Investor & Analyst Day

November 20, 2024

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This presentation includes “forward-looking statements” within the meaning of the “safe harbor” provisions of the United States Private Securities Litigation Reform Act of 1995. The actual results of the Company may differ from its expectations, estimates, and projections and, consequently, you should not rely on these forward-looking statements as predictions of future events. Words such as “expect,” “estimate,” “project,” “budget,” “forecast,” “anticipate,” “intend,” “plan,” “may,” “will,” “could,” “should,” “believes,” “predicts,” “potential,” “continue,” and similar expressions (or the negative versions of such words or expressions) are intended to identify such forward-looking statements. These forward-looking statements include, without limitation, the Company’s expectations with respect to future performance and development and commercialization of products and services, its anticipated cash runway and its financial guidance for the full year 2024. These forward-looking statements involve significant risks and uncertainties that could cause the actual results to differ materially from those discussed in the forward-looking statements. Most of these factors are outside the Company’s control and are difficult to predict. Factors that may cause such differences include, but are not limited to: the inability to maintain the listing of the Company’s Class A common stock on The Nasdaq Stock Market; the ability of the Company to grow and manage growth profitably and retain its key employees; the Company’s ongoing leadership transitions; changes in applicable laws or regulations; the ability of the Company to raise financing in the future; the success, cost and timing of the Company’s product development and commercialization activities; the commercialization and adoption of the Company’s existing products and the success of any product the Company may offer in the future; the potential attributes and benefits of the Company’s commercialized Platinum® protein sequencing instrument and kits and the Company’s other products once commercialized; the Company’s ability to obtain and maintain regulatory approval for its products, and any related restrictions and limitations of any approved product; the Company’s ability to identify, in-license or acquire additional technology; the Company’s ability to maintain its existing lease, license, manufacture and supply agreements; the Company’s ability to compete with other companies currently marketing or engaged in the development or commercialization of products and services that serve customers engaged in proteomic analysis, many of which have greater financial and marketing resources than the Company; the size and growth potential of the markets for the Company’s products and services, and its ability to serve those markets once commercialized, either alone or in partnership with others; the Company’s estimates regarding future expenses, future revenue, capital requirements and needs for additional financing; the Company’s financial performance; and other risks and uncertainties described under “Risk Factors” in the Company’s most recent Annual Report on Form 10-K and Quarterly Reports on Form 10-Q and in the Company’s other filings with the SEC. The Company cautions that the foregoing list of factors is not exclusive. The Company cautions readers not to place undue reliance upon any forward-looking statements, which speak only as of the date made. The Company does not undertake or accept any obligation or undertaking to release publicly any updates or revisions to any forward-looking statements to reflect any change in its expectations or any change in events, conditions, or circumstances on which any such statement is based.

Investor Day Agenda

Jeff Hawkins, CEO	**Proteomics Market: Current & Future Perspective**	10:00–10:20 AM
Todd Rearick, CTO	**Technology Architecture for the Future**	10:20–10:40 AM
Brian Reed, PhD	**Innovating Discovery Applications in Proteomics**	10:40–11:00 AM
John Vieceli, CPO	**Platform Roadmap**	11:00–11:20 AM
Jeff Hawkins, CEO	**The Proteomics Lab of the Future**	11:20–11:30 AM
Management	**Q&A Session**	11:30 AM–Noon

Proteomics Market: Current & Future Perspective

Proteins are the Core of Biological Discoveries

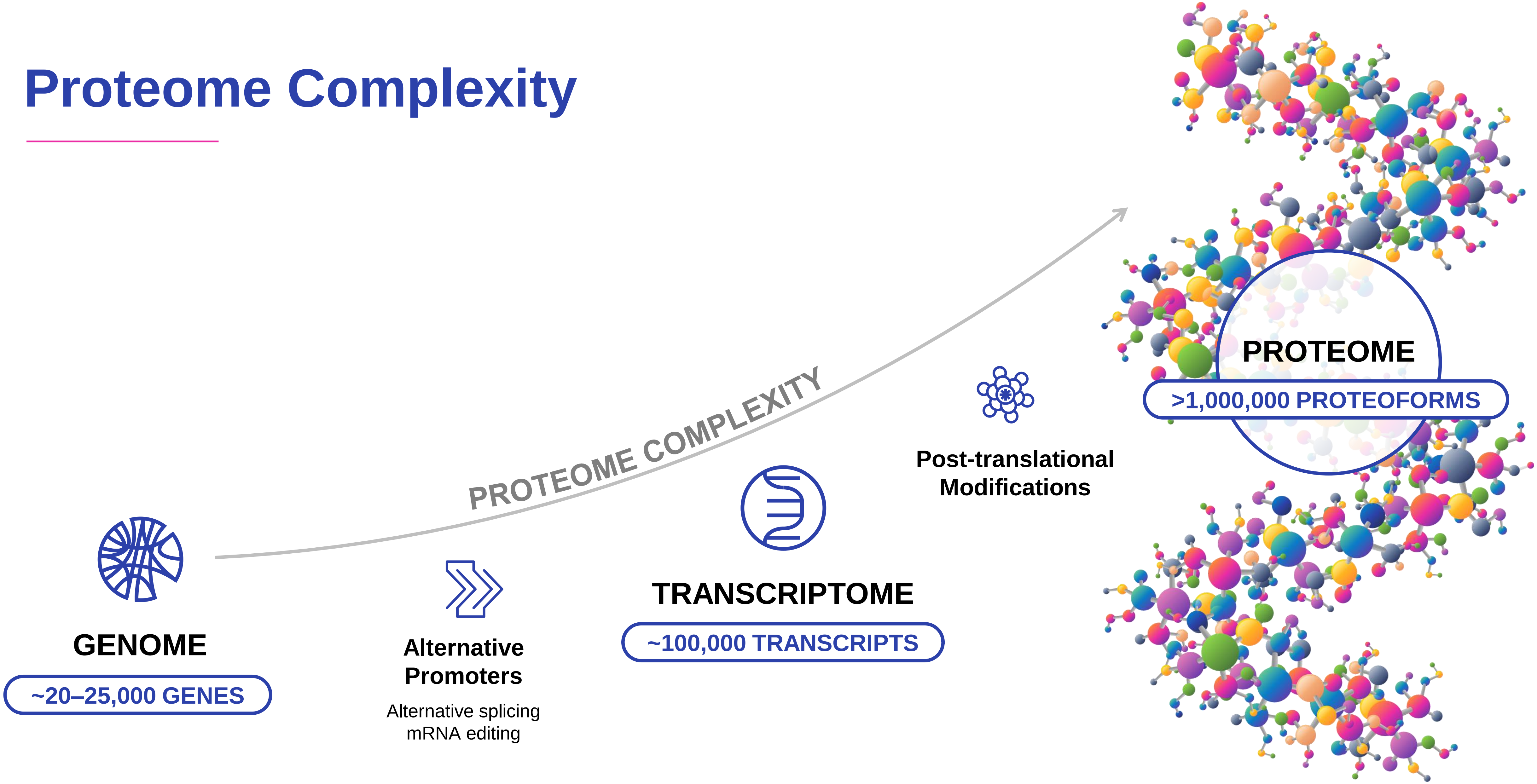
Disease Biomarkers

Therapeutic Development

Biotech Innovation

Proteins are the vital engines of biological systems, playing crucial roles in both health and disease

