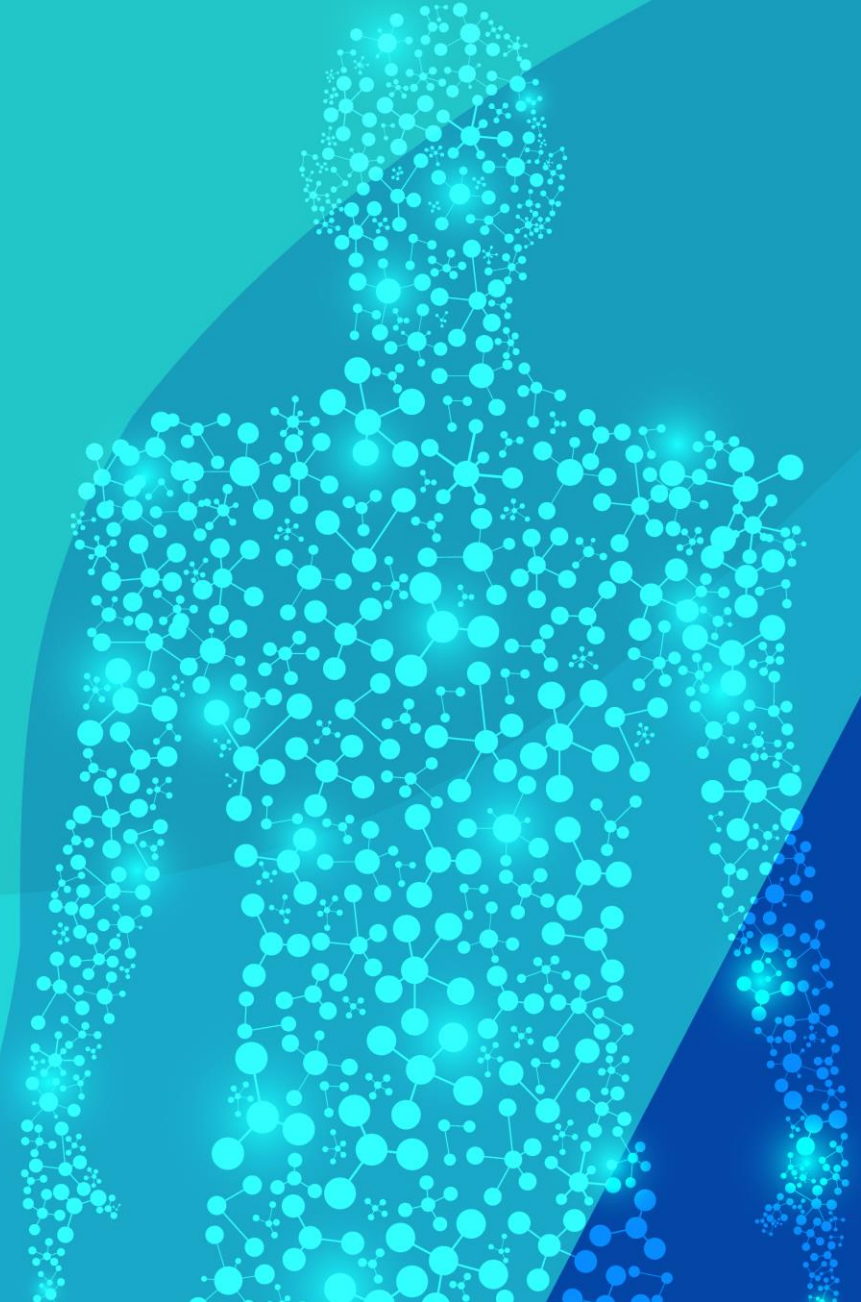
**Seer**  
**40<sup>th</sup> Annual J.P. Morgan**  
**Healthcare Conference**

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Omid Farokhzad, M.D.

CEO, Seer

*January 10, 2022*



# 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 Seer, Inc. (the “Company”)’s 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 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.

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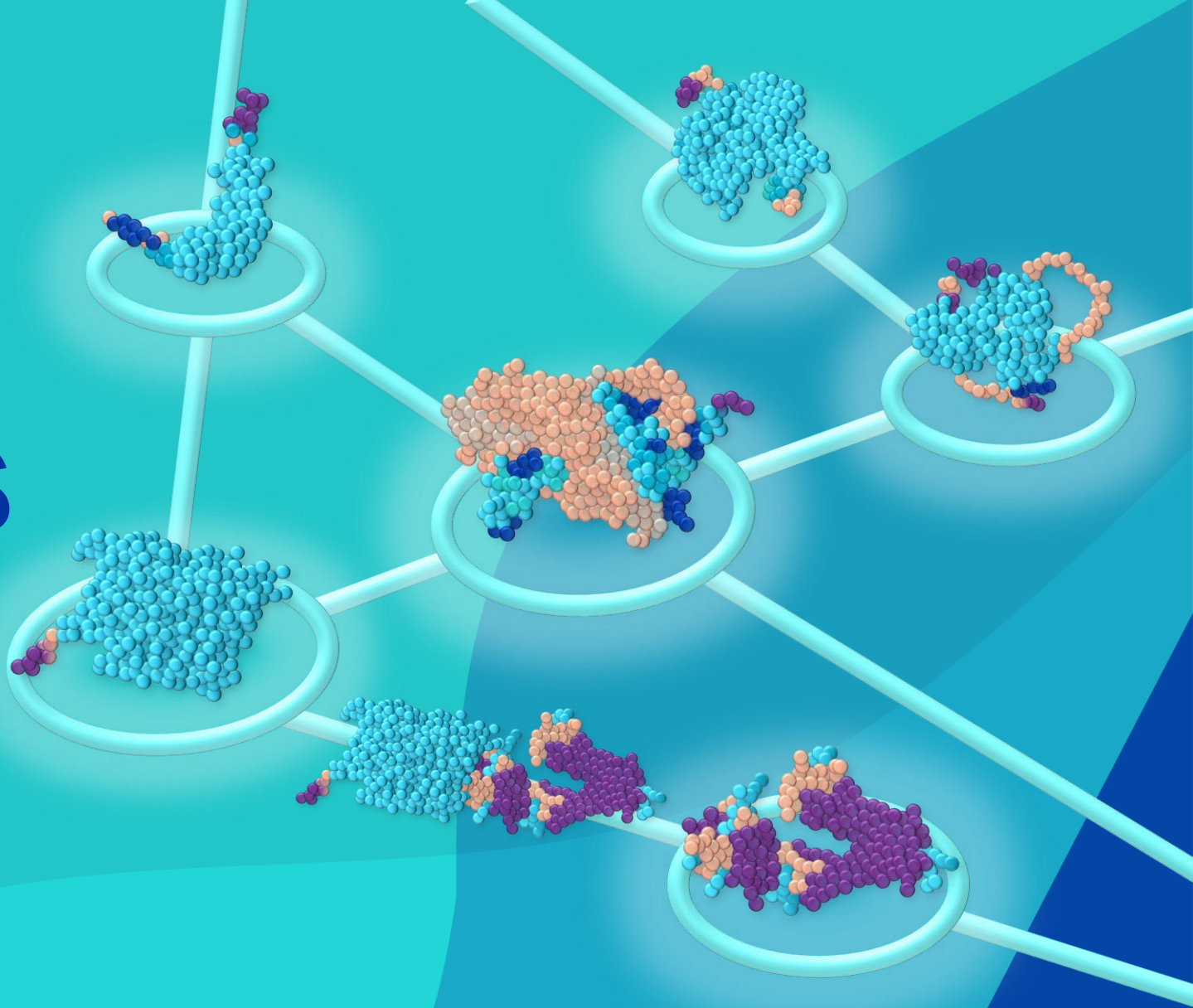
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We imagine and  
pioneer new ways to

