

# Quantum-Si

# Disclaimer

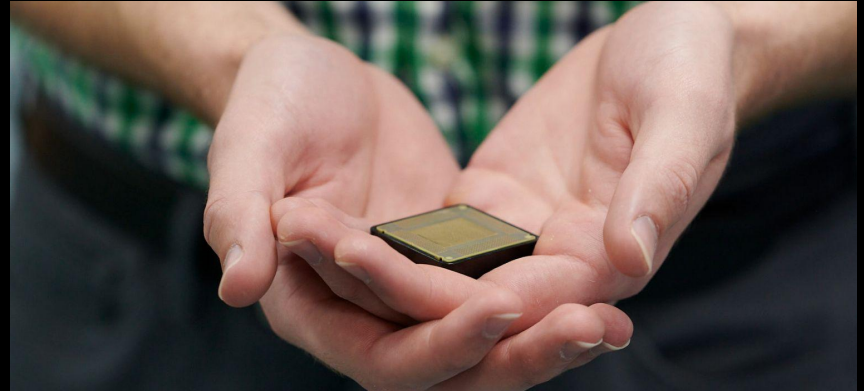
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# Quantum-Si | Enabling Next Generation Protein Sequencing

## Company Overview:

- Founded by Dr. Jonathan Rothberg in 2013
- Publicly traded on the NASDAQ (QSI) in June-2021
- ~\$435M in cash (as of the end of 1Q22)
- >900 patents issued & applications pending
- Established sites in Guilford, CT and San Diego, CA
- Focused on launching the first **Next Generation Protein Sequencing** instrument to interrogate proteins at amino acid resolution

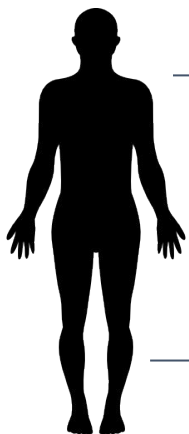
The power of semiconductor chip technology...



...enables massively-parallel, single molecule protein sequencing

We harness the power of  
semiconductor technology for  
Simplicity Speed Scale





20,000 Genes  
(DNA)

A blueprint of "what could be"

1,000,000+ Proteoforms  
(Protein)

A view of "what is happening"

*Proteins are the main structural and functional components of cells and they are extremely diverse*

**\$50B Market**

# 90%

of FDA-approved drugs target a protein<sup>1</sup>

85% of the **human proteome** is currently undrugged<sup>2</sup>, potential for game changing drug development.

**Protein modifications** are real-time indicators of health and disease, making them ideal markers for disease, drug response and health.

Source(s):

1. The Human Proteome Tissue Atlas - Druggable Proteome, 2015, The Human Protein Atlas Project
2. A Quest to Drug the Undruggable, June 2018, Chemical & Engineering News

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# 150,000

research papers found

thousands of protein biomarkers

yet less than

# 100

are used routinely today<sup>1</sup>

Source:

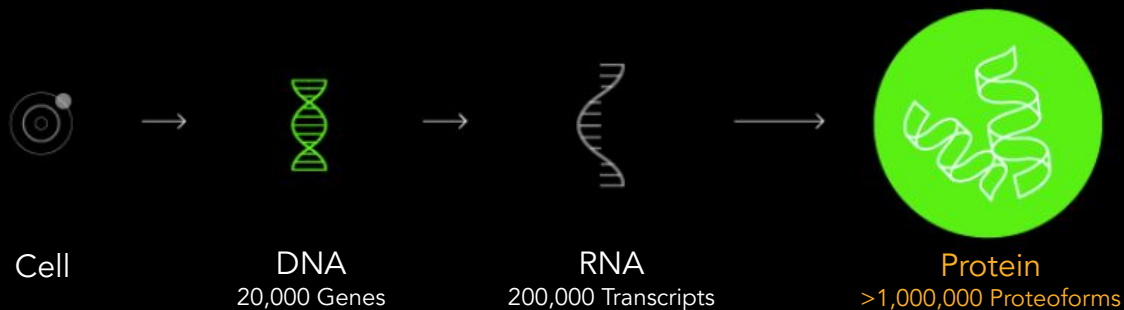
1. <https://www.technologynetworks.com/proteomics/blog/using-protein-biomarkers-increases-the-chances-of-success-in-clinical-trials-329018>

Current tools limit the use of protein biomarkers.

Routine tests for Serum & Cerebrospinal Fluid (CSF) are constrained by number of analytes they can look at, sensitivity, and specificity.



# Digital Technologies Transform Markets – We've Seen This Before



*Analog*  
Microarrays

*DNA (Genomics)*

Affinity Arrays

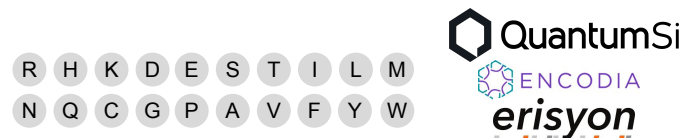
*Proteins*  
(Proteomics)



Analog → Digital transition  
creates new market  
opportunities.

*Digital*  
DNA sequencing

Protein Sequencing



# Approaches to Proteomics

## Digital Sequencing-based Approaches

Decode Novel Sequences

### Quantum-Si

Direct Kinetic  
Real-Time

### Encodia

Binding +  
Degradation with  
NGS readout

### Erisyon

Labeling +  
Degradation  
with scanning

Detection Method

Instrument/Run Costs

AA Sequencing

Read Length Scaling

PTM Detection

Notes

Kinetics for  
amino acids &  
PTMs

\$\$ - \$\$\$

LIMITED

LOW

?