Proteome Complexity



PROTEOME COMPLEXITY

GENOME

~20–25,000 GENES

Alternative Promoters

Alternative splicing
mRNA editing

TRANSCRIPTOME

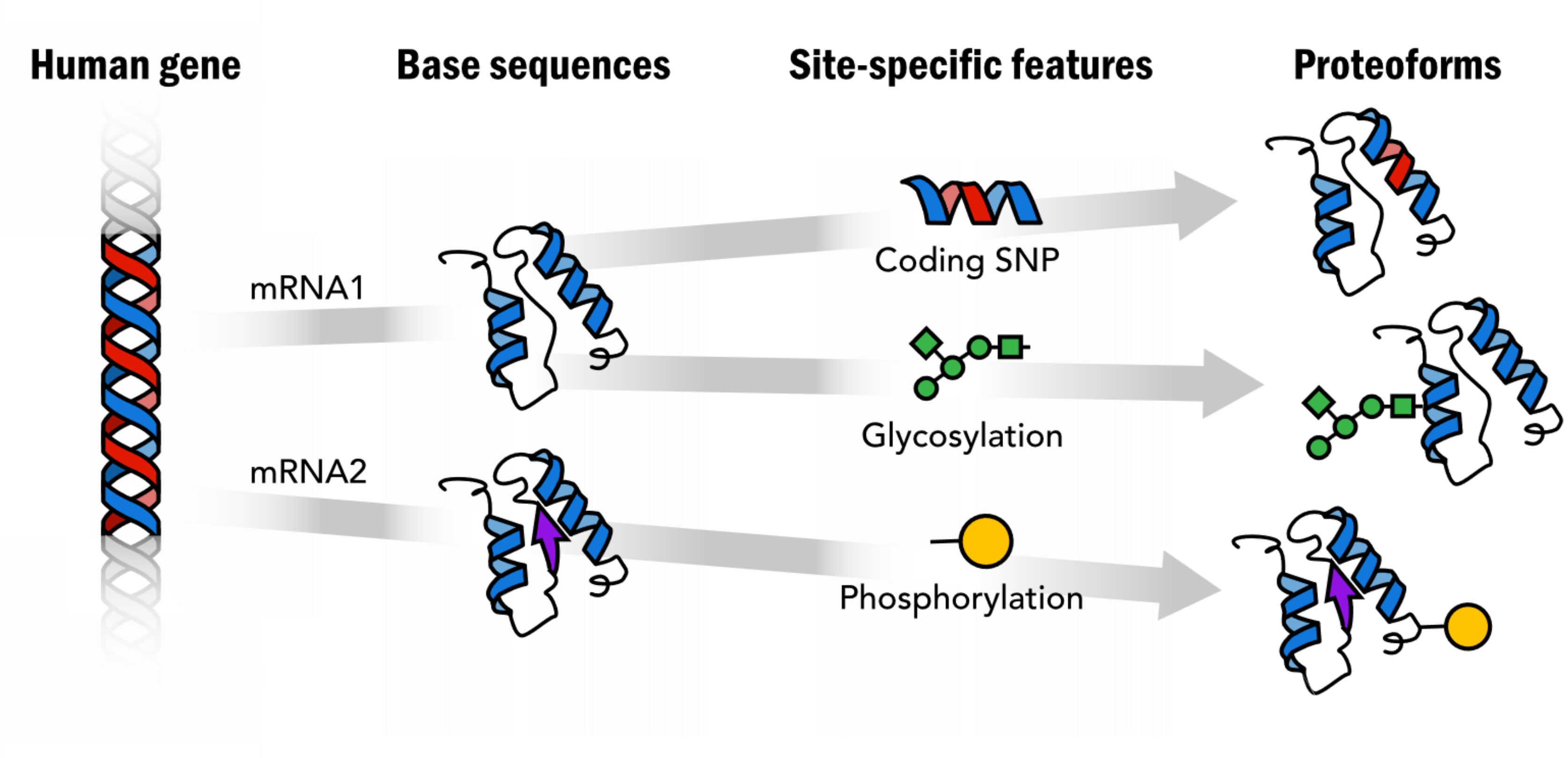
~100,000 TRANSCRIPTS

Post-translational Modifications

PROTEOME

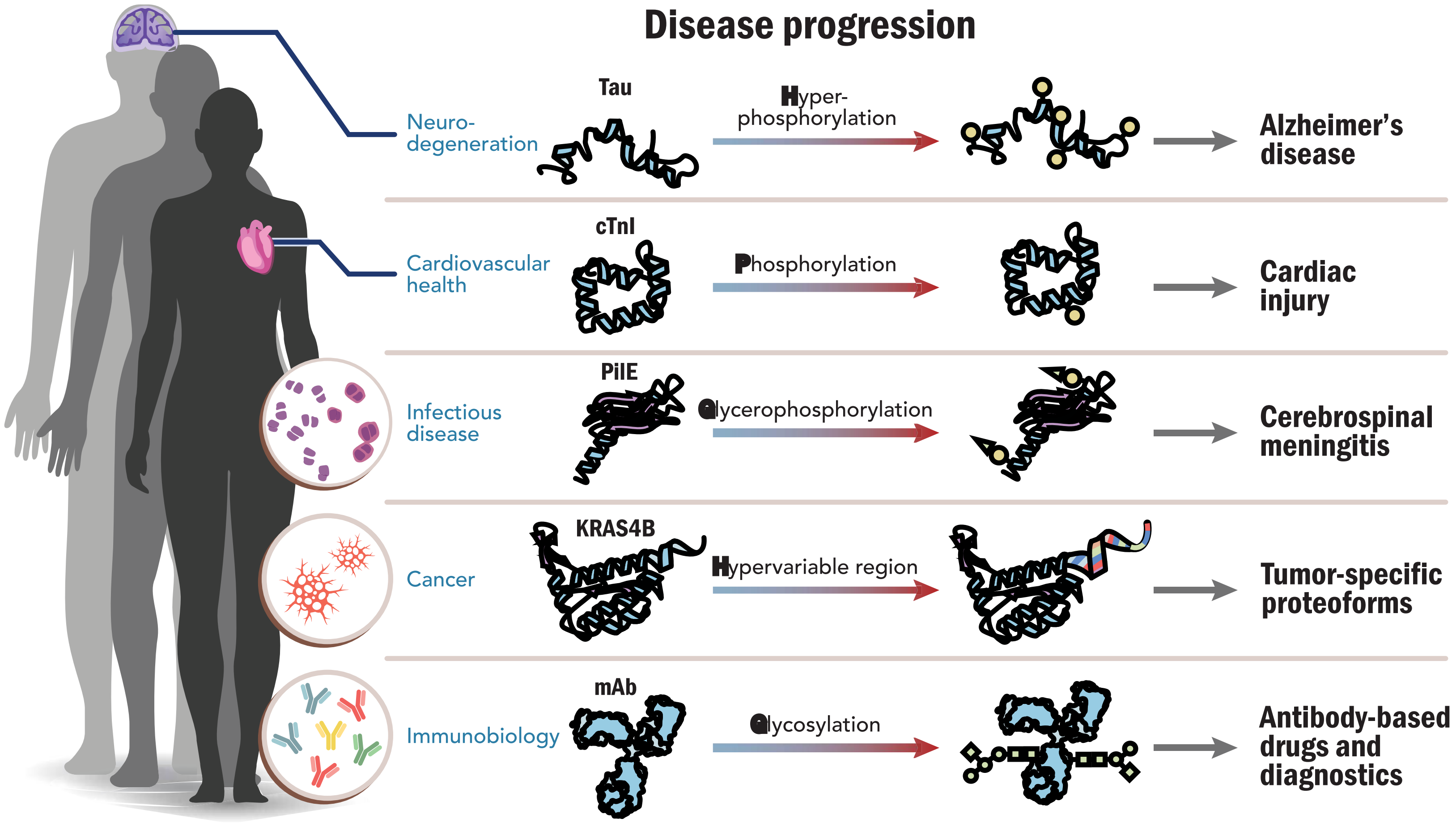
>1,000,000 PROTEOFORMS

Transcriptomics Does Not Accurately Predict Protein Profiles



Human Proteoform Project: https://www.science.org/doi/10.1126/sciadv.abk0734

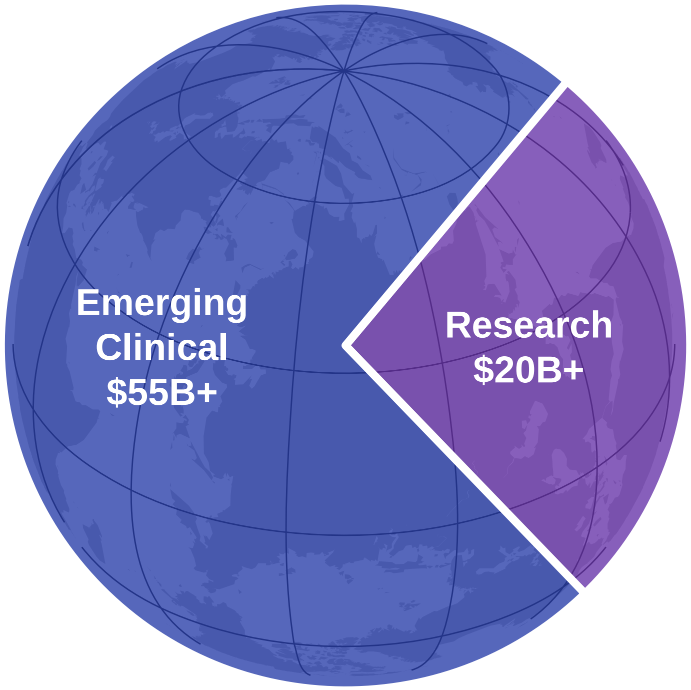
Disease Progression Goes Beyond the Protein Level



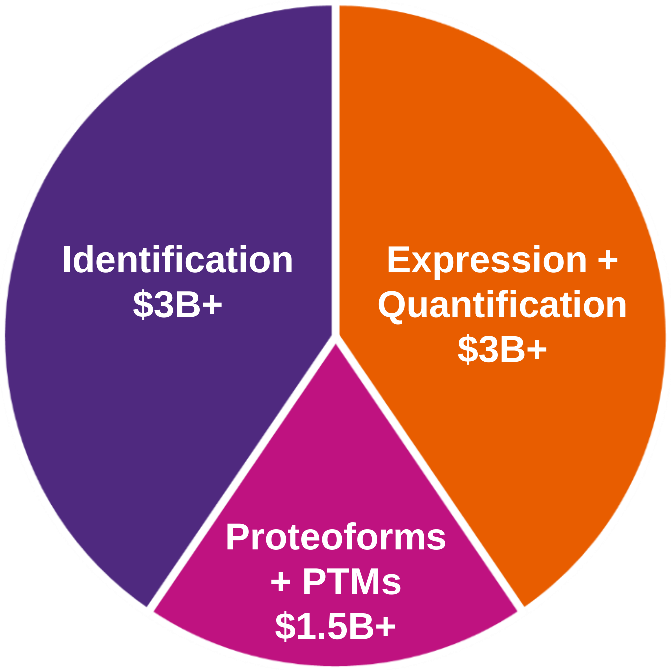
Human Proteoform Project: https://www.science.org/doi/10.1126/sciadv.abk0734

Proteomics is a Large and Growing Market Opportunity

$75B+ Proteomics Market[1]



$8B+ Initial Target Market[2]



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1. SVB Leerink Research, "*Proteomics: The Next Frontier in Life Science Tools and Diagnostics.*" September 28, 2021
2. DeciBio Consulting Evaluation, June 2020

Platinum Use Cases Today

Identify Proteins Critical to Biology

- In-gel digest of bio samples
- Characterize antibodies
- Identify co-IP proteins

Uncover + Understand Proteoforms

- Post-translational modifications
- Amino acid variants
- RNA isoforms

Screen and Characterize Proteins with Barcodes

- Protein/antibody engineering
- mRNA vaccine development
- Lipid nanoparticle delivery

How QSI Customers Are Leveraging Platinum

Liberate Bio

MRNA screening with protein barcodes for gene therapy

Cedars Sinai

Studying citrullination PTMs

Weill Cornell Medicine

Characterizing far-flung extremophiles

Johns Hopkins University

Studying mRNA translation and PTMs

University of Virginia School of Medicine

Studying disease isoforms

Stony Brook University

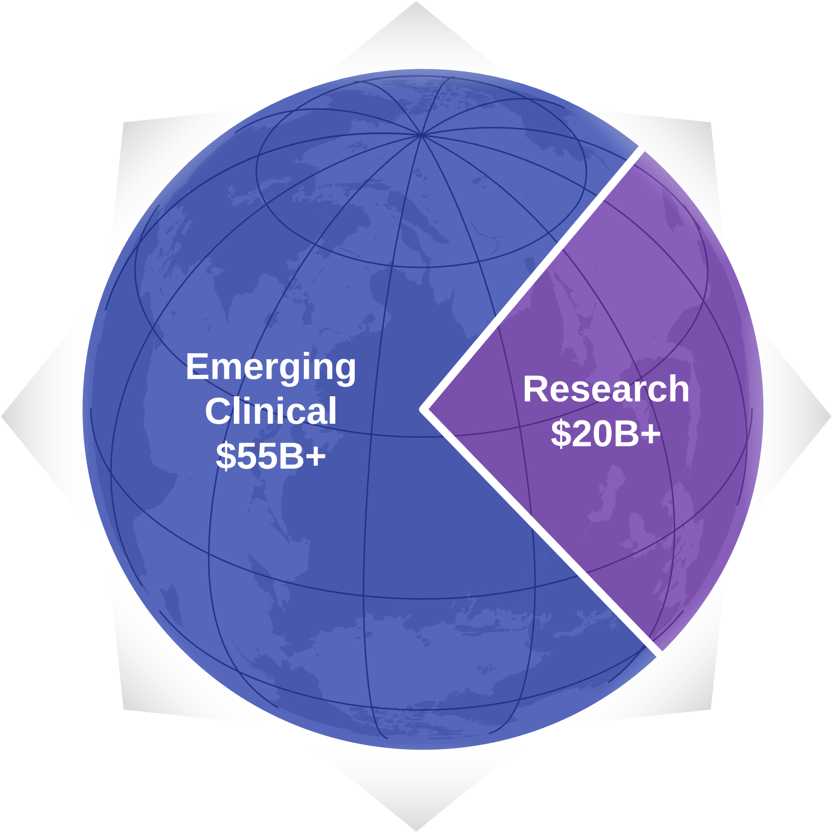
Mapping protein conformations using protein barcodes

The Proteomics Market is Poised for Significant Growth

Large-scale screening studies designed to identify clinically relevant biomarkers are increasing

Deep proteoform-level analysis will be needed to fully define and characterize the biomarkers with highest medical value

Population-scale studies will be needed to characterize what a “healthy” profile looks like



Routine use of multiomics requires creating new data analysis tools — these tools will require large amounts of training data

AI-driven drug development will drive the need for deeper proteomic data (amino acid level) to better inform and train the models

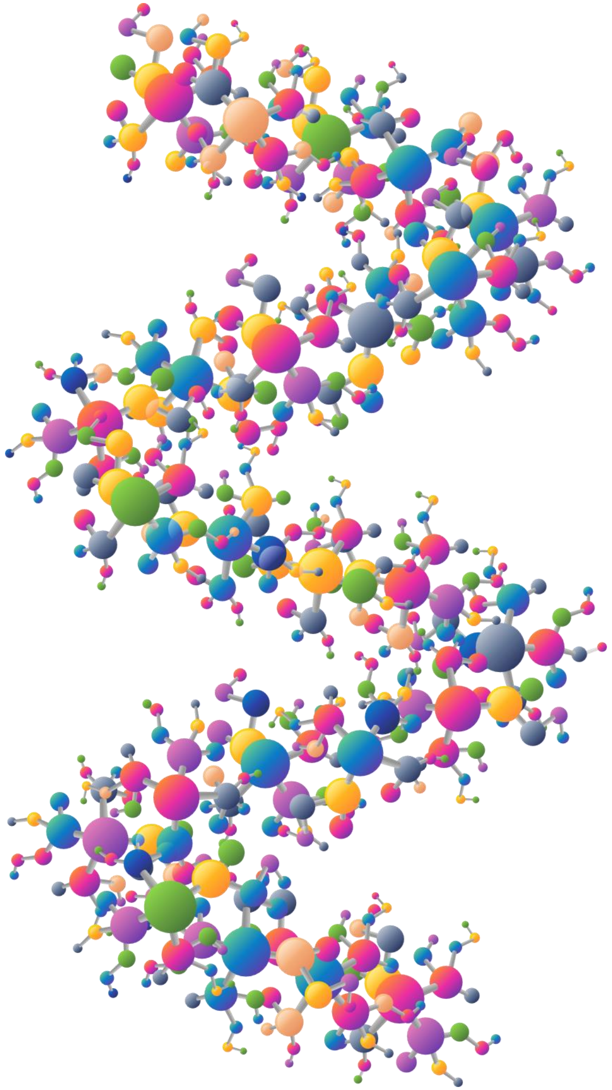
The proteome is dynamic — longitudinal data will be needed (i.e., repeat testing)