# decode the secrets of the proteome

to improve human health

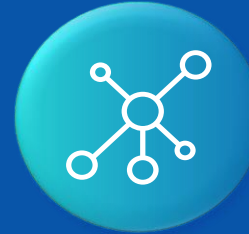


# Seer is leading the proteomics revolution



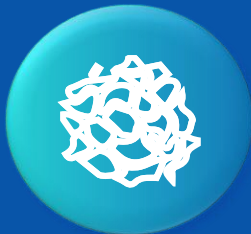
## Leading customers and collaborators

Lighthouse customers  
Well designed customer experience



## Creating new markets

Industry leading partners  
Geographically positioned



## Best in class technology

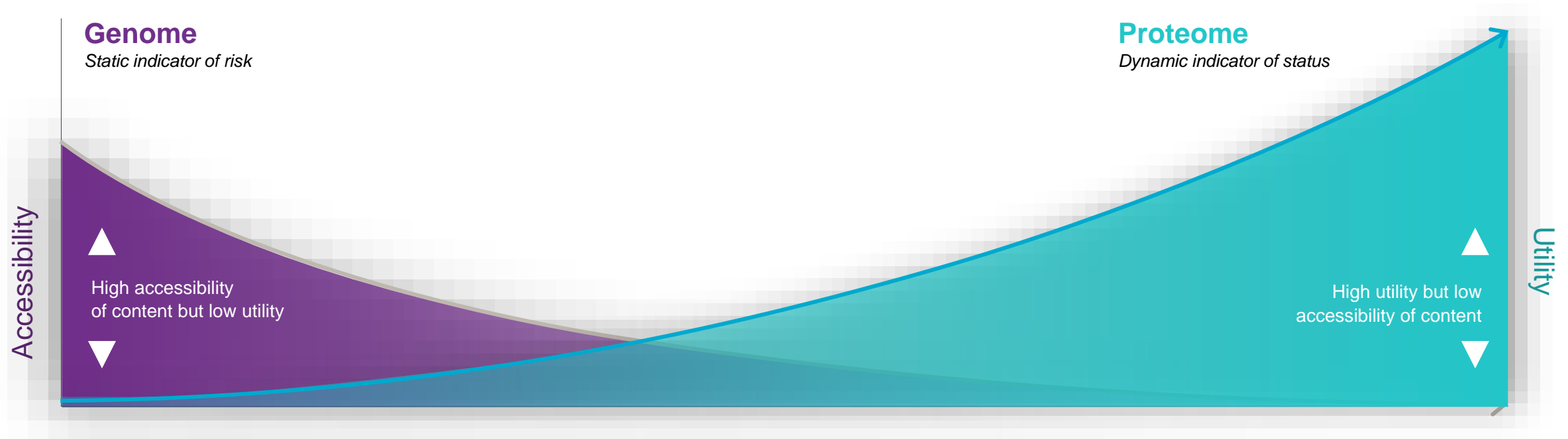
Uniquely enabling technology  
Data demonstrating impact



## Leading team with multi-omics expertise

Culture of innovation  
Industry-leading talent

# Full characterization of the proteome is essential



10M+ human exomes and  
1M+ genomes and counting



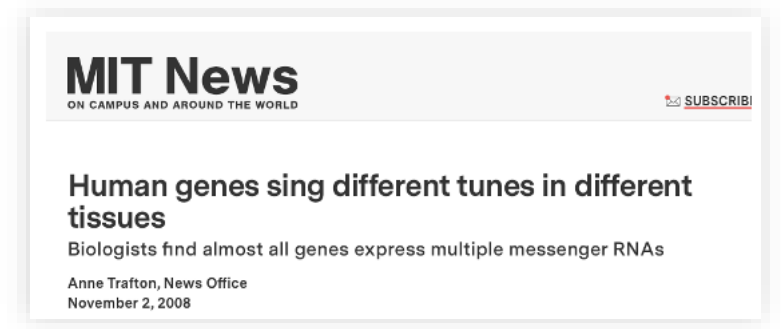
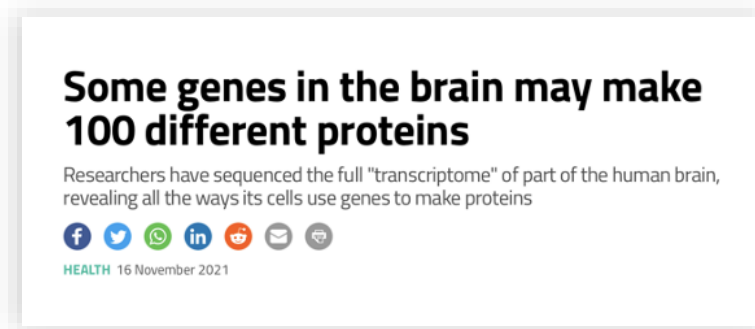
~1B genetic  
variants catalogued