NGS erases  
quantitative  
information

Harsh acidic  
environment  
limits utility

## Analog Affinity-based Approaches

Identify Known Proteins

### SomaLogic / Olink / Nautilus

Antibodies / Aptamers

\$ - \$\$\$

NO

N/A

?(Affinity Reagent)

\*Need to create proteoform specific  
affinity reagent





# Quantum-Si unique solution

## Next Generation Protein Sequencing

### END-TO-END BENCHTOP SYSTEM

Decentralization by enabling the scientific and clinical community

### TIME DOMAIN SEQUENCING™

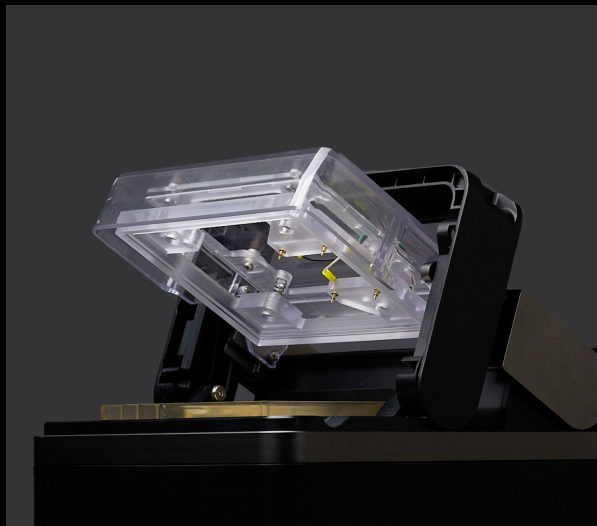
Novel sequencing method that provides interrogation at the amino acid level

### SINGLE MOLECULE RESOLUTION

Absolute (versus relative) measurement of unbiased biology providing novel insights into variant and modifications



# Quantum-Si's End-to-End Benchtop Proteomics Solution



## Sample Prep

**CARBON: \$20,000**

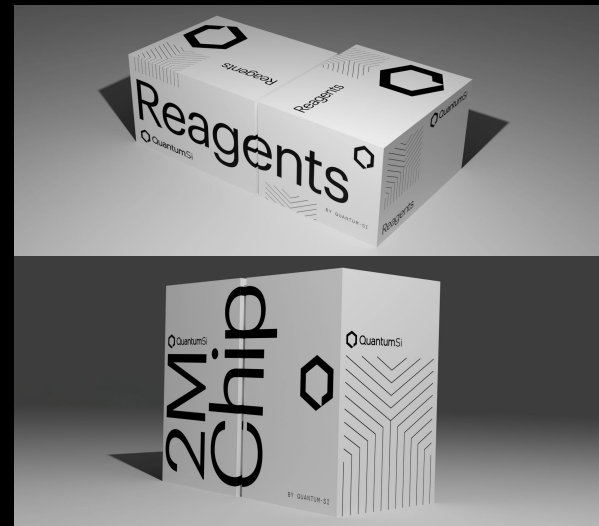
Universal cartridge based sample preparation and automation



## Sequencing & Cloud Analysis

**PLATINUM: \$70,000**

Real-Time, Massively Parallel, Single Molecule Detection



## Reagents & Chips

**CONSUMABLES: \$1,000/each**

Library Prep & Protein Sequencing

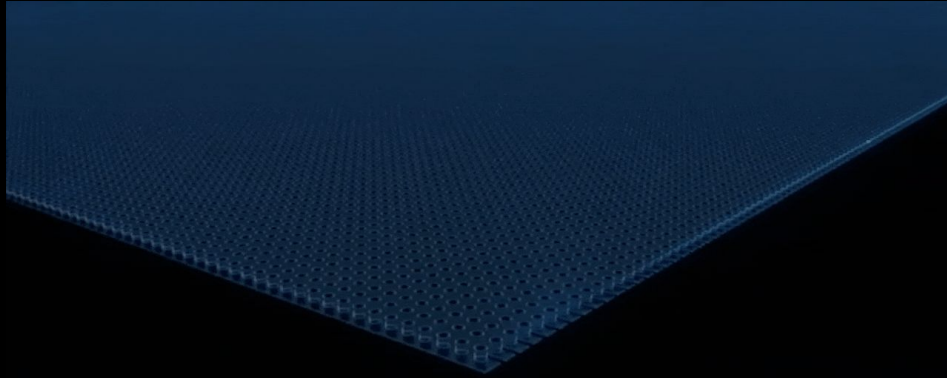


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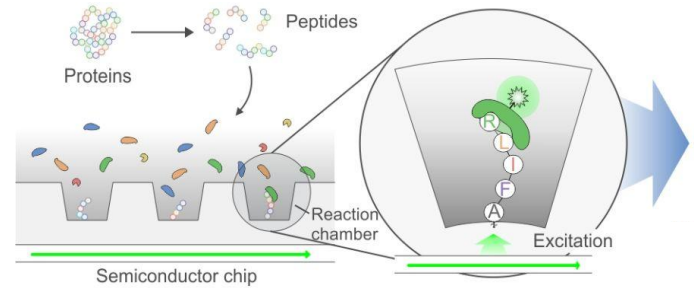
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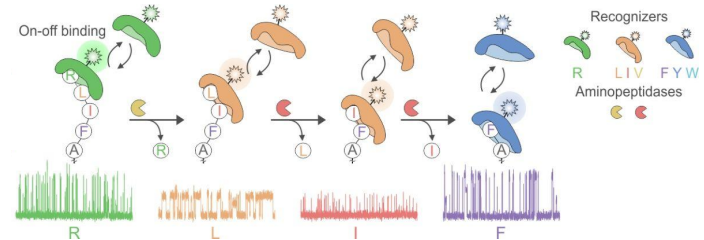
# Time Domain Sequencing™