Technical Challenges in Proteomics Today

Top-down
vs
Bottom-up

Throughput
+
Costs

Sensitivity
vs
Dynamic Range



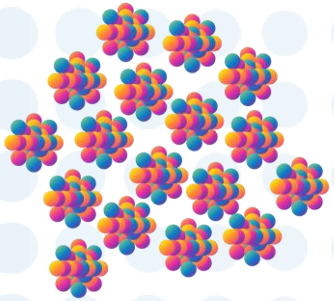
Unbiased
vs
Biased

Breadth
(# of Proteins)
vs
Depth
(Amino Acid, PTM)

Standardization
+
Reproducibility

Multiple Specialized Platforms Required to Fully Interrogate the Proteome

Protein-level Screening



Samples: 100s–1,000s per study
Proteins: 100-1,000s per sample
Resolution: Protein

Focused + Deep Characterization

Samples: 10s–100s per study
Proteins: <50 per sample
Resolution: Amino acid; single-molecule

- Mass Spec
- HT Affinity Assays
- Ultra-Sensitive Protein Detection
- Western Blots + ELISA
- Edman Degradation
- QSI™

QSI is Best Positioned to Usher in a New Paradigm in Proteomics

Proteus™

Core technology is the only commercially available tech that can enable single-molecule, top-down, and bottom-up proteomics methods

New architecture (Proteus™), combined with other ongoing technology development initiatives, creates clear path to *de novo* sequencing

Ultrarapid sequencing chemistry can enable significant increase in sample throughput per day and unlock time-sensitive applications (e.g., clinical diagnostics) in the future

Platinum® Pro

Distribution Agreement in Place to Scale Adoption Across the US + Canada

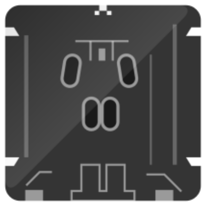
avantor™

Technology Development Pipeline

Quantum-Si Core Technologies

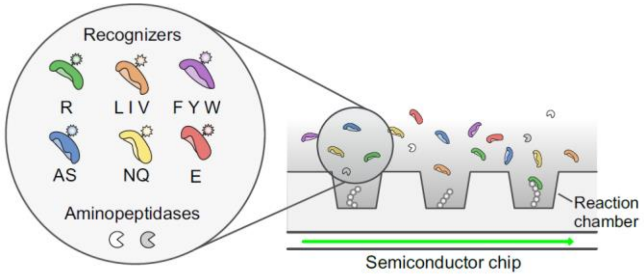
Platinum® System

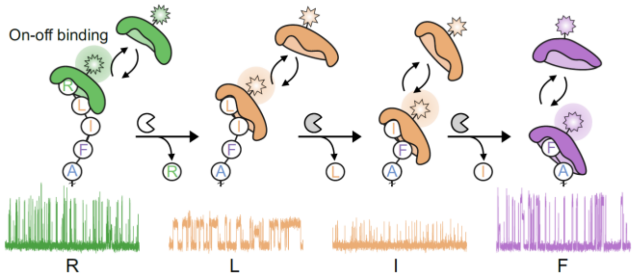
2M Chip



Chemistry

Biomolecules





Algorithms

Applications

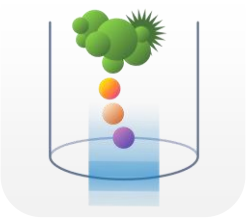
- **Peptide Mapping**
- **Barcode Applications**
- **Variant Calling**
- **PTM Characterization**
- **Protein Identification**

End-to-End Protein Analysis

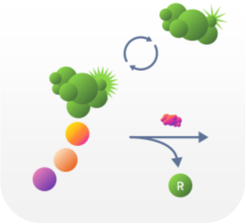
Protein

Peptides

Wells Prepared

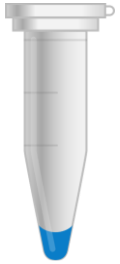


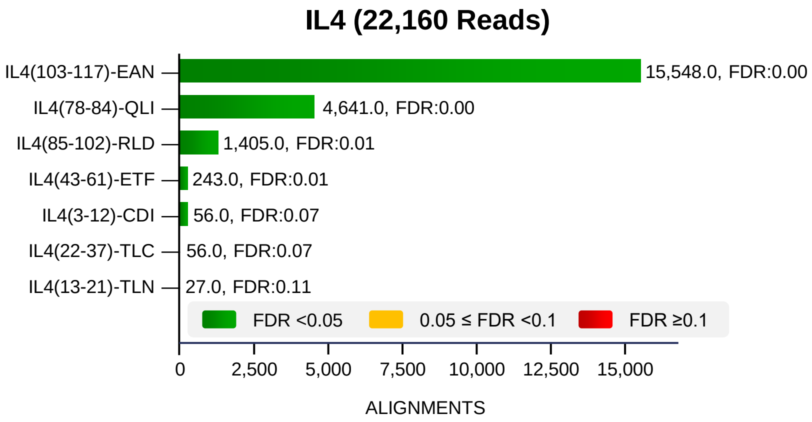
Excitation



'R' Sequenced

Data Analyzed

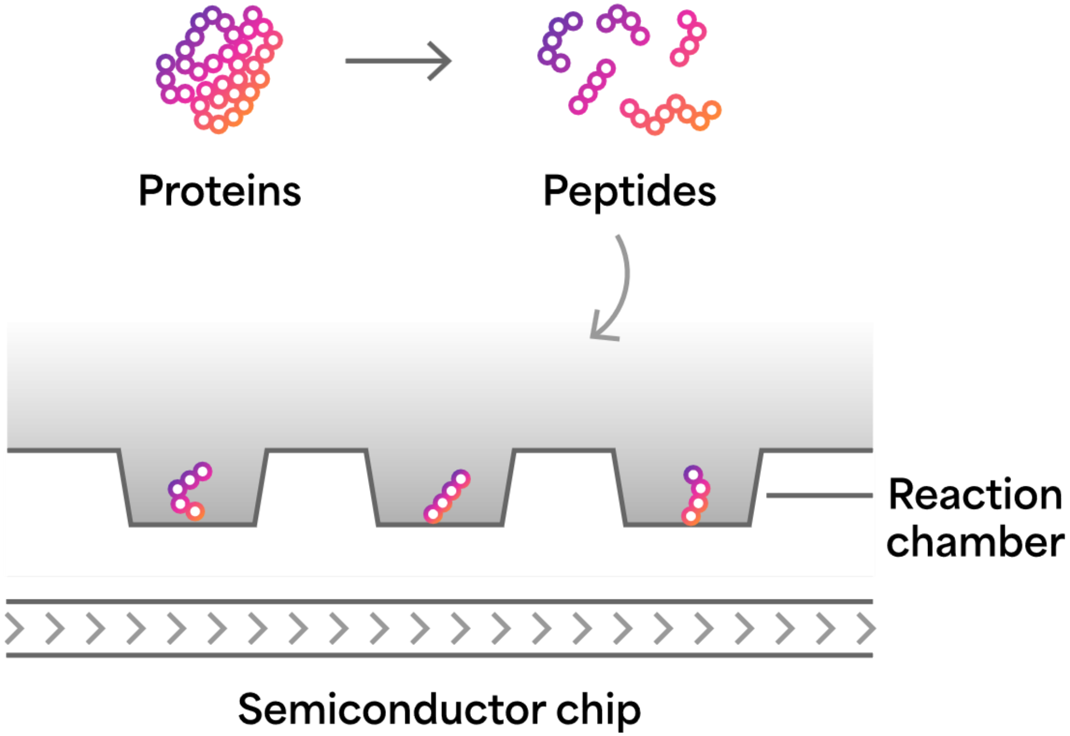




Prepare Proteins for Sequencing

Proteins are digested into short fragments (peptides)

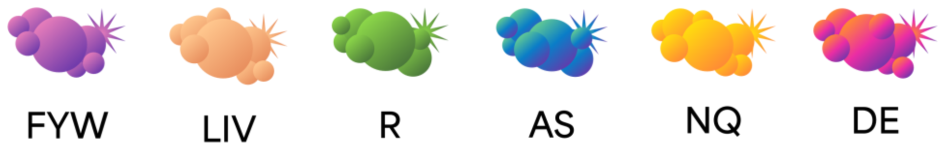
Peptides are immobilized at the bottom of reaction chambers on our chip

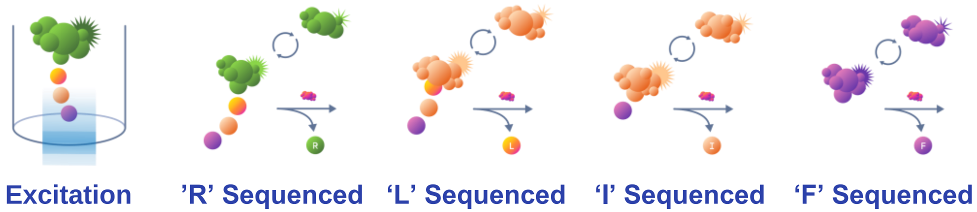


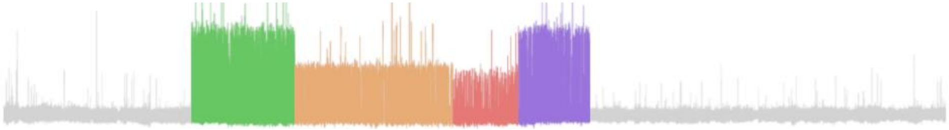
Kinetic Signatures Uniquely Identify Proteins + Proteoforms

Recognizers bind amino acids in sequence

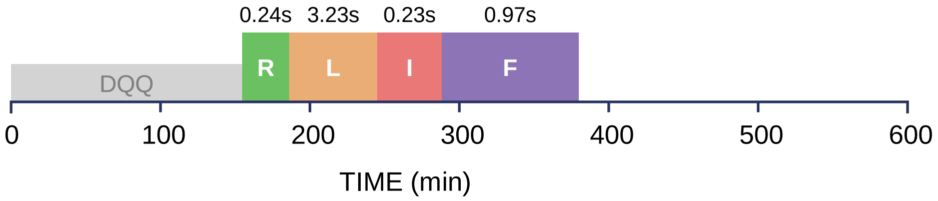
Recognition events produce kinetic signatures