< 0.2% of genetic variants  
fully characterized



# Biology is a dynamic and complex matrix of interactions



**~20,000**  
Genes



**Genome**

**>200,000**  
Transcripts



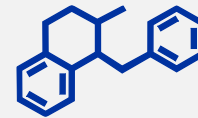
**Transcriptome**

**>1,000,000**  
Proteoforms



**Proteome**

**>200,000**  
Metabolites



**Metabolome**

**STATIC**

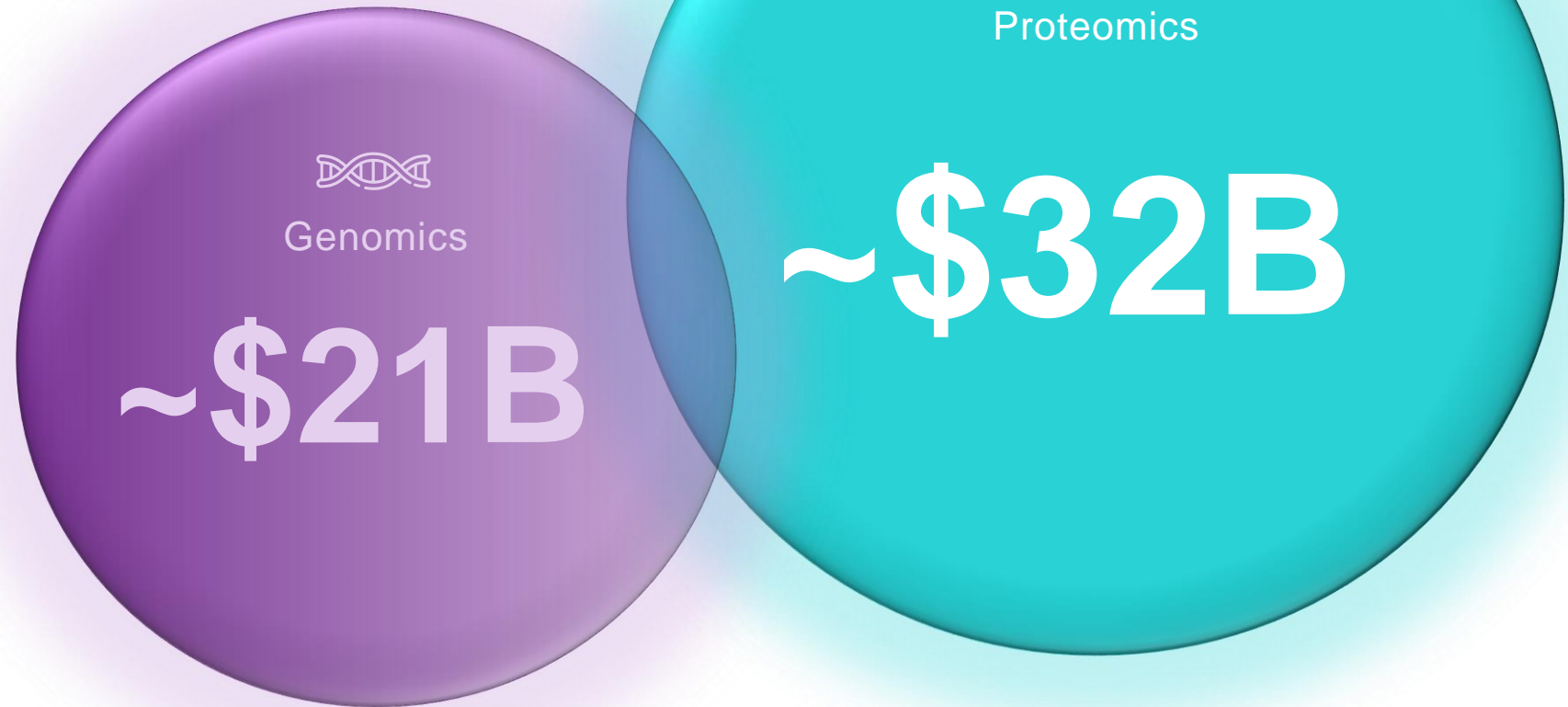


**DYNAMIC**

**Phenotype**



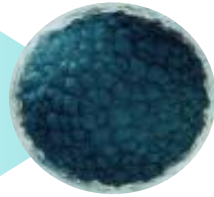
Opening a **new frontier** with  
unbiased, deep, rapid  
proteomics at scale



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



Conventional  
Proteomics Lab



Lab on a  
nanoparticle



## seer

Unbiased

Deep

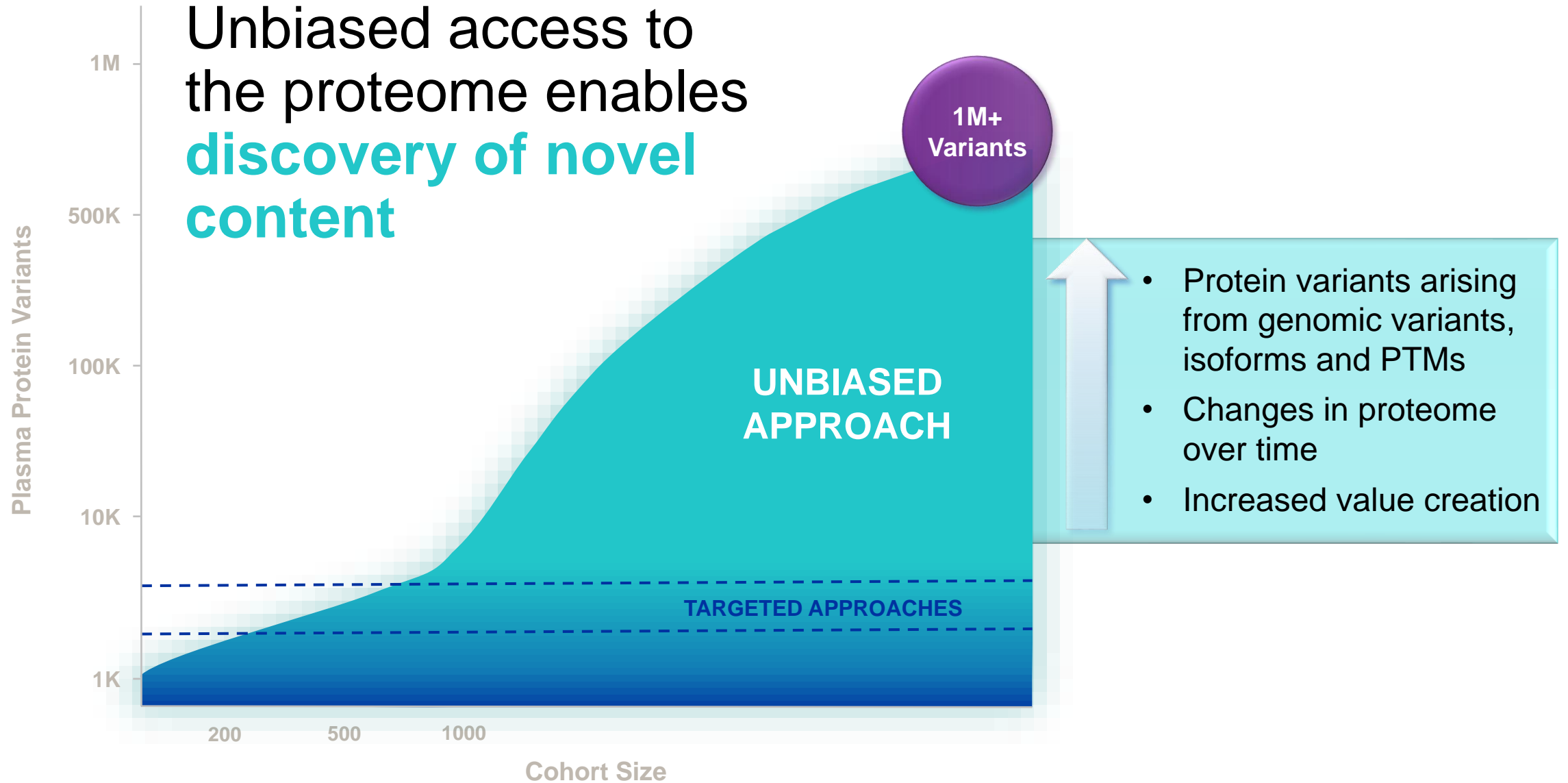
Rapid

Large-scale

A New Gateway to the Proteome



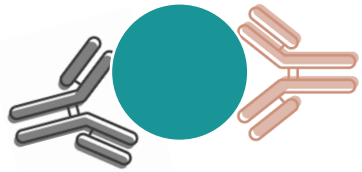
Unbiased access to the proteome enables **discovery of novel content**