## Library Preparation and Loading



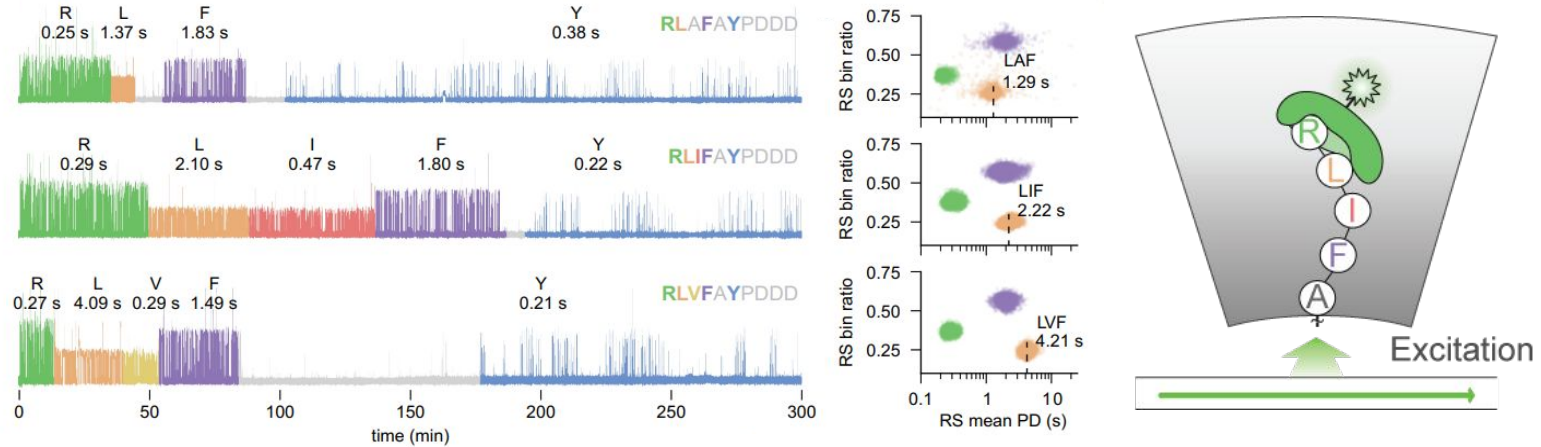
## Protein Sequencing



Additional details are available in our preprint on [bioRxiv](#) and foundational whitepaper [online](#)

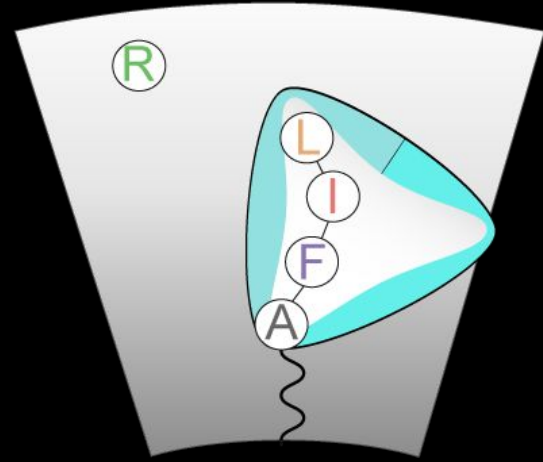
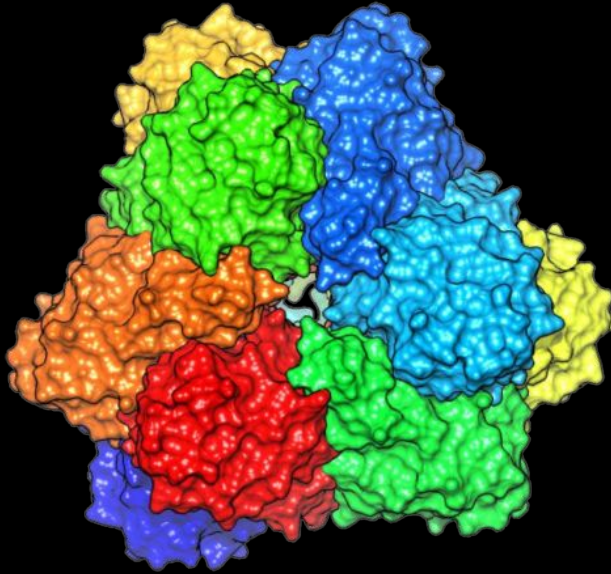