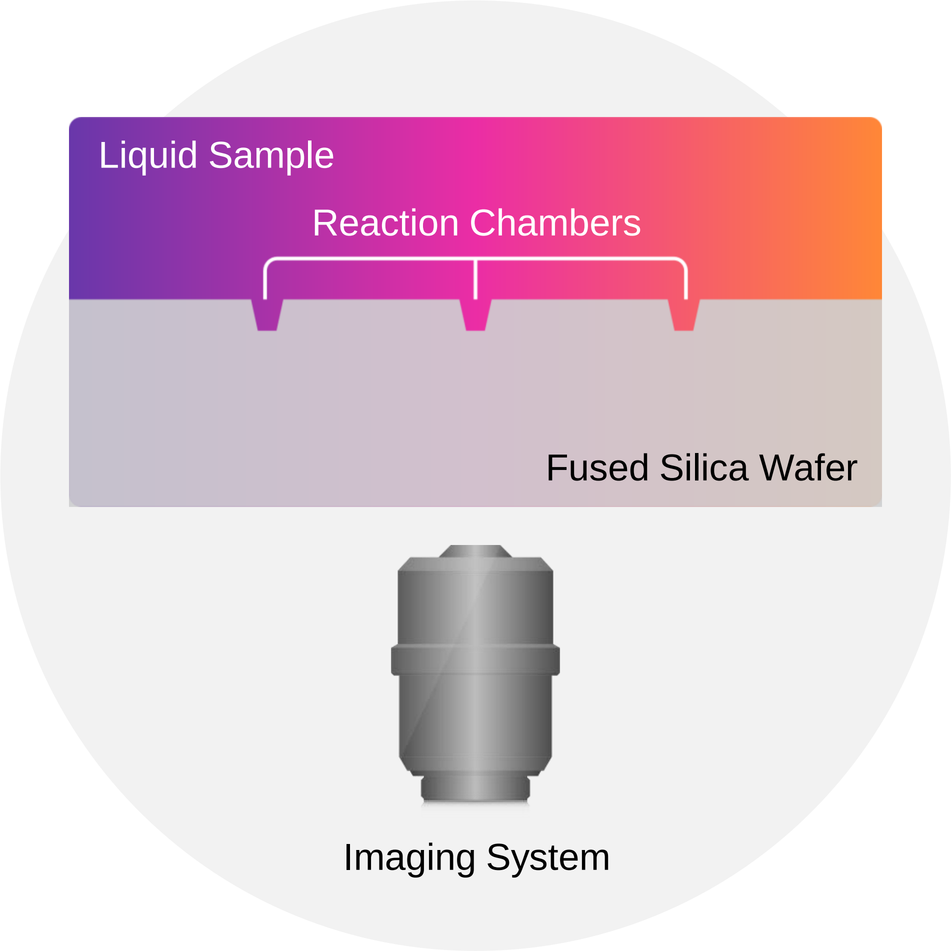


Kinetic signature plot

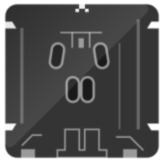


Rationale for New Technology Architecture

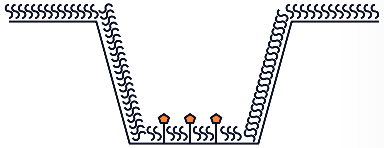
- **Semiconductors** require large R&D investment
- **Re-partitioning of system** allows for less expensive consumable
- **Leverage optical magnification** to pack wells closer together and scale to billions of reads
- **Leverage high-performance**, commercially-available imaging components



QSI Core Technologies



Chip



Surface Chemistry

Instrument

Library Prep + Sequencing Reagents

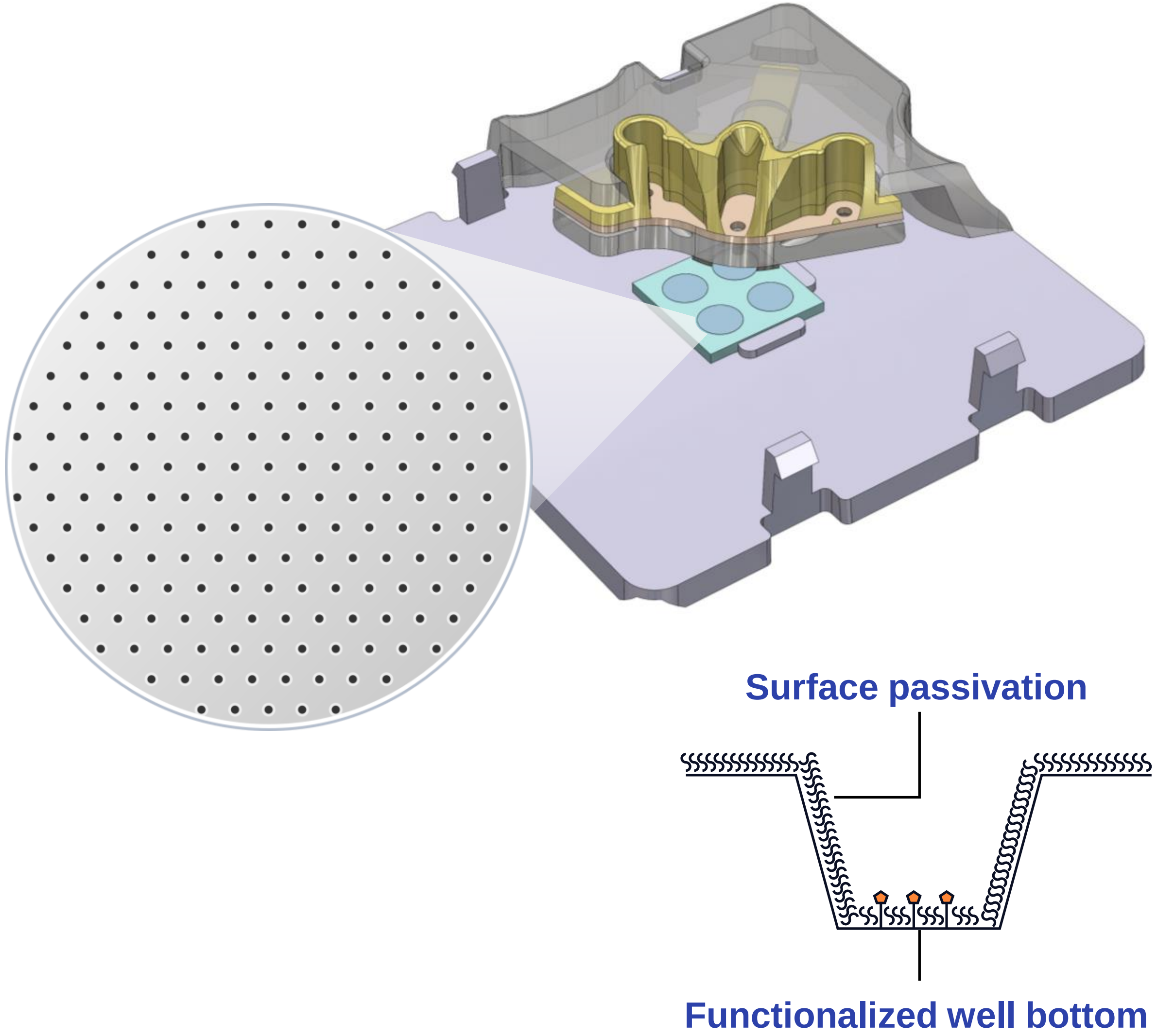
Software

Chip + Surface Chemistry

Simple passive device with approximately 20M wells (per flow cell) at initial launch

Heavily de-risked — leverages existing design, materials, and fabrication methods

Compatible with existing surface chemistry

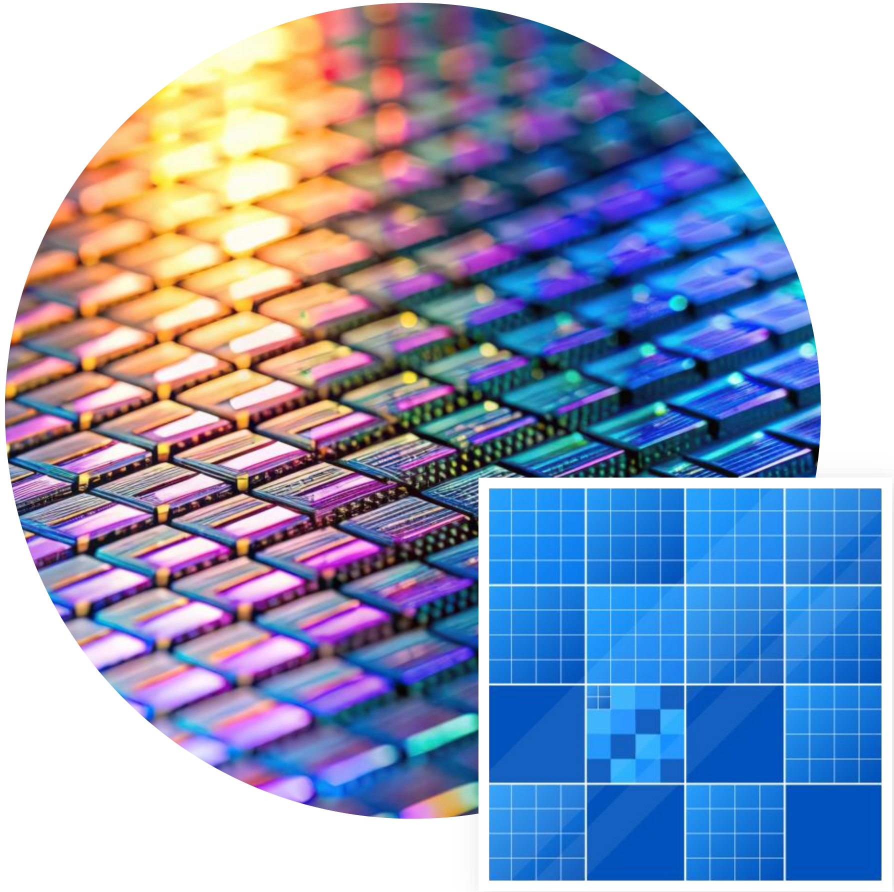


Proteus™ Consumable Development

Wafer process flow developed in production foundry

Prototype wafers fabricated and tested

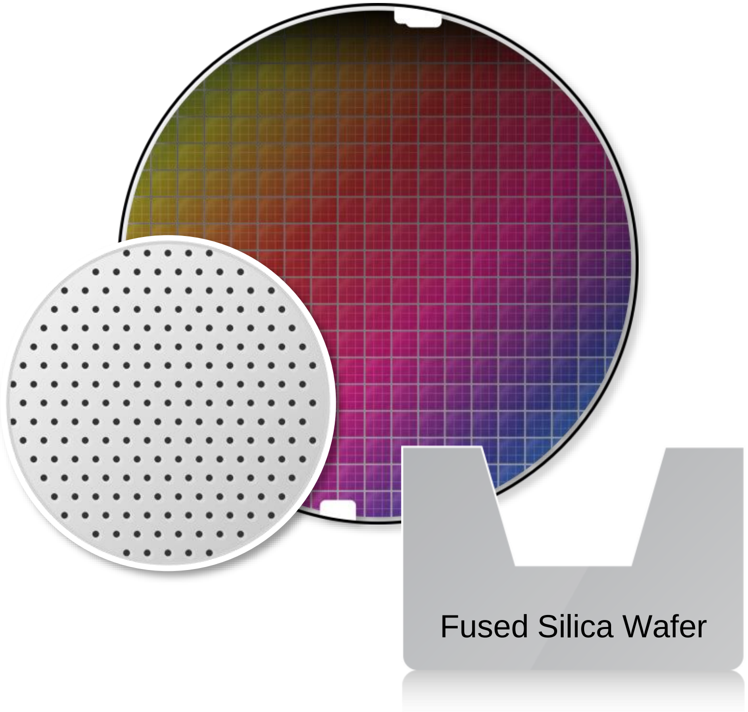
Simple process has low-risk path to high-volume production