# Unbiased approaches identify peptide level insights

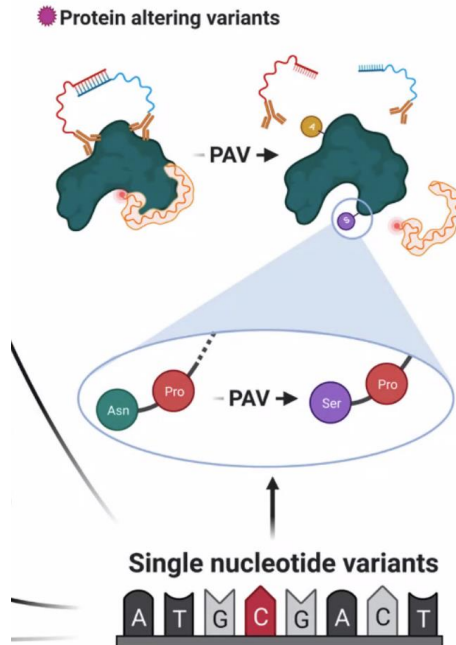
## Targeted Approaches

Miss the Vast Majority of Protein Altering Variants



Average human protein:  
472aa long

Average epitope:  
5-8 aa long



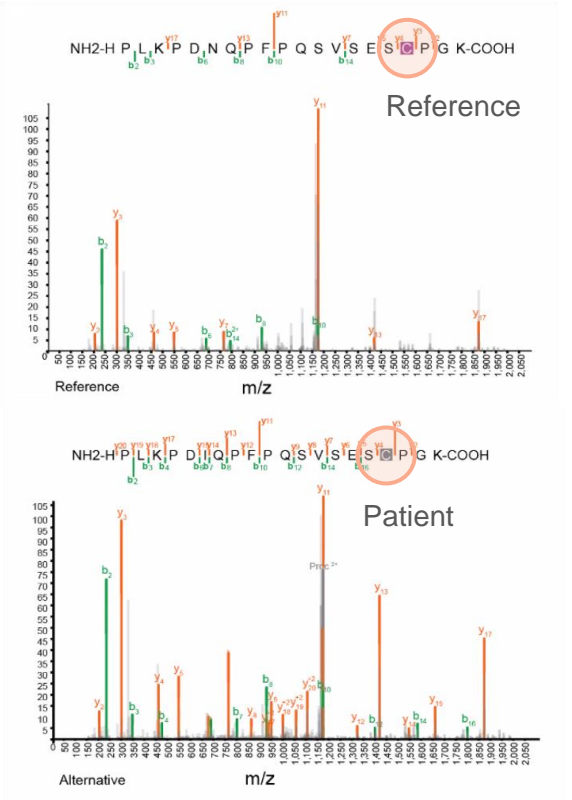
Pietzner, et al Nature Communications, Nov 2021

**“Protein–phenotype  
colocalisation ... goes  
beyond missing target  
specificity and can be  
explained by alternative  
proteoforms induced  
by genetic variants  
altering the amino acid  
sequence of the protein  
and the effects of  
alternative splicing”**

*Pietzner, et al Nature  
Communications*

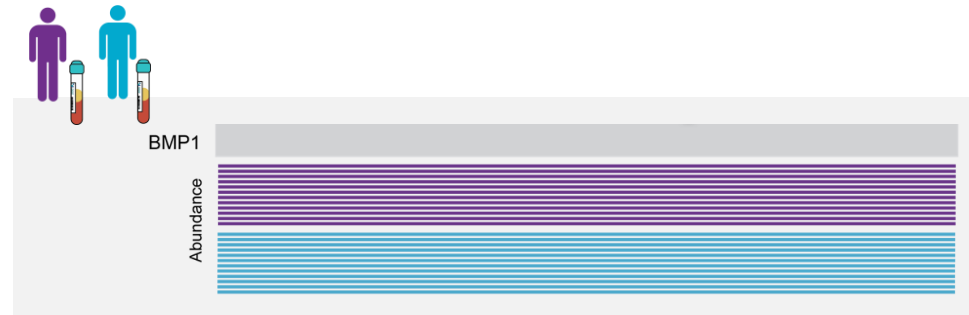
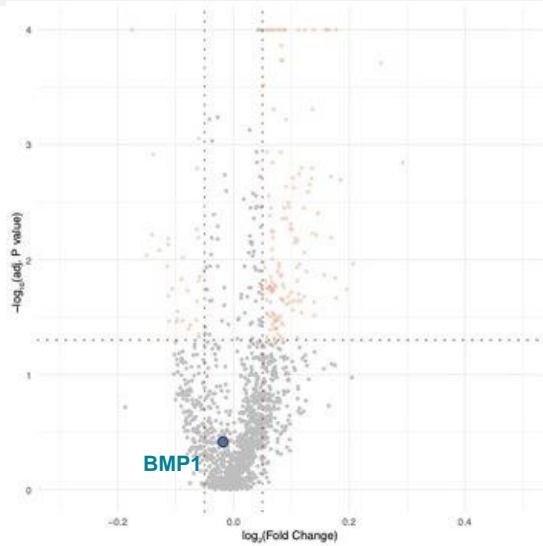
## Unbiased Approaches

Capture Common and Rare Variants

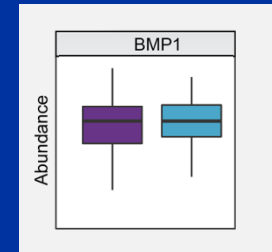


# Unbiased approaches identify peptide level insights

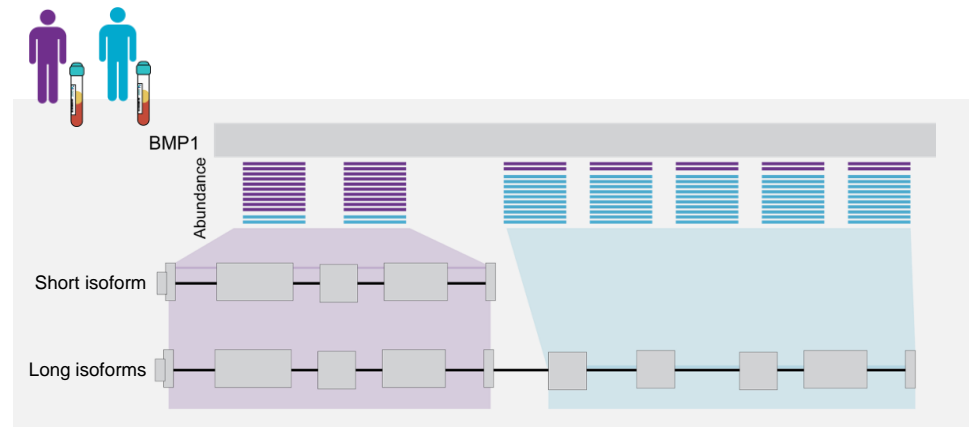
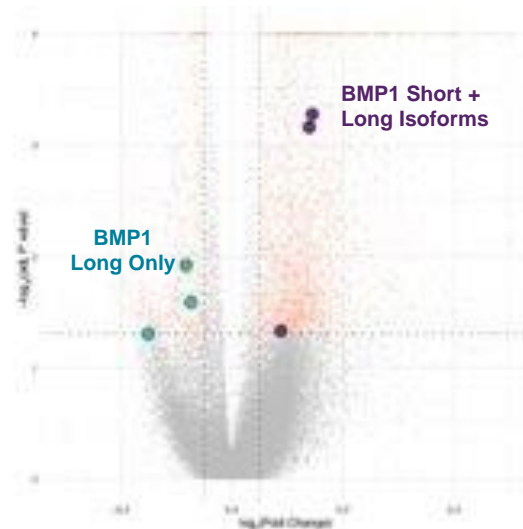
## Protein Level