# Sequencing Peptides to Decode Proteins and Modifications



Quantum-Si's recognizers interrogate more than just the N-terminal amino acid

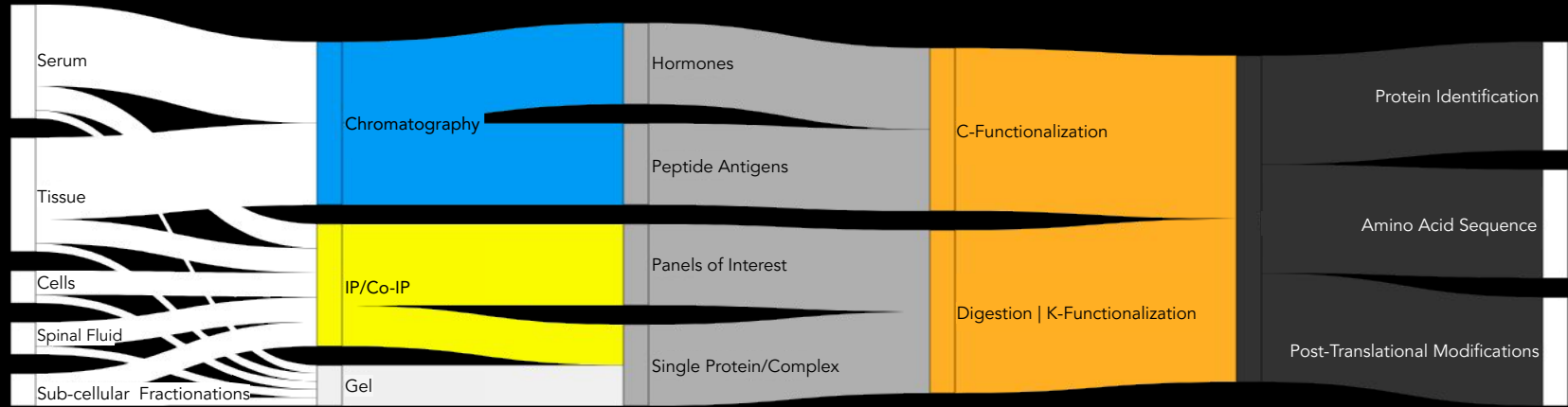
# The Magic Enabling Broad Coverage of the Proteome



While each protein is unique, the enzyme machines we engineer (aminopeptidases) have evolved to make all peptides behave the same in our system!

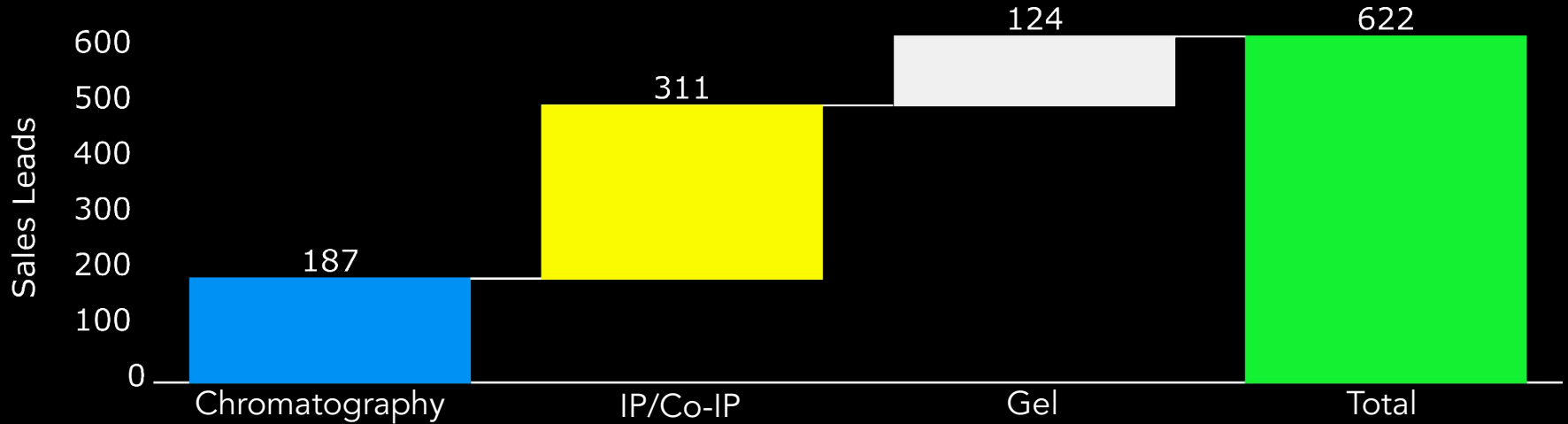


# Universal Process for Protein Sequencing



Fits into existing proteomic workflow.

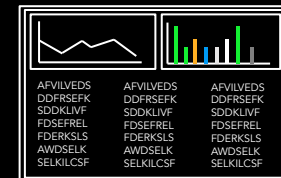
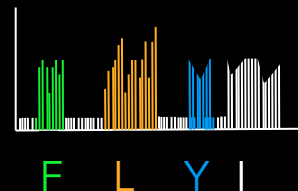
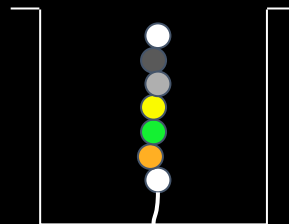
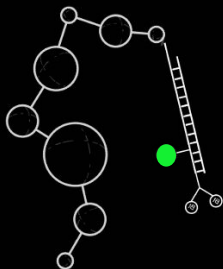
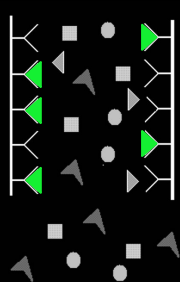
# 500+ Advanced Leads by Workflow



Estimates based on 50% IP/Co-IP, 30% Chromatography, and 20% Gel of 500+ advanced leads



# Workflow for Quantum-Si's Next-Gen Protein Sequencing™



Enrichment

Library Prep

Loading

Sequencing

Results

Enrich proteins of interest

Digest and add Linker for loading (multiple samples or single cell proteomics)

Immobilize peptides in wells (2 Million wells per chip)

