

Investor Presentation

September 2022

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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 888

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





< 0.2% of genetic variants fully characterized



Biology is a dynamic and complex matrix of interactions

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, 20}, Gloria M. Sheynkman ^{1, 2, 3, 17}, Tong Hao ^{1, 2, 3, 17}, Aaron Richardson ^{1, 2, 3}, Song Sun ^{7, 8, 9, 10}, Fan Yang ^{7, 8, 9}, Yun A. Shen ^{1, 2, 3}, Ryan R. Murray ^{2,} ^{3, 21}, Kerstin Spirohn ^{1, 2, 3}, Bridget E. Begg ^{1, 2, 3, 22}, Miquel Duran-Frigola ¹¹, Andrew MacWilliams ^{2, 3, 23},

Some genes in the brain may make 100 different proteins

Researchers have sequenced the full "transcriptome" of part of the human brain, revealing all the ways its cells use genes to make proteins

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HEALTH 16 November 2021

MIT News

SUBSCRIB

Human genes sing different tunes in different tissues Biologists find almost all genes express multiple messenger RNAs Anne Trafton, News Office November 2, 2008







Advances and limitations of genomics has crystalized the need for **novel proteomics discovery at scale**



Unmet Need:

Unbiased deep proteomics at scale to power discovery of novel insights

Seer is uniquely positioned to address this need across range of customers, applications and geographies



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

Genomics

~\$21B



Proteomics

~\$32B



Seer enables unbiased, deep and rapid proteomic analysis at scale



Conventional Proteomics Lab Lab on a nanoparticle





A New Gateway to the Proteome



Seer's **Proteograph™ Product Suite**

Designed to enable researchers globally to access the proteome in a new way





Proteograph outperforms traditional deep unbiased methods

Proteograph reproducibly captures more proteins and low abundant proteins than other deep methods



Seer identifies ~4x more protein groups than neat plasma³

Seer covers more proteins at lower intensity than alternative workflows³

Seer median CV <20% and deep fractionation 1.5X higher (31.2%)³



11 2 Keshishian, et al. Nature Protocols (2017)

3 Ferdosi et al. PNAS (2022).







Unbiased approaches identify peptide level insights





Unbiased approaches identify what is present in a sample



The Proteograph captures protein variants...



...including Isoforms PTMs Alleles (at any frequency in the population) Small open reading frame (smORFs)



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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 all 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





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



Margaret K. R. Donovan, Yingxiang Huang, John E. Blume, Jian Wang, Daniel Hornburg, Iman Mohtashemi, Sangtae Kim, Marwin Ko, Ryan W. Benz, Theodore L. Platt, Serafim Batzoglou, Omid C. Farokhzad, Asim Siddiqui doi: https://doi.org/10.1101/2022.01.07.475393



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Proteograph enables unbiased access to low abundant chemokines and cytokines at scale





Enabling new applications & insights in customers' hands







Examples of Customer Data at the Most Recent 2022 ASMS Conference

Multiple abstracts from customers as well as Seer demonstrating unique capabilities of the Proteograph

Pancreatic Cancer	Serum Proteome	Spaceflight Plasma Proteome
Case-control multi-omic study	Ultra-high proteome coverage	Deep proteome interrogation
	evotec	SPACEX Weill Cornell Medicine
 92 cancer and 104 healthy subjects 	 105 patient study shows unprecedented proteome 	 Changes in Reactive Oxygen Species, Telomeric DNA Binding,

- Achieves high predictive power driven by biomarker signatures compared to other published pancreatic cancer studies
- Found novel signatures for pancreatic cancer with multiple statistically significant differences in abundance

- unprecedented proteome coverage and depthProteome coverage of 5,000
- Proteome coverage of 5,000 proteins across cohort and >3,000 per sample
- Identified 30% more cytokines vs other deep proteomic workflows
- and Ribosomal Assembly and
 Biogenesis
 3,000 unique protein groups
 identified agrees the small study at
- identified across the small study at 1% false discovery rate
- Found 50 differentially abundant proteins primarily indicative of oxidative stress and metabolic pathways



Enabling proteogenomics by impedance matching genomics

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





Making deep, unbiased proteomics analysis more accessible

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





High-resolution, Proteogenomics At-Scale with PAS 2.0

First-of-its-kind Proteogenomics Workflow paves the way for new, biological insights



PAS enables the visualization of identified peptides' relationship to gene structure, protein domain information, and functional regions



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

*soul*brain



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Strong progress with Proteogenomics Consortium

- Discovery Life Science Updates
 - Targeting initial customer projects in Q4
 - Building out proteomics facility in Boston area
 - In the process of installation and validation, will run a 500-sample internal study
- Seer / Sciex instruments are in place



BRINGING PROTEOMICS TO

GENOMICS CUSTOMERS



Growing revenue and strong balance sheet





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





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