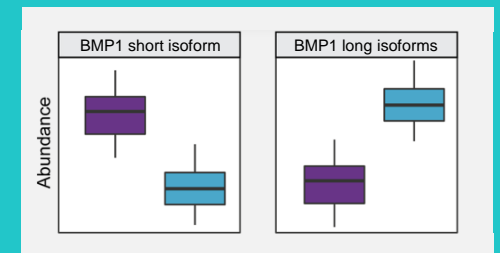
No Difference  
Detected



## Peptide Level

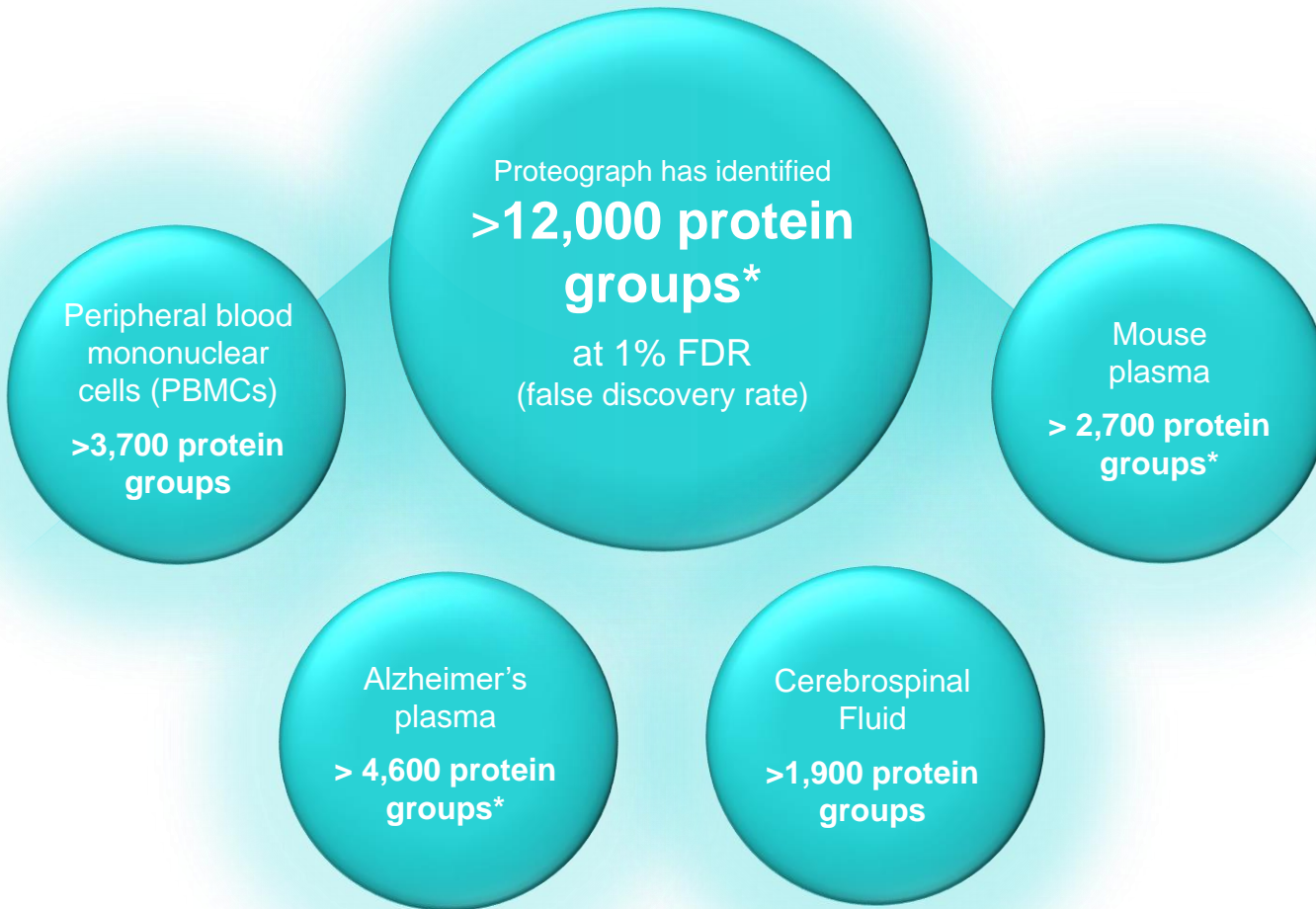


Meaningful Difference  
Detected

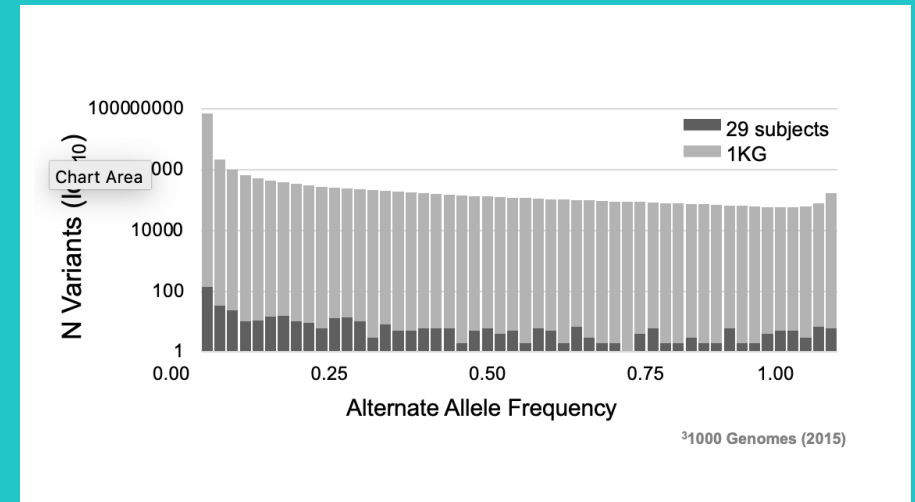


# Unbiased approaches **identify what is present** in a sample

The Proteograph identifies what is present in the sample at a controlled FDR



The Proteograph captures protein variants...



...including

Isoforms

PTMs

Alleles (at any frequency in the population)

Small open reading frame (smORFs)

# Strong finish to 2021



Completed first two phases  
of commercial release



25+ unique abstracts



Established industry-  
leading partnerships



Systems sold in US,  
Korea, China, EMEA



Doubled organization



# Announcing Broad Commercial Release of the **Proteograph Product Suite**

Uniquely enabling technology for deep, unbiased proteomics

Streamlined workflow and analysis to enable large-scale studies

Simplified solution accessible to nearly any lab



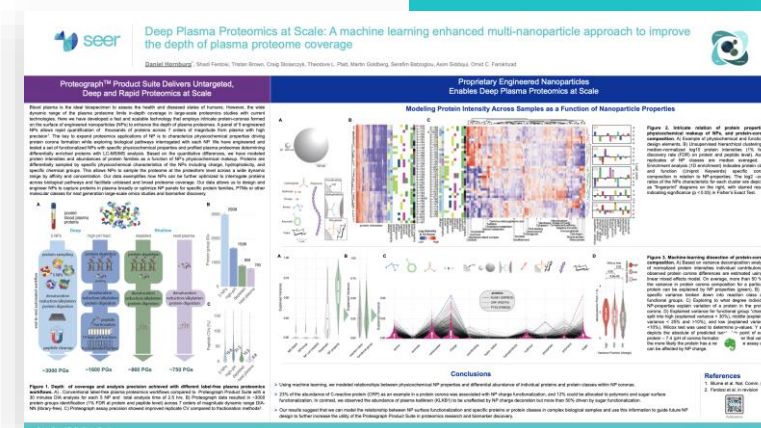
# Positioned to **lead the proteomics revolution**