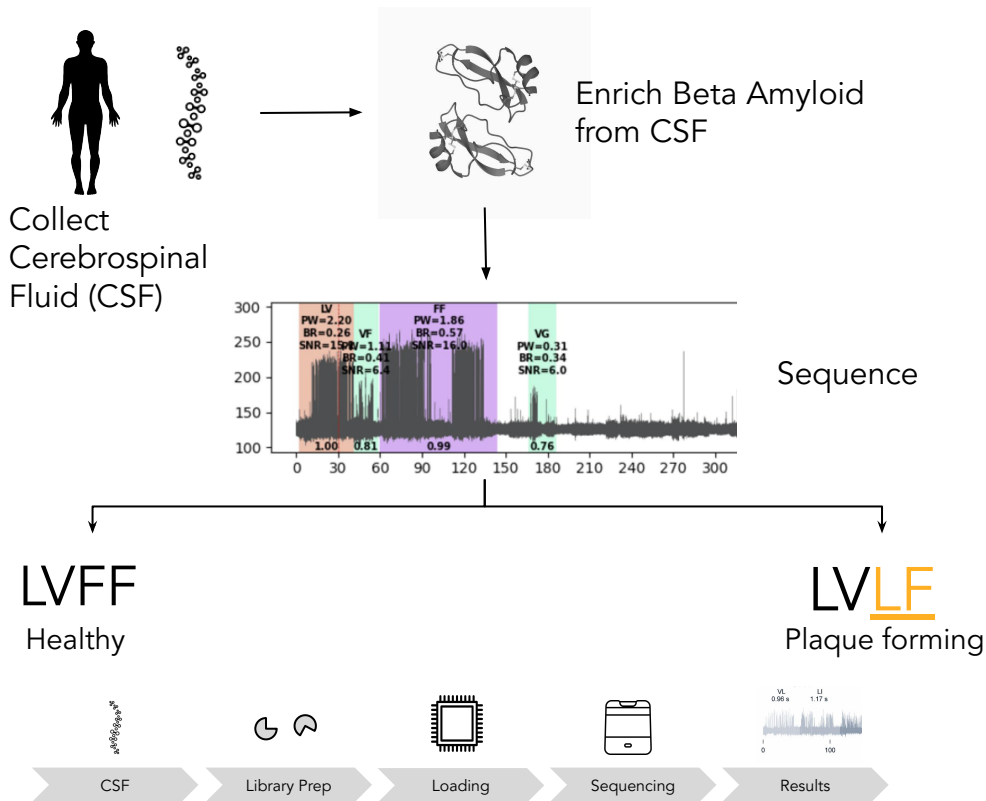
Sequence by recognizing the amino acids at the end, removing it, and recognizing the next ones

Analyze sequence to discover new proteins, decode amino acid sequence & post-translational modifications





# Alzheimer's Risk Assessment



## How Can You Test for Early Onset Disease?

### Biological & Clinical Challenge:

- Less than 1% of Alzheimer's caused by an inherited single gene.
- Somatic mutations - mutations accumulated over a lifetime.

### Technical Challenge:

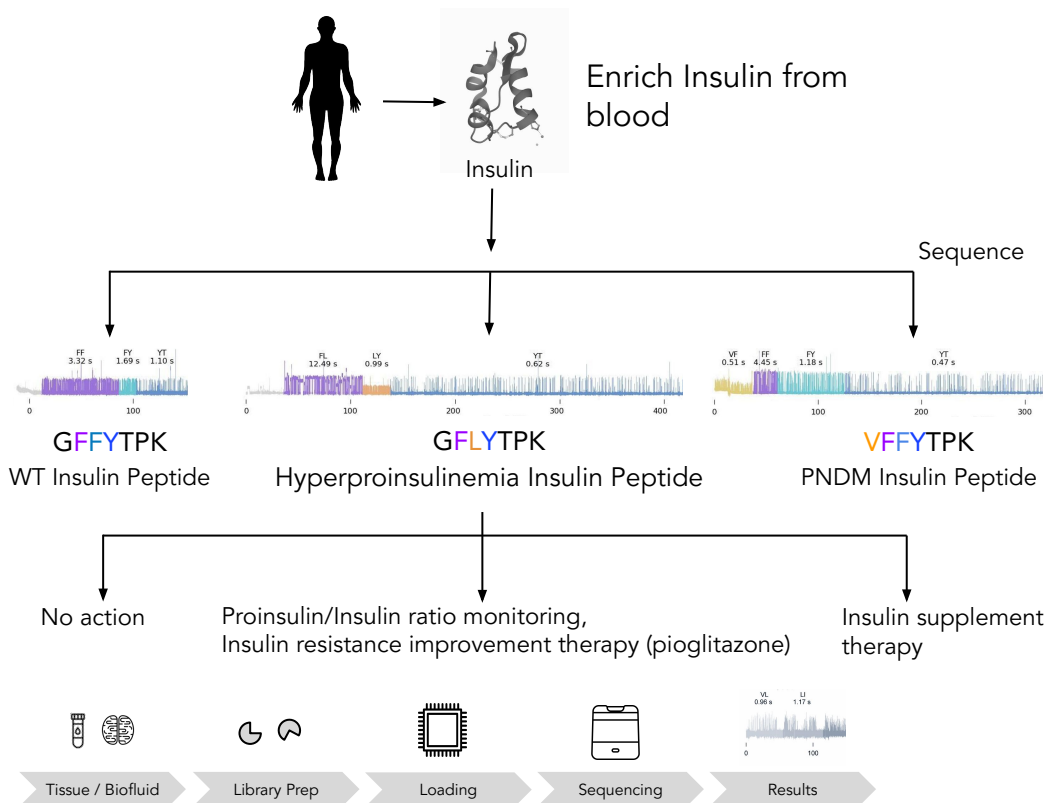
- Source of mutation not known.
- Mass spec is expensive, inconsistent, and often not sensitive enough.

### Solution:

- Sequencing of the peptides to identify changes in amino acid sequence.
- See our beta-amyloid protein sequencing application note [online](#).



# Metabolic Disease



## How Can You Identify Modification of Critical Peptide Hormones?

### Biological & Clinical Challenge:

- Heterogeneous populations of variants.