Wafer Fabrication Process Development

Foundry process modules work
and produce the desired well structure

Foundry partner for development
and production is in place



skywater

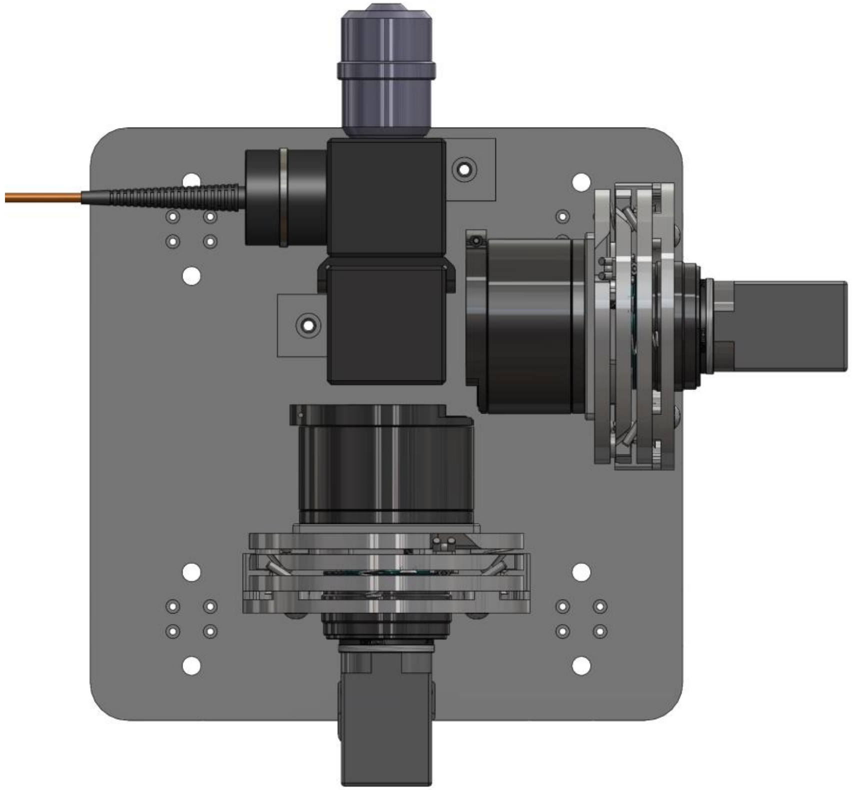
Proteus™ Instrument Development

Move imaging components to the system

Increase workflow automation

Leverage commercially available technologies for imaging and liquid handling

Takes advantage of significant investment in optics driven by NGS industry



Planet Innovation

Library Prep + Sequencing Chemistry

Existing library prep and sequencing chemistry are completely portable

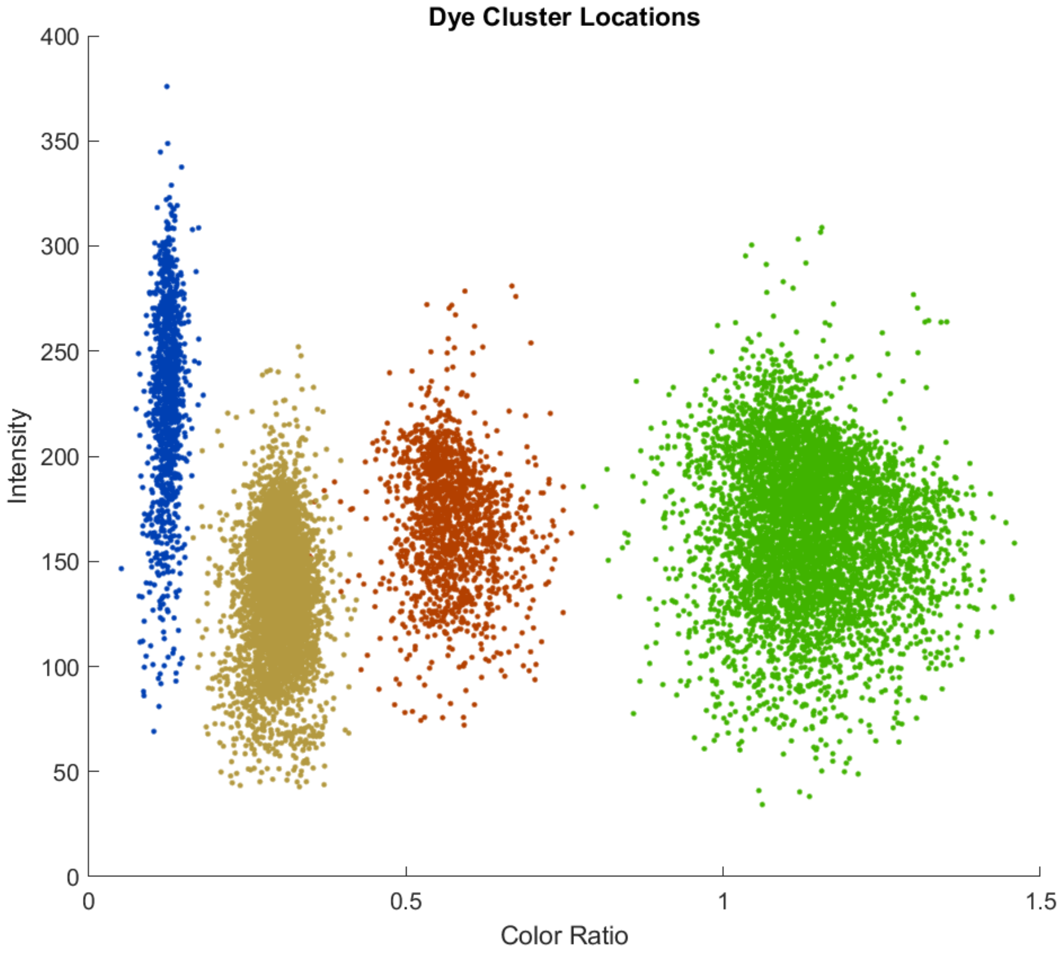
New system discriminates dyes with color rather than lifetime

Some new dye development is necessary, but is underway and low risk

Color Ratio is a Viable Alternative to Current Lifetime Detection

Key elements have already been de-risked

Move to color means we can leverage off-the-shelf camera technology


Dye Cluster Locations

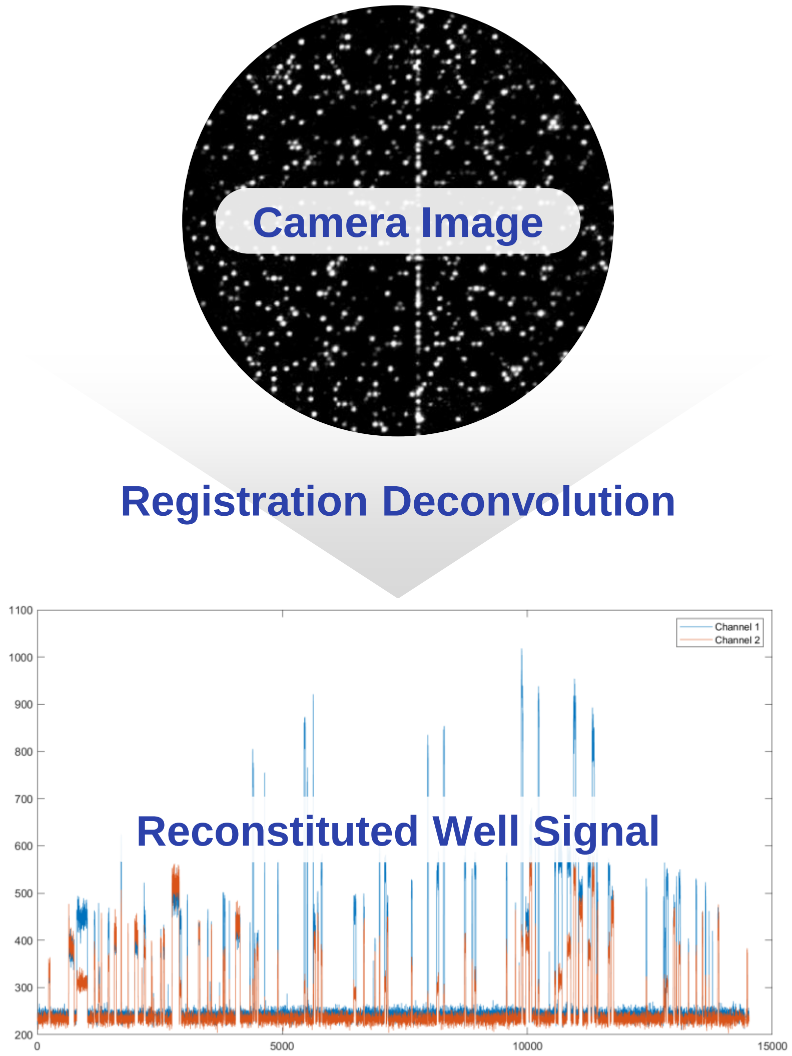
Analysis Software

Backend processing is completely portable to new system

- Pulse detection, ROI calling, alignment, protein inference, and other applications

Development required for frontend image processing

Well within state-of-the-art capability



Camera Image

Registration Deconvolution

Reconstituted Well Signal

Instrument Roadmap

New architecture scales up to 10B reads per consumable

Enables shotgun proteomics of complex samples

Puts us on path to *de novo* sequencing

Platinum (**2M**)

Proteus^{TM} 1.0 (**50M+**)

Proteus^{TM} 2.0 (**10B**)

Innovation Toward the Most Advanced Set of Discovery Applications in Proteomics

Brian Reed

Agenda

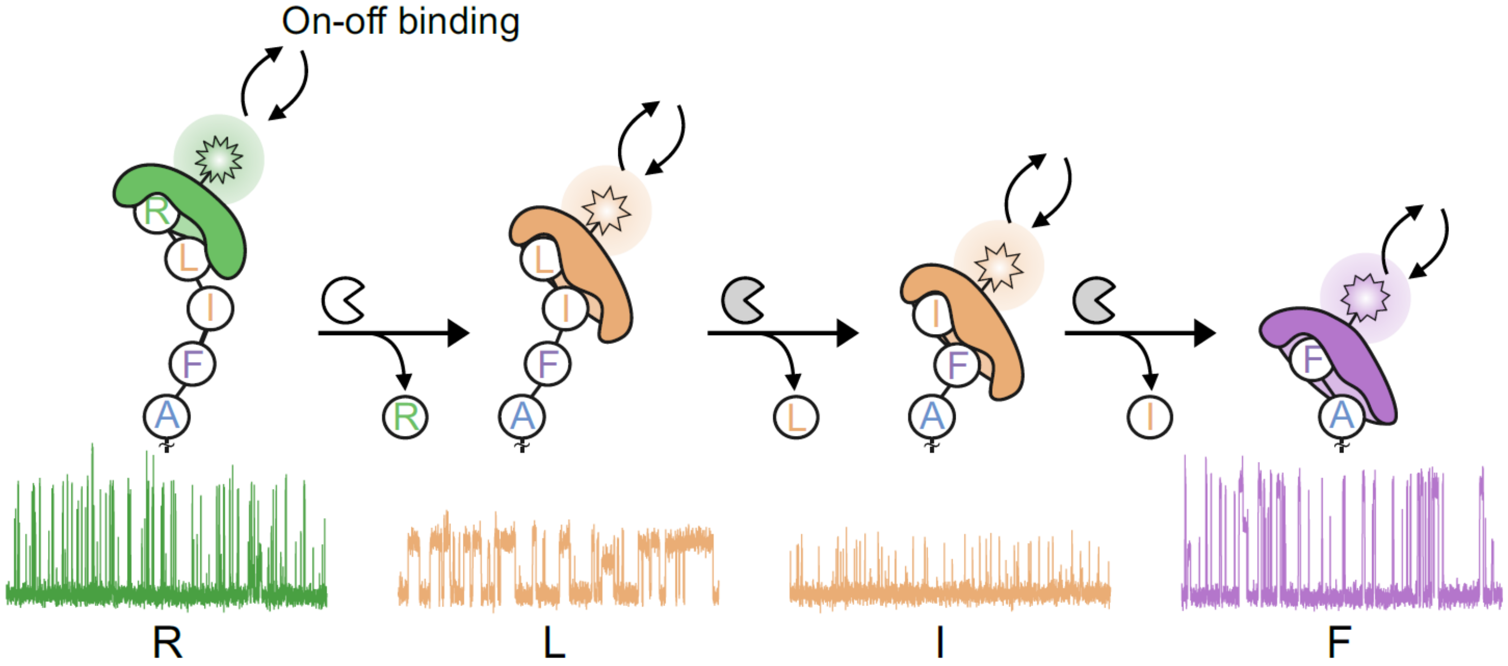
Innovation at the Forefront of Proteomics

1. **The path to complete proteome coverage**
2. **Ultrasensitive PTM detection for proteoforms**
3. **Deep, unbiased interrogation of high-complexity samples**
4. **Beyond sequencing: the first platform for top-down single-molecule proteomics**