*Building an ecosystem around unbiased, deep proteomics*



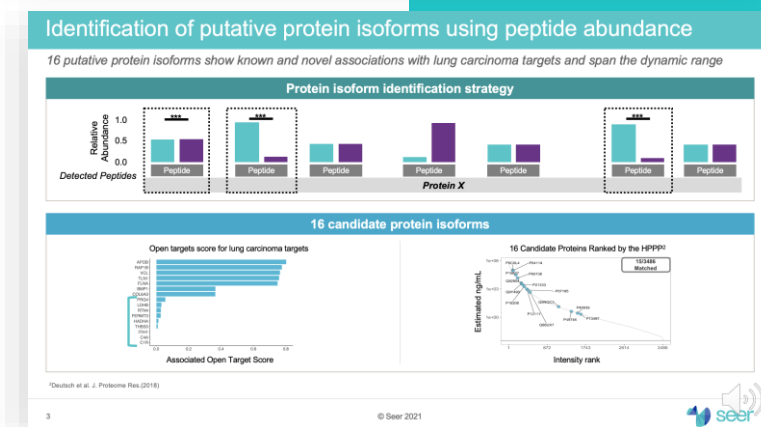
# Technology uniquely positioned to enable deep, unbiased proteomics

Seminal publications demonstrate the power of Seer's proprietary engineered nanoparticles



Deep and precise coverage of the plasma proteome  
*Ferdosi, et al, in press, PNAS*

Optimization of protein coronas to increase proteome depth  
*Manuscript in pre-print\**

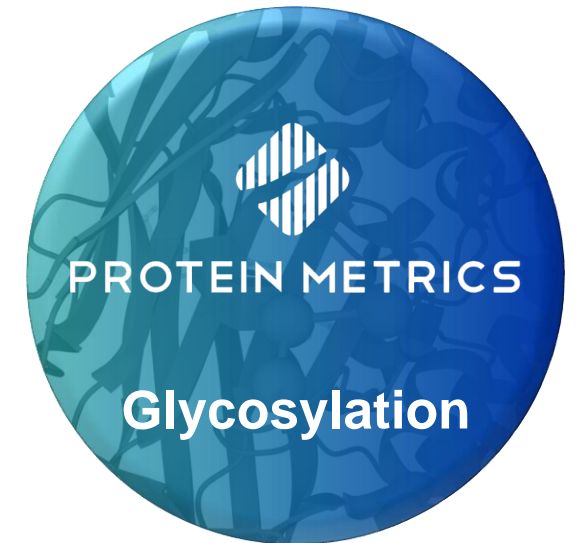


Proteoform detection with peptide-centric analysis  
*Manuscript in pre-print\**

Hornburg D, et al., 2022. Enhanced competitive protein exchange at the nano-bio interface enables ultra-deep coverage of the human plasma proteome. *bioRxiv*.

Donovan MKR, et al., 2022. Peptide-centric analyses of human plasma enable increased resolution of biological insights into non-small cell lung cancer relative to protein-centric analysis. *bioRxiv*.

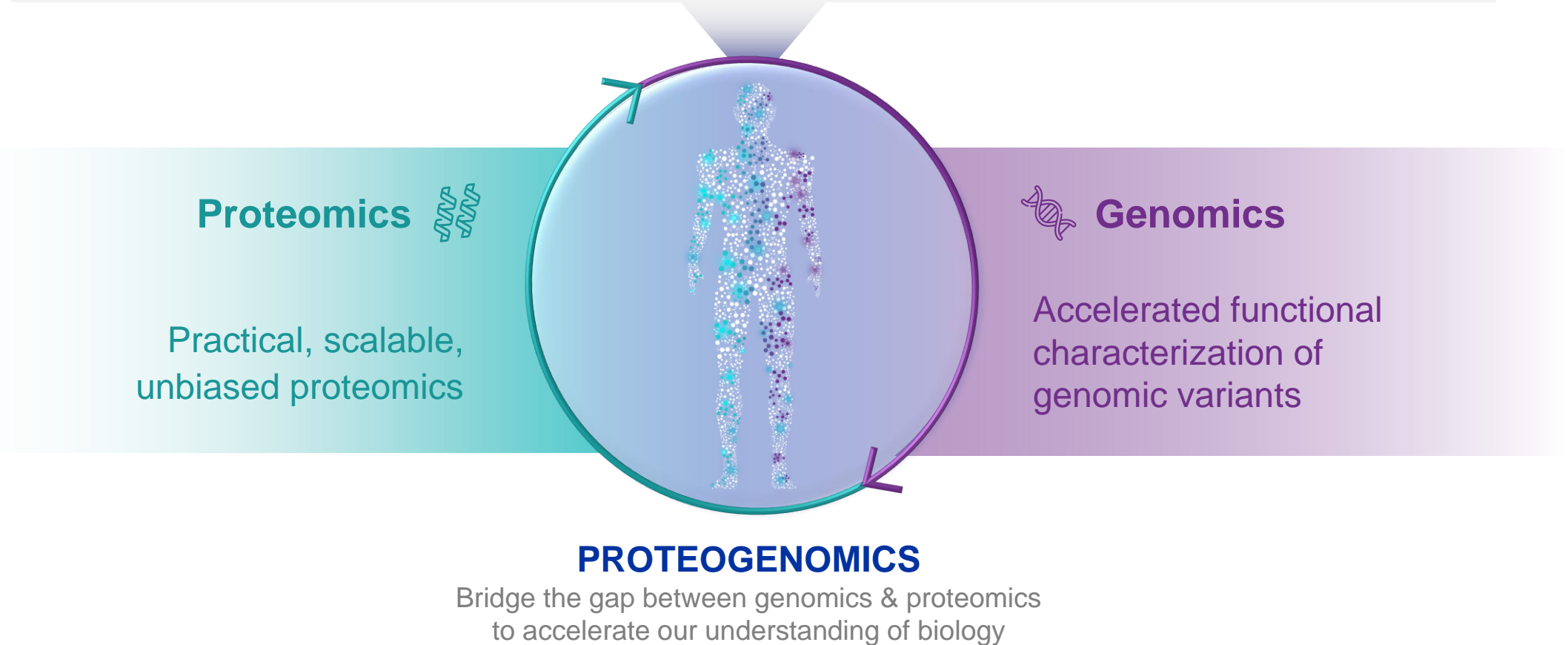
# Enabling new applications & insights in customers' hands



# Enabling proteogenomics by impedance matching genomics

*Unmet need to functionally characterize genomic variation and deepen our understanding of biology*

Oncology   Diagnostics   Complex Disease   Infectious Disease   Rare Disease   Therapeutics   Reproductive Health



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# Empowering unprecedented studies for unbiased plasma proteomics

*Prior to Seer, the largest published deep, unbiased plasma proteomics studies were in the 10s of samples*