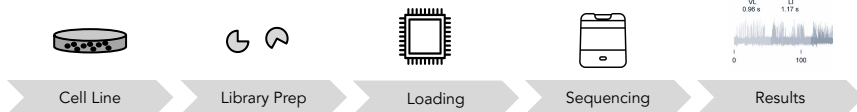
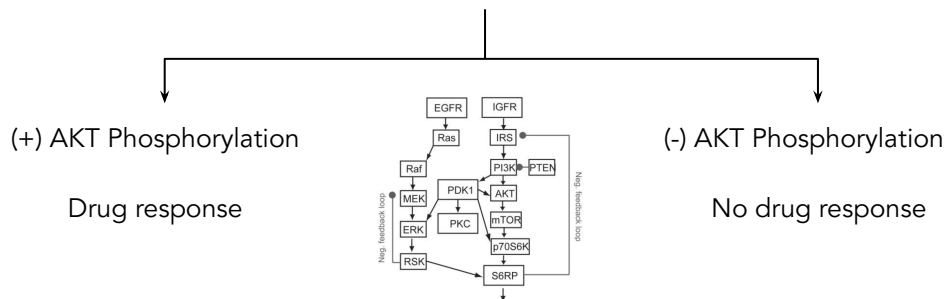
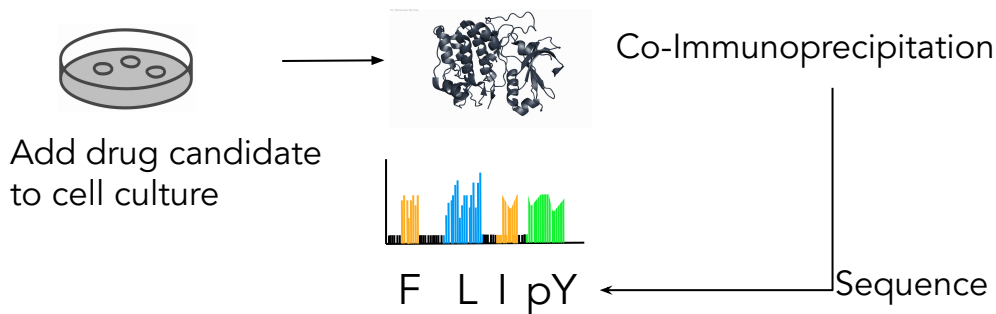
### Technical Challenge:

- Mass spec is expensive and inconsistent.
- Sensitivity challenging for less abundant modifications.

### Solution:

- Immunoprecipitation and Sequencing of the peptides to identify point mutations.

# Drug Development



How Do You Identify Proteins that Interact with Target Proteins of Interest?

## Biological & Clinical Challenge:

- New proteins in my pathway?
- How does the complex change in disease?

## Technical Challenge:

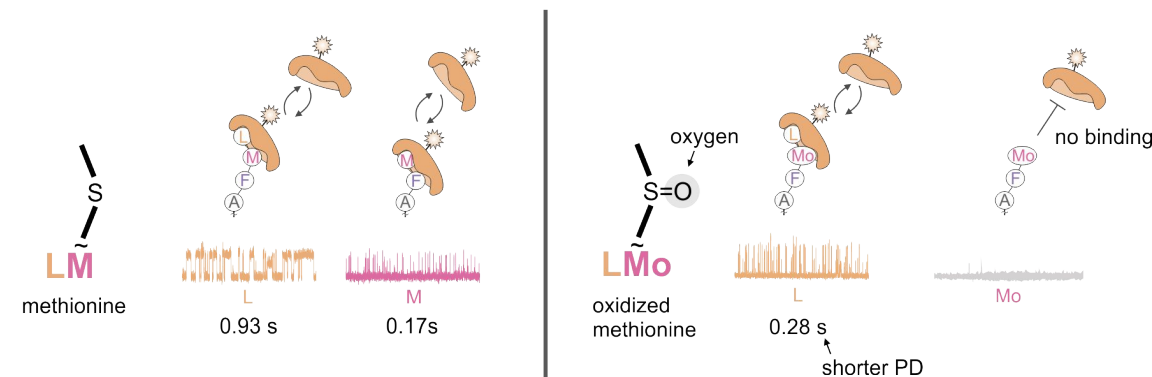
- Routine, robust, scalable, sensitive tools to discover new proteins and post-translational modifications.

## Solution:

- Peptide sequencing to discover new proteins.
- Comparisons between samples to identify new post-translational modifications.



# Single Molecule, Single Atom Detection



No *a priori* knowledge needed to detect new biological markers.

The oxidation of the penultimate residue is detected by a reduction in the average pulse duration of the N-terminal recognizer (as well as by the blocking of recognition of methionine when it becomes the N-terminal amino acid, as sequencing proceeds).

1,000,000+ Protein Variations!

## Biological & Clinical Challenge:

- A protein's modifications determine its function.
- What biomarkers can we discover?