QUANTUM SI™

Acceleration on the Path to Complete Proteome Coverage

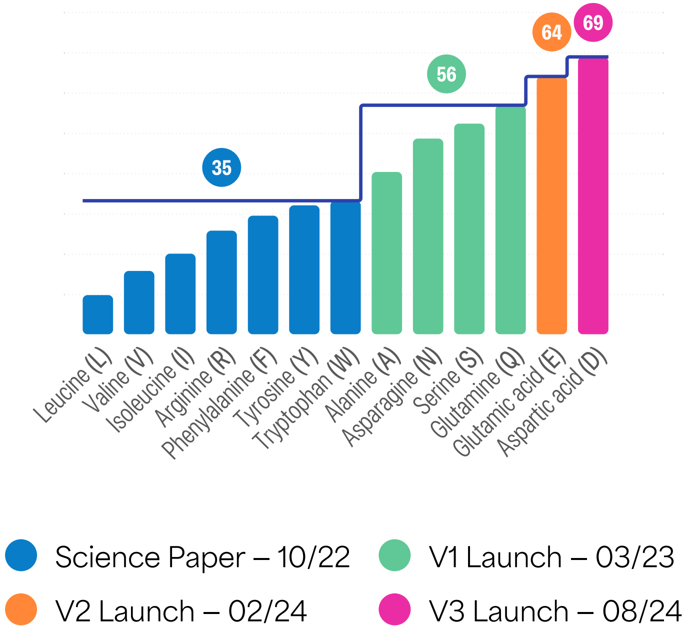
Sequence Proteins on Platinum



- **Each recognizer binds** 1-3 cognate N-terminal amino acids (NAAs)
- **Rapid on-off binding** generates a pulsing pattern detected by the chip
- **Extremely information-rich** data output: 10s-100s of pulsing events per amino acid

A Rapid Path to Complete Amino Acid Coverage

Our team has mastered the engineering and evolution of amino acid recognizers

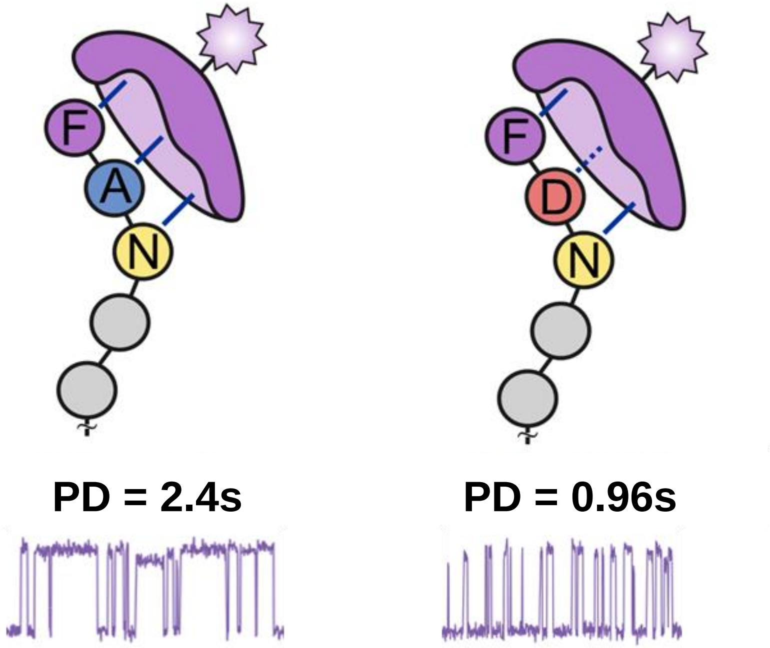


Recognition Progress

Human proteome AA prevalence with recognizers

- **As a result of our rich kinetic output**, we have more data on our recognizers than possibly any other set of proteins in biotechnology
- Recognizers in the V3 kit recognize **13 of the 20 types of amino acids** (69%)
- **New recognizers** have already been developed and are on track for release in our next kit update
- We are on track to enable complete reference-free sequencing: **enables key applications like sequencing antibodies and cancer neoantigens *de novo***

Kinetic Signatures are Sensitive to Downstream Sequence



PD = 2.4s

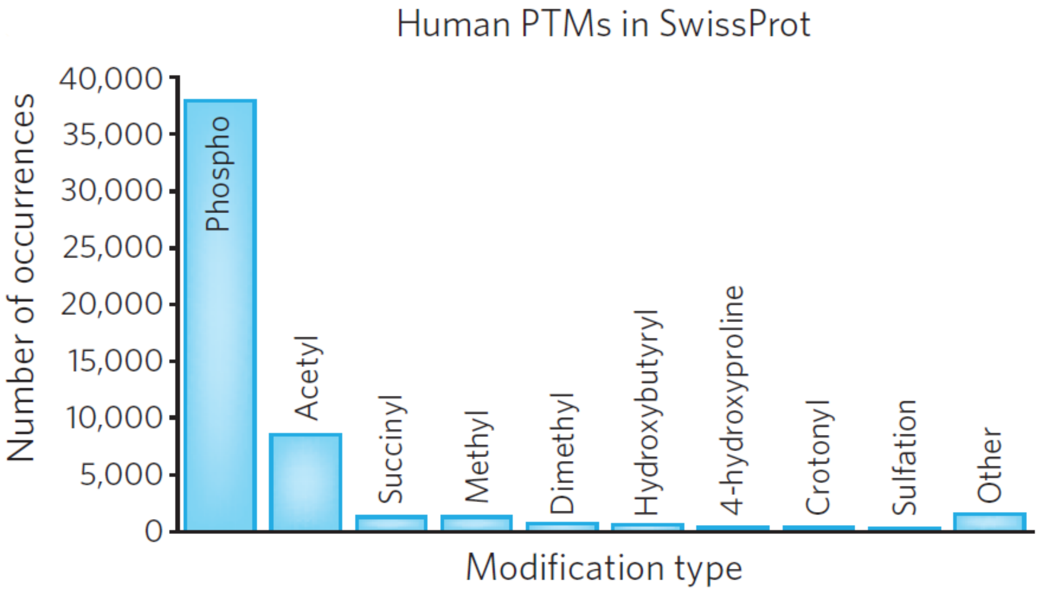
PD = 0.96s

- **Recognizers physically contact residues** downstream of bound NAA
- **Influence is encoded in the peptide's kinetic signature** and is highly predictable
- **Kinetic signatures are a unique and powerful feature** of Quantum-Si's core technology
- **The acquisition of single-molecule kinetic information** gives us unprecedented insight into binding interactions

QUANTUM SI™

Ultrasensitive PTM Detection for Proteins and Proteoforms

Phosphorylation is the Most Abundant PTM in the Human Proteome



Nat Chem Biol 14, 206–214 (2018). https://doi.org/10.1038/nchembio.2576

- **Post-translational modifications** (PTMs) are central to protein function and implicated in human diseases
- **There are more than 400 different types of PTMs;** phosphorylation is the dominant type (~72% of all PTM sites)
- **Phosphorylation has the largest disease association:** 81% of all discovered PTM-associated diseases[1]

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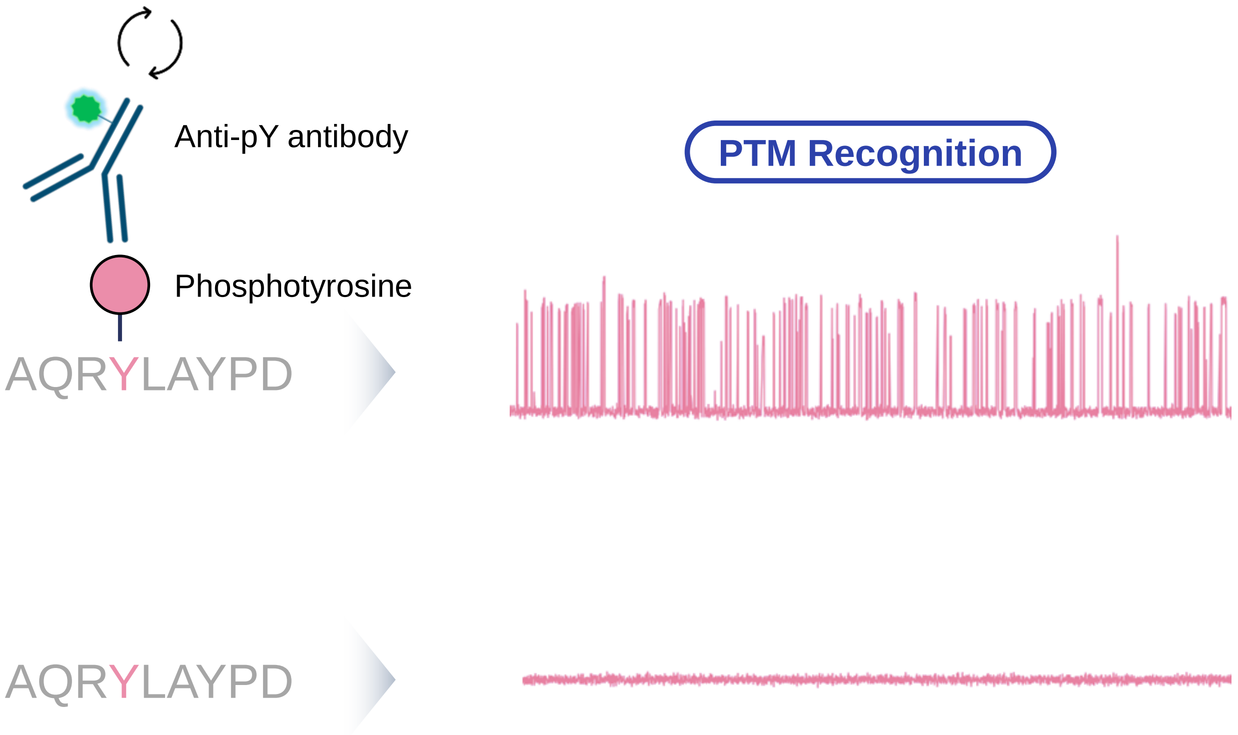
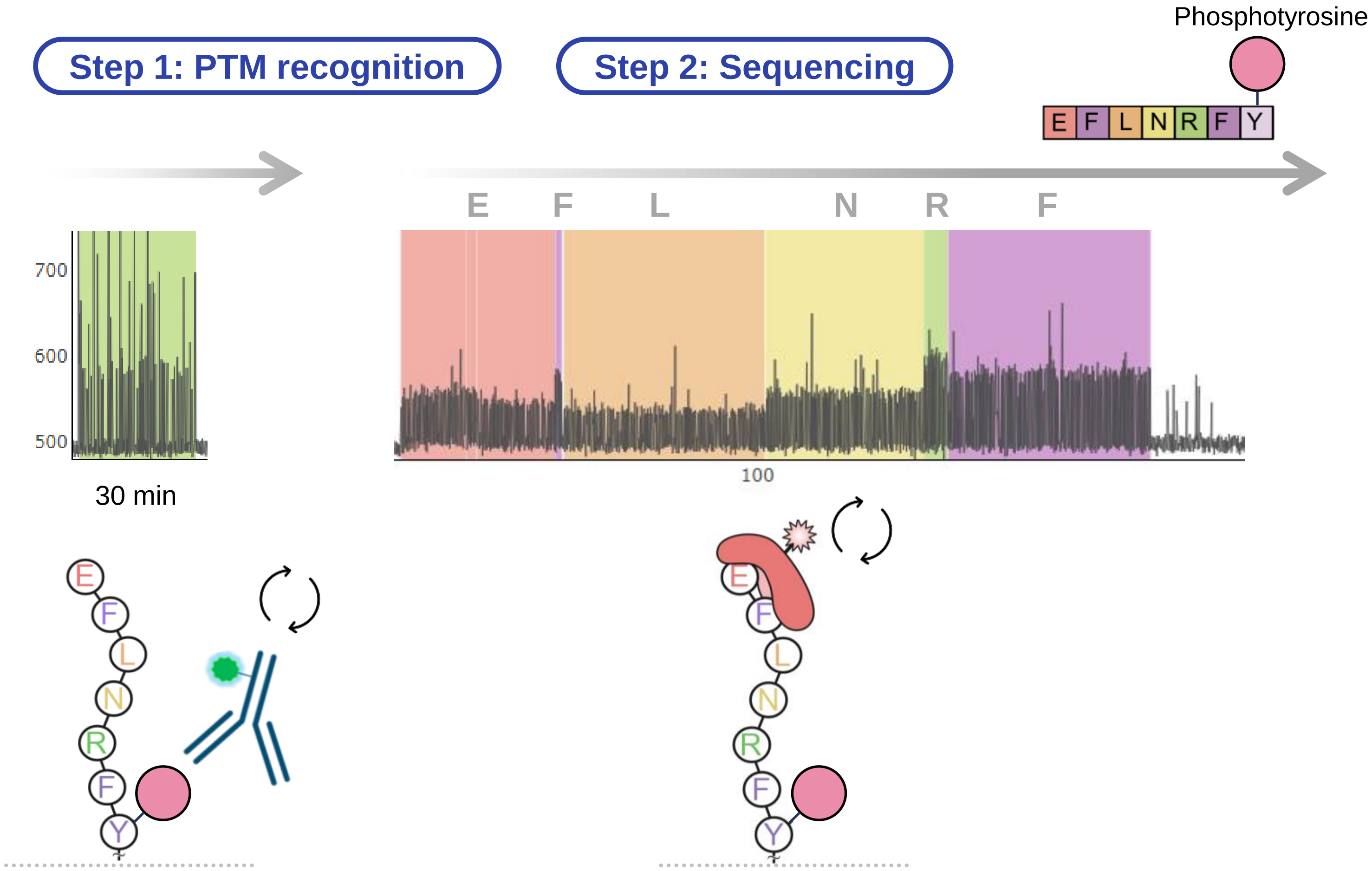
1. https://doi.org/10.1016/j.gpb.2018.06.004