**Prostate Cancer**

**1,000 samples**



**Disease Multi-omics**

**2,000 samples**



**Aging**

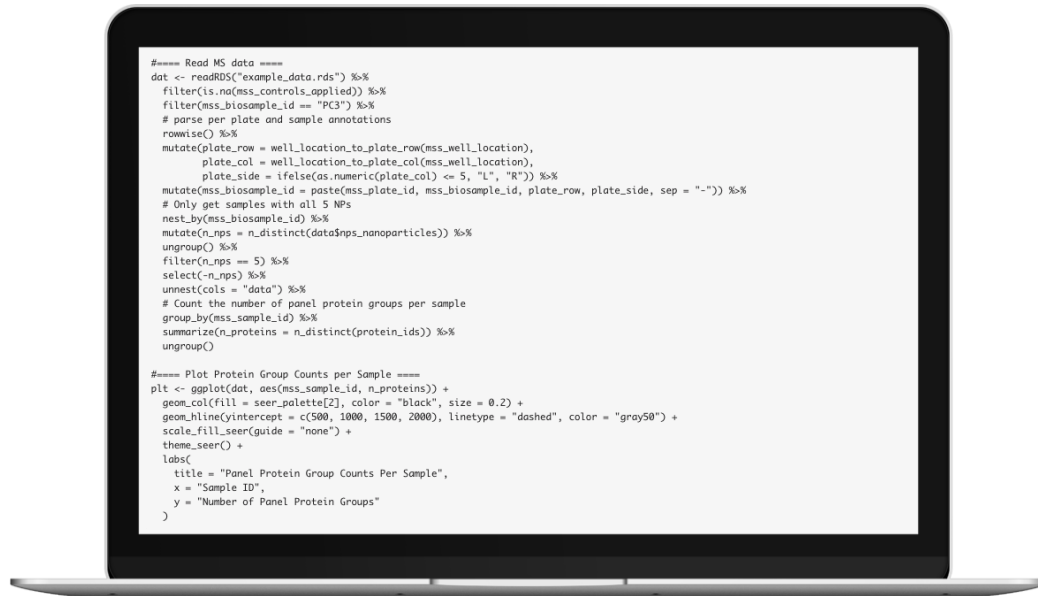
**1,500 samples**

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# Making deep, unbiased proteomics **analysis more accessible**

*Making it easier to access deep, unbiased, rapid proteomics at scale with Proteograph Analysis Suite*

## Past



Advanced  
Data  
Analysis



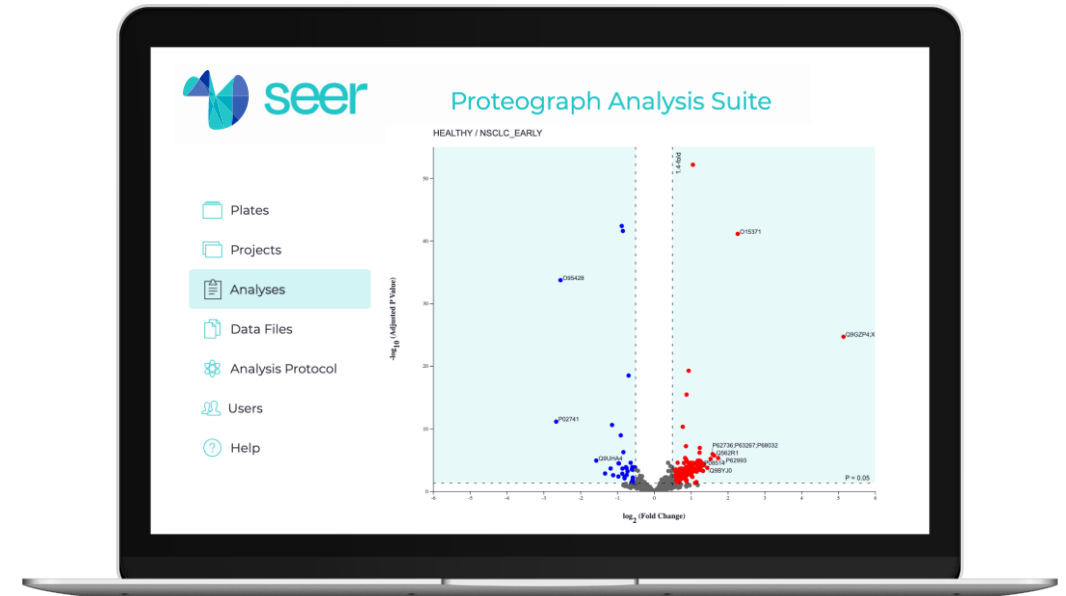
Multiple experts



Weeks+



## Today



*Recapitulates Nature Communications results*



1 user



9 clicks, <1 minute  
to visualization

© Seer 2022

# Making deep, unbiased proteomics **geographically more accessible**

*Building access to deep, unbiased, rapid proteomics with key partners and Centers of Excellence program*

## Key partnerships to expand access across geographies and customer groups



Increase access in **Europe**  
with one of the world's  
premier service providers



Accelerate and simplify  
adoption especially among  
**academic/pharma** customers



Provide access to research  
and healthcare customers in  
**Asia Pacific**



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# Making deep, unbiased proteomics **more accessible to more labs**

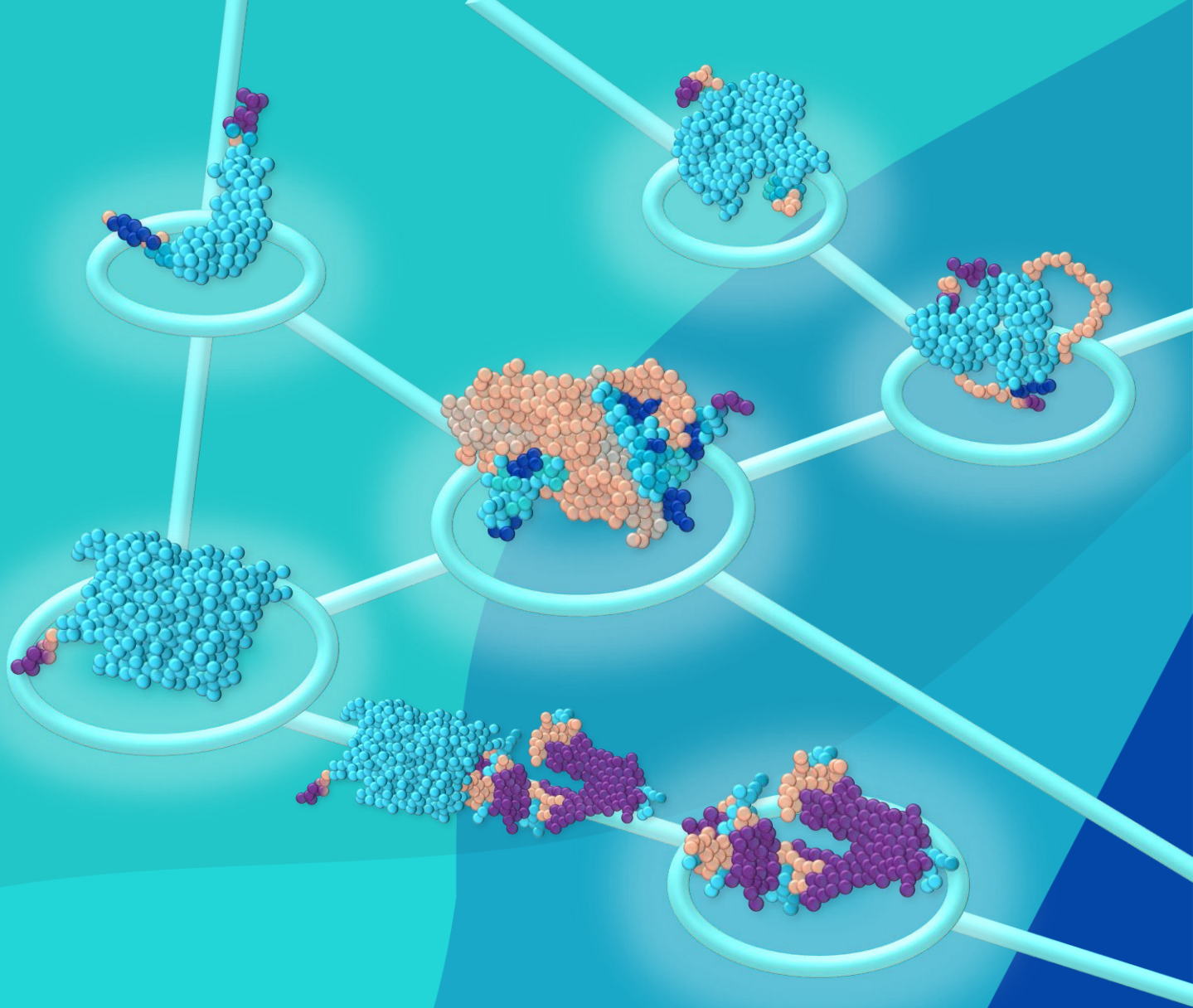
*Announcing the Proteogenomics Consortium to expand the availability of proteomics to genomics customers*