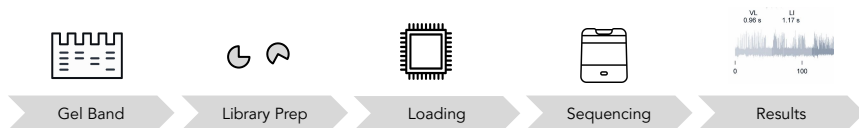
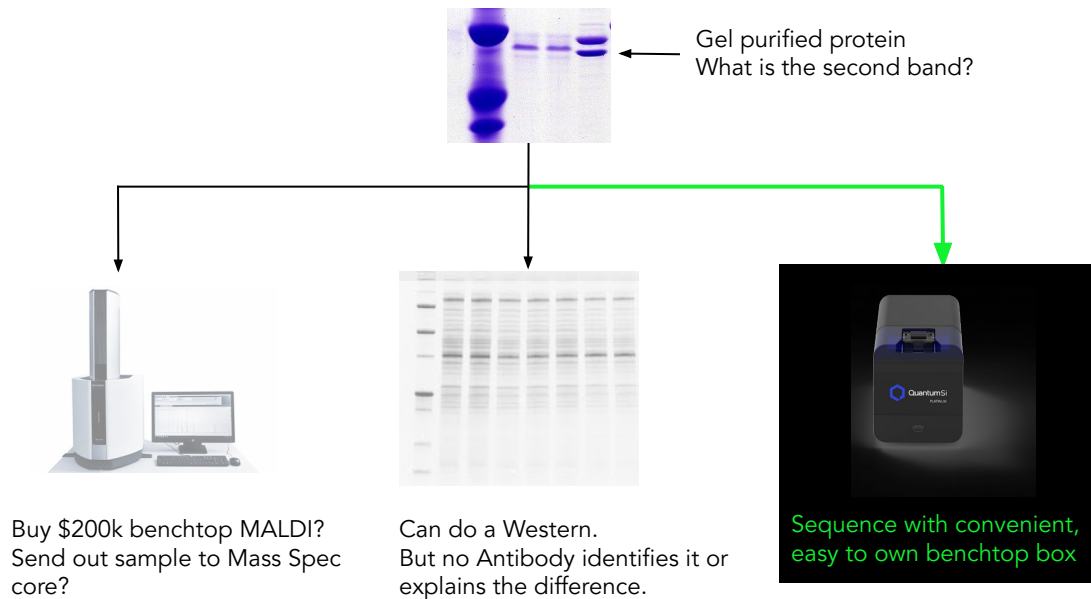
## Technical Challenge:

- Impossible technical challenge to generate affinity reagents to ALL PTMs in context (over 1 million).

## Solution:

- Q-Si detects modifications without *a priori* knowledge.
- Powerful new method for comparing disease & treatment states to find biomarkers.
- Kinetics enable the detection of post-translational modifications; oxidation, phosphorylation, glycosylation (in the penultimate amino acids).

# Proteomics Core on Your Benchtop



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## Sequence Proteins like We Sequence DNA

### Biological & Clinical Challenge:

- What is this protein?
- How is it modified?

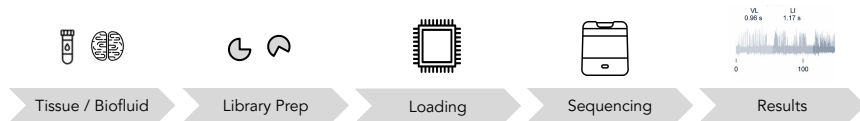
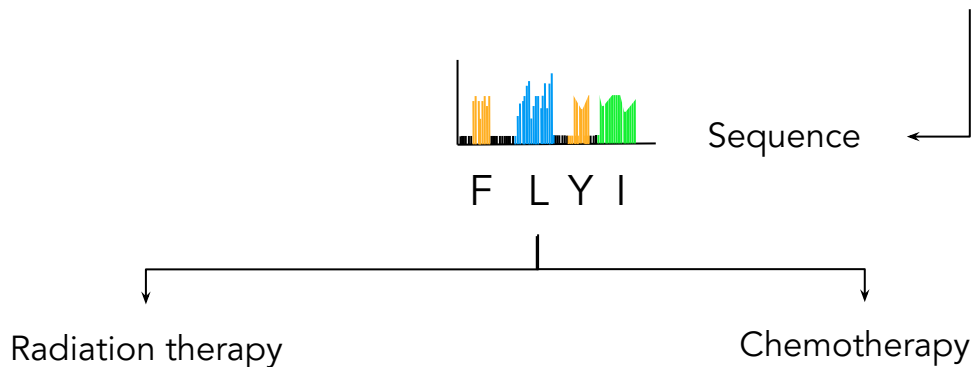
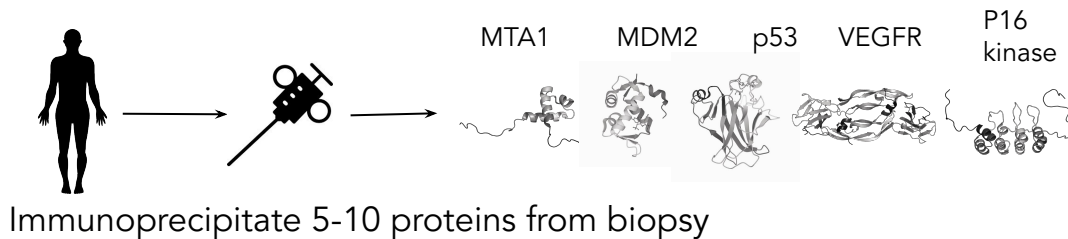
### Technical Challenge:

- Weeks waiting for answers from a mass spec core facility.
- Antibodies don't provide new insights.

### Solution:

- Discover new proteins of interest.
- Identify new protein variations and post-translational modification.

# Future of Therapy Selection



## Profiling Cancers to Guide Therapy

### Clinical Challenge:

- Survival depends on early correct therapy selection and modifications of treatment regimens.

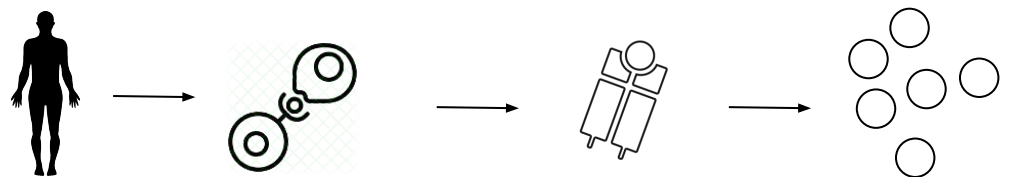
### Technical Challenge:

- Genetic tests detect chromosomal aberrations, not protein alterations.
- Disease instability requires frequent testing & new understanding.