Affinity Reagents as Ultrasensitive PTM Recognizers



- **Anti-PTM antibodies and other affinity reagents** work on chip for ultrasensitive PTM detection
- **Deliver the same real-time kinetic information** as NAA recognizers
- **Recognize PTMs anywhere** in the peptide (not just at the N-terminus)

Affinity Reagents as Ultrasensitive PTM Recognizers



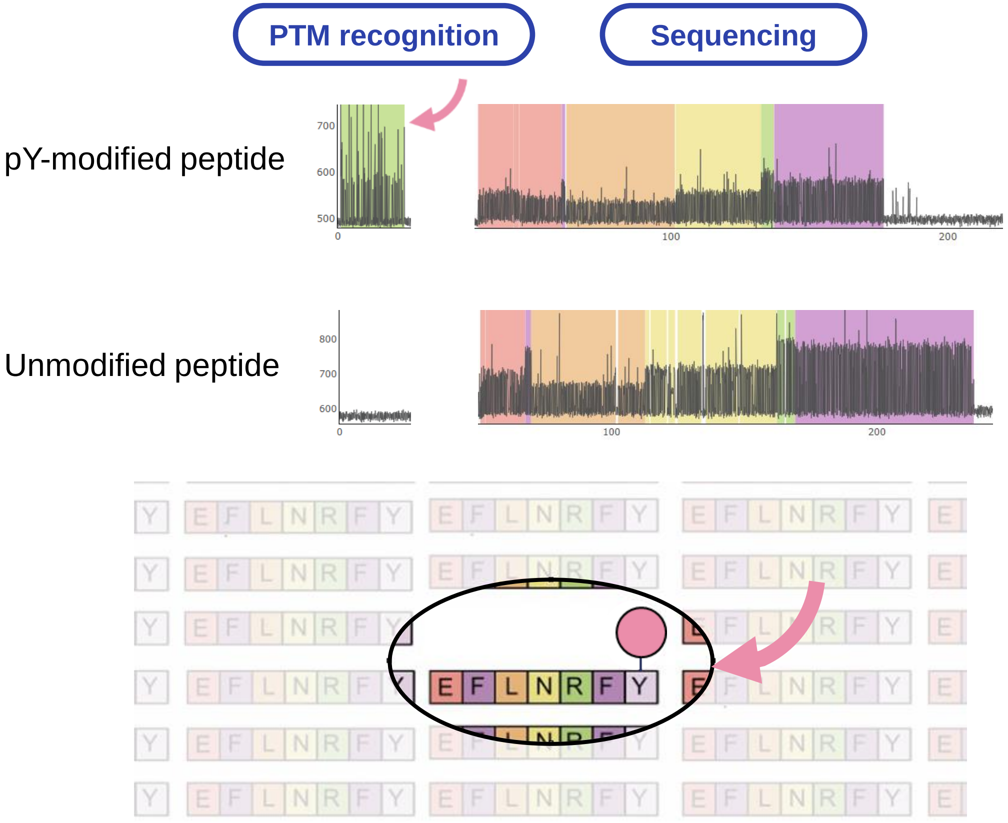
Step 1: PTM recognition

Step 2: Sequencing

- **Step1:** PTM detection for 30 minutes with PTM recognizer
- **Step 2:** Normal protein sequencing with NAA recognizers
- **PTM recogizers can be multiplexed and combined** with kinetic signatures to pinpoint PTMs in multisite configurations

Ultrasensitive Phosphotyrosine Detection with CDNF

CDNF_HUMAN
..QEAGGRPGADCEVCK **EFLNRFYK** SLIDRGVNFSLDTIEK ELISFCLDTK..

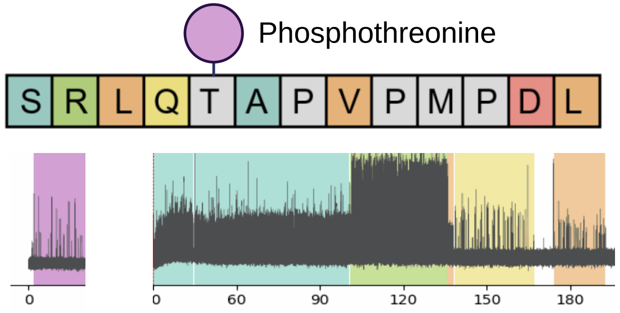


Detection of less than **1** PTM-modified peptide **in 1,000**

- **Extreme sensitivity to PTM stoichiometry** due to the clear pulsing pattern from PTM recognition
- **Example:** a CDNF peptide is detected at a ratio of less than 1 phosphorylated peptide in 1,000
- **Method can be extended to other types of PTMs,** e.g., ubiquitination, glycosylation; works with commercially available affinity reagents

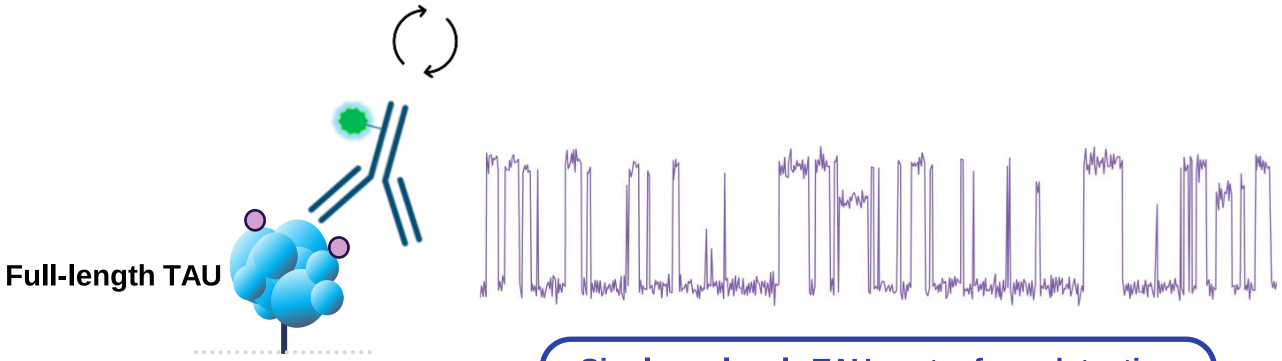
Recognition of Human TAU Proteoforms

TAU_HUMAN
..VAVVRTPPKSPSSAK **SRLQTAPVPMPDLK** NVK SK IGSTENLK HQPGGGK VQIINK K..



PTM recognition

Sequencing



Full-length TAU

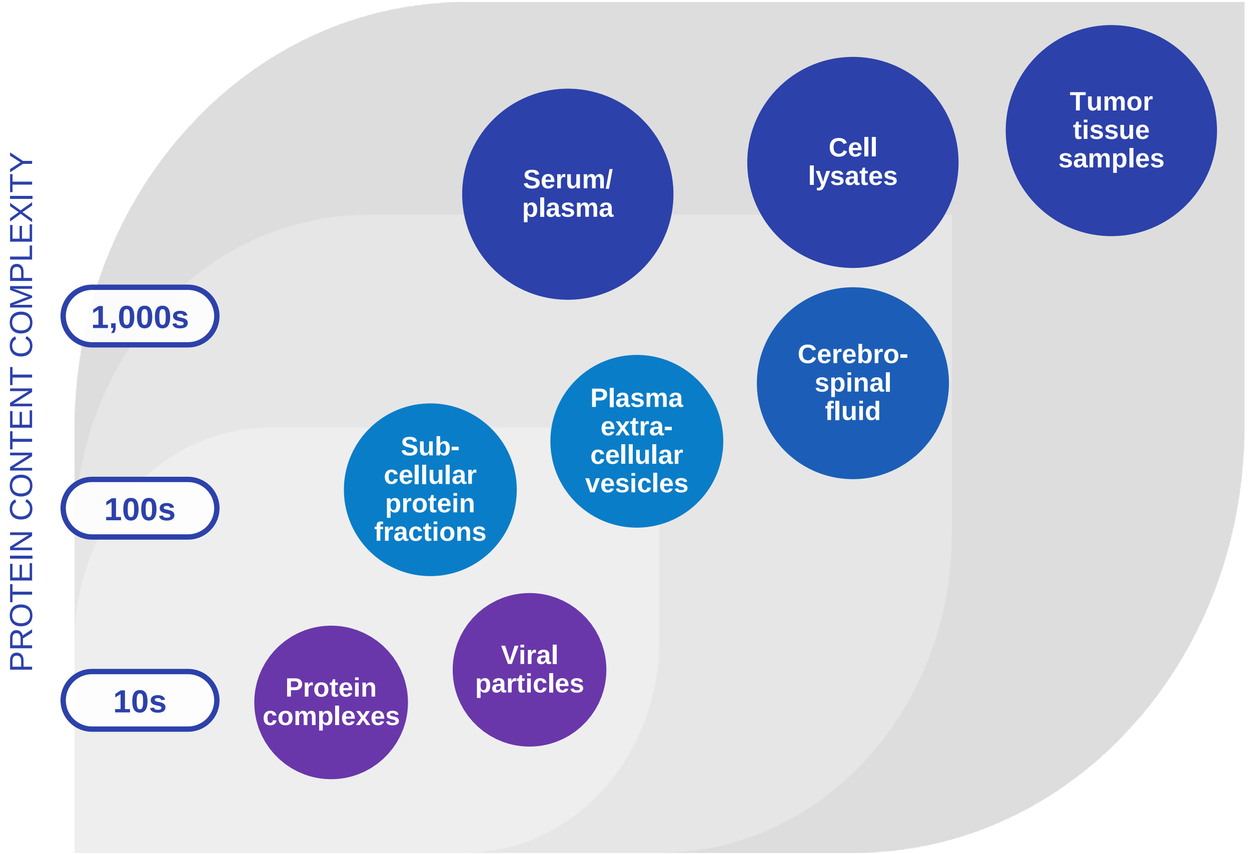
Single-molecule TAU proteoform detection

- **Affinity reagents** can be used in a bottom-up or top-down configuration
- **Example:** bottom-up recognition of pT* on human TAU peptides, top-down detection of immobilized full-length TAU proteoforms
- **Real-time approach enables proteoform detecting** reagents to be run simultaneously
- **First commercially available platform** for detection and differentiation of full-length proteoforms