**BRINGING PROTEOMICS TO GENOMICS CUSTOMERS**



# Looking ahead...





# Our vision is to understand biology in a **dynamic, broad way**

TODAY

FUTURE



Protein Variants

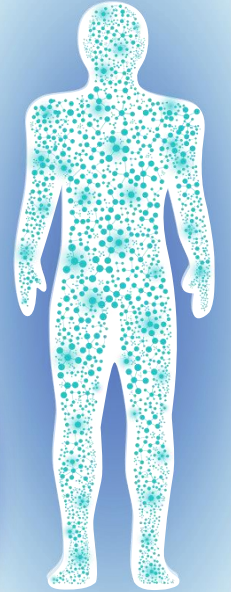
Proteogenomics

PTMs

Other biomolecules

Deep  
Proteomics

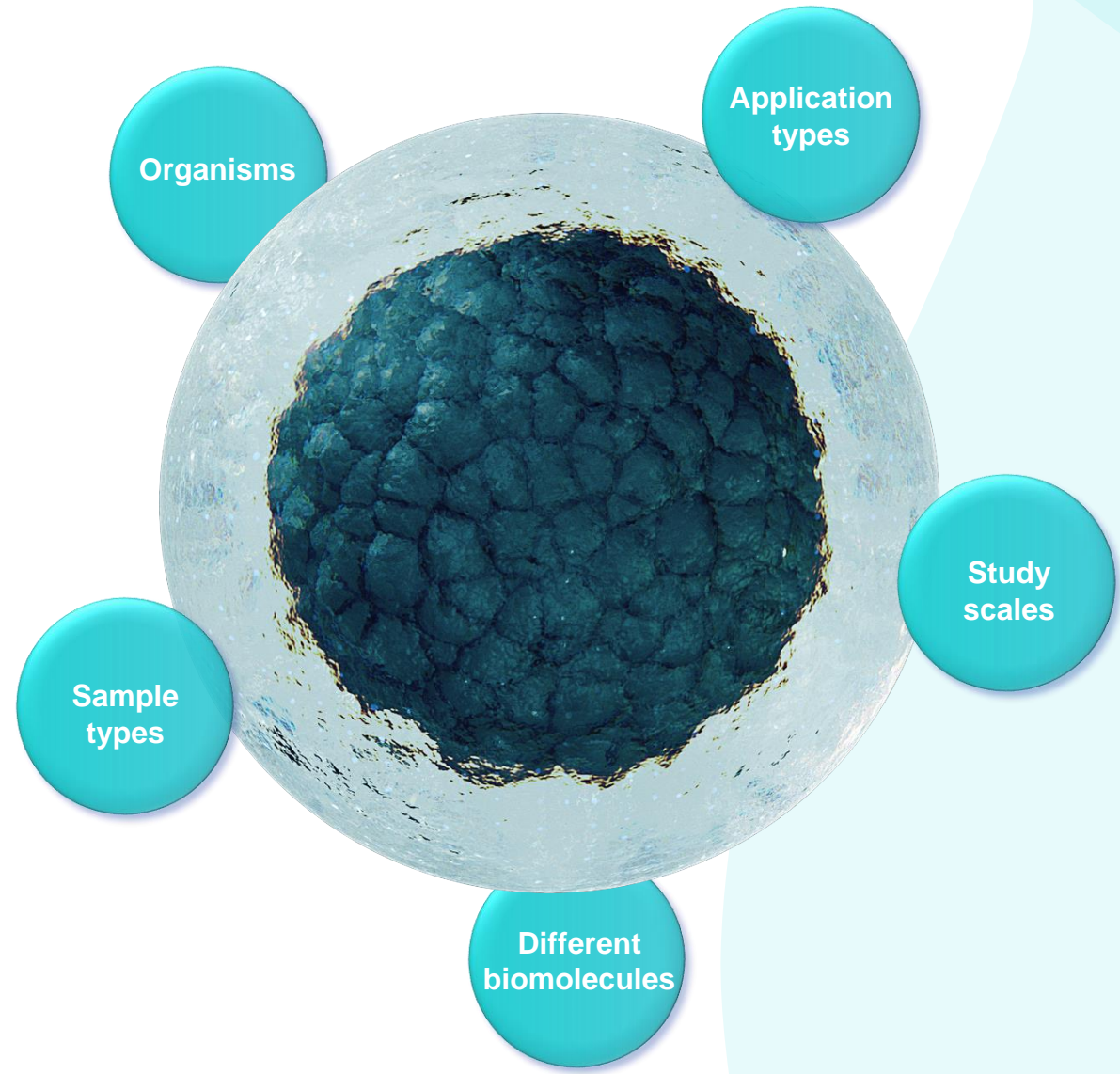
+  
Deep  
Multi-omics



COMPREHENSIVE  
MOLECULAR  
PHENOTYPE

FROM A PINHOLE TO A PANORAMA

# Unconstrained interrogation of biology enabled by proprietary nanoparticles



# Continued execution in 2022



## Leading customers and collaborators

- ✓ Continue to grow installed base
- ✓ Facilitate the execution of large-scale studies using the Proteograph Product Suite



## Best in class technology

- ✓ Further product roadmap to open up a new gateway to biology
- ✓ Pave the way for future clinical validation of our technology
- ✓ Exemplify how deep unbiased proteomics enables discovery of novel content



## Creating new markets

- ✓ Partner in novel ways to standardize deep proteomics workflows and insights
- ✓ Broadly enable proteogenomics



## Leading team with multi-omics expertise

- ✓ Continue to build a team of world-class talent
- ✓ Expand global infrastructure and team to support expanding customer base

seer

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# Q & A

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Omid Farokhzad, M.D.