### Solution:

- Quantum-Si sequencing enables biomarkers select therapy.

# Enabling Personalized Medicine



Isolate antigen  
presenting cells

Elute MHC peptides



Sequence



Synthesize personal  
cancer vaccine

Assess infection  
(long-haul COVID)



Tissue / Biofluid



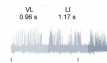
Library Prep



Loading



Sequencing



Results

Identify Antigens for Personalized  
Immunotherapy or to Understand  
Infection

## Clinical Challenge:

- Highly diverse peptides of unknown origin.
- Need to identify modifications.

## Technical Challenge:

- Peptides missed by mass spec
- Relevant neoantigens or antigenic pathogens relatively low abundant.

## Solution:

- Quantum-Si sequencing to identify antigen targets.
- Understanding of new Covid variants.



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# Goals for Commercial Launch

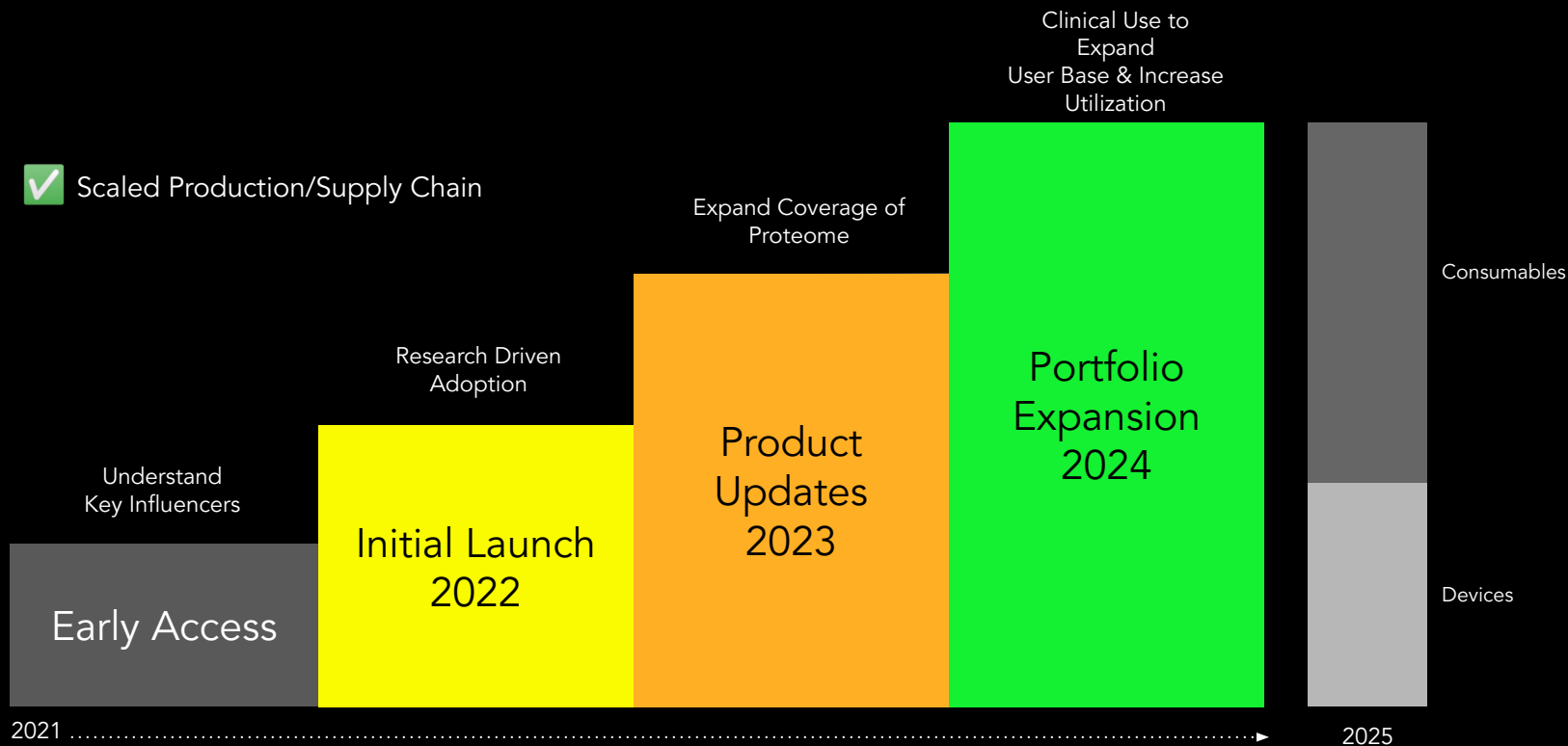
**~70%** loading of proteome after library prep into **5 to 25 amino acid** long peptides

**200,000+** reads per run, with **10 to 20 reads** for each high confidence call

**5 to 50+** proteins over **3 or 4 logs** concentration range



# Roadmap for Customer Adoption & Growth



# ~\$435 M

to fund work through 2024

## Experienced

team of

# 175+

With team members that invented and commercialized the first Next Generation DNA Sequencing and put DNA sequencing on a Semiconductor chip, we are well positioned to launch the World's First Next Generation Protein Sequencing



# Strategic Focus for 2022



QuantumSi

## 2022 Focus:

1. Launch in 2H 2022
2. Deliver Product Development and Application Pipeline
3. Establish Market Leadership in Next Generation Protein Sequencing



Thank You