* - Phosphothreonine

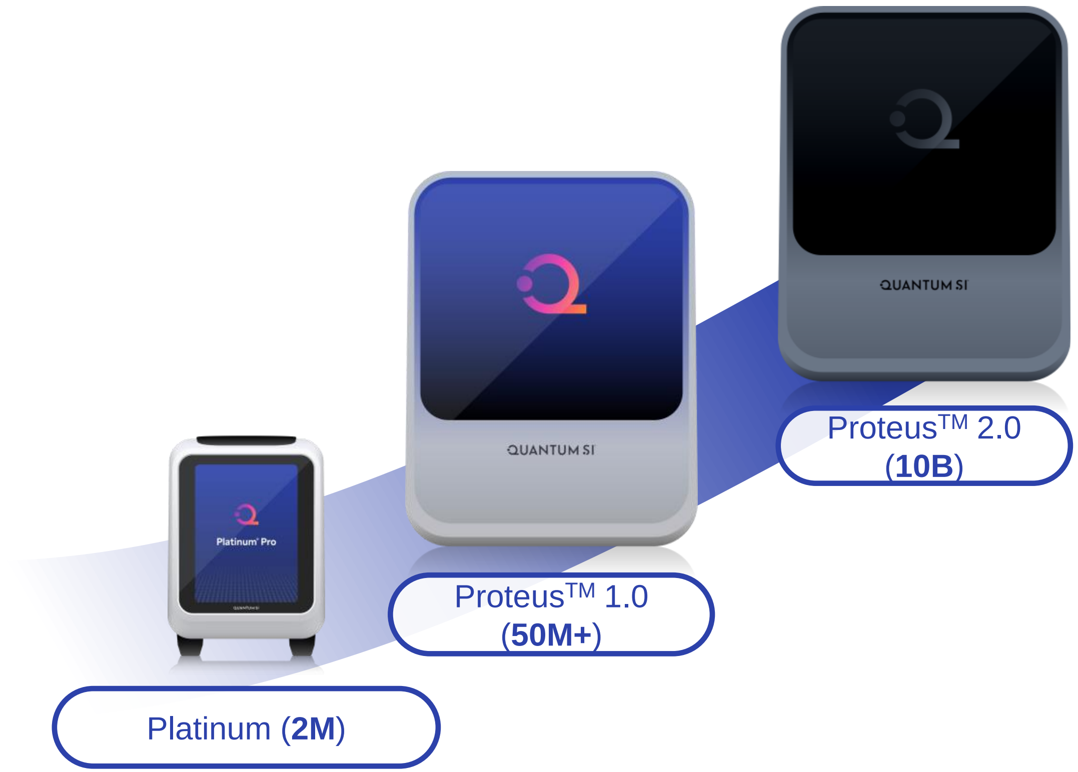
Unbiased Interrogation of High-Complexity Samples with Quantum-Si's Core Technology

Sequencing Complex Biological Samples Unlocks Broad Access to Proteomics



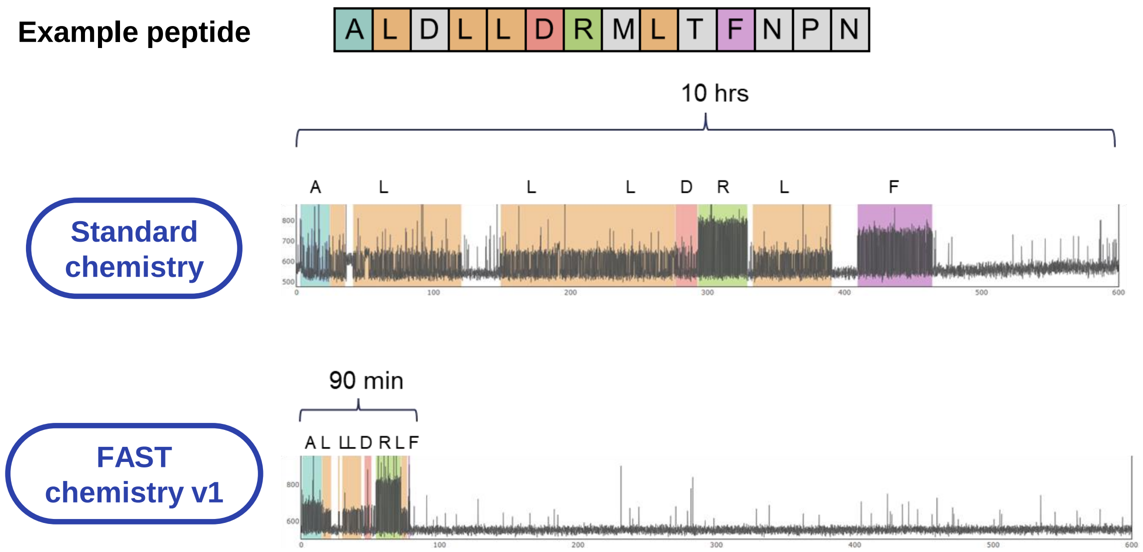
- **Biological samples like serum** contain hundreds to thousands of proteins with wide dynamic range of abundance
- **Unbiased, consistent, accessible interrogation** of these samples is a challenge in proteomics
- **Sequencing is not limited to predefined content:** enables discovery of changes in proteins and proteoforms that other methods are unable to access

Unbiased Interrogation of High-Complexity Samples



- **New chip architectures** and advances in sequencing chemistry will enable sequencing biological samples at ever-increasing depth
- **Future versions of the platform** will see shotgun sequencing with thousands of proteins identified
- **Barcoding approaches** and flowcell designs will enable sample multiplexing
- **Innovative methods to fractionate proteins** and to reduce sample complexity will be combined with these improvements

Fast Sequencing for Deep Coverage and Rapid Sample-to-Answer



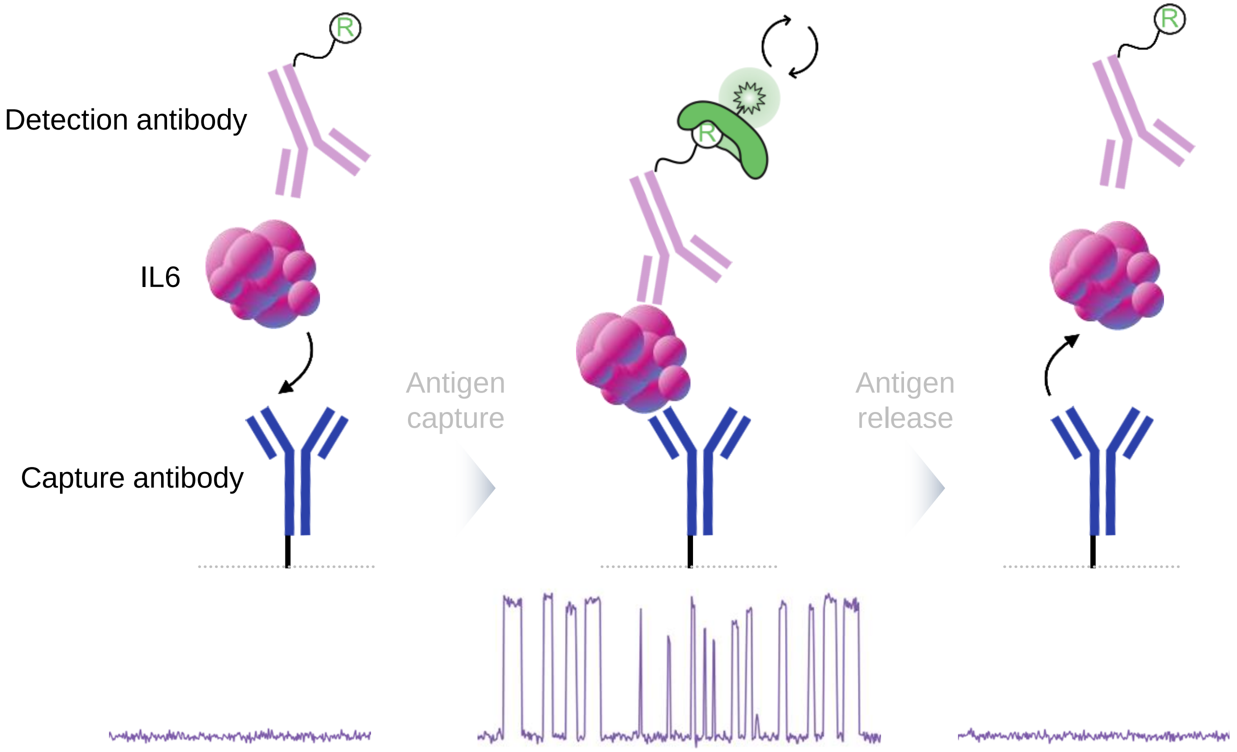
- **We have developed new sequencing chemistry** with a much faster rate of sequencing
- **With FAST chemistry**, we achieve equal performance to 10-hour runs in just 90 minutes (version 1)
- **Path to runs <30 minutes** for some applications with further development
- **Enables deep sample coverage** via iterative FAST sequencing and rapid sample-to-answer methods for clinical applications

QUANTUM SI™

Beyond Sequencing: the First Commercially Available Platform for Top-Down Single-Molecule Proteomics

Detecting Antibody Binding Events with the Power of Real-Time Kinetics

Dye-cycling enables ultrasensitive real-time detection of biomarkers

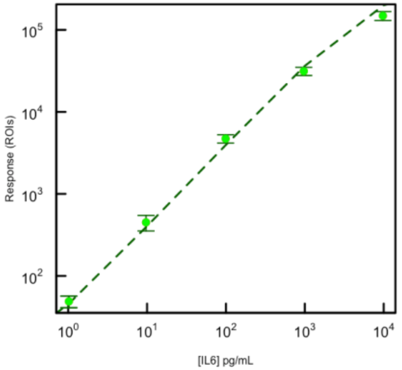


- **Detection of fixed protein panels** with high sensitivity is an increasingly important application in proteomics
- **We developed a single-molecule sandwich assay** that enables real-time detection of biomarkers
- **Dye-cycling approach uses our existing kits** to translate immune complex formation into a readily detected pulsing segment

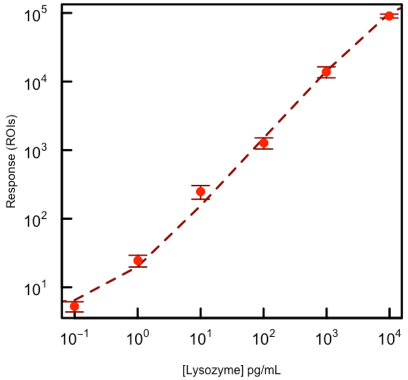
Ultrasensitive Detection of Proteins in Serum

Direct detection of proteins in serum with high sensitivity

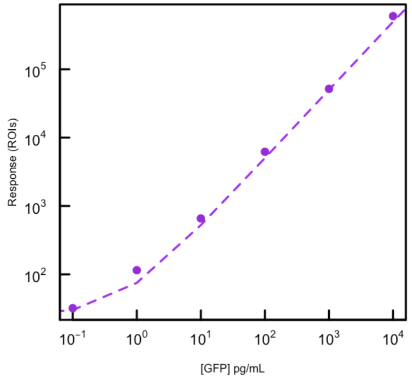
Interleukin 6



Lysozyme



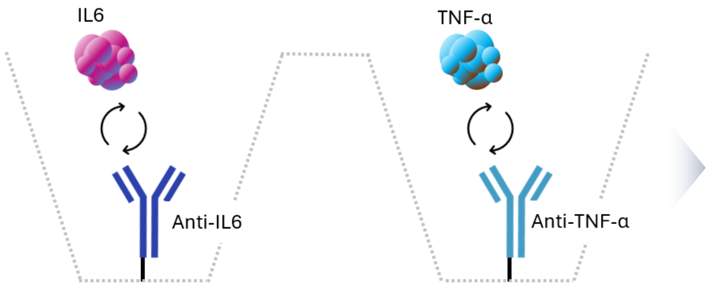
GFP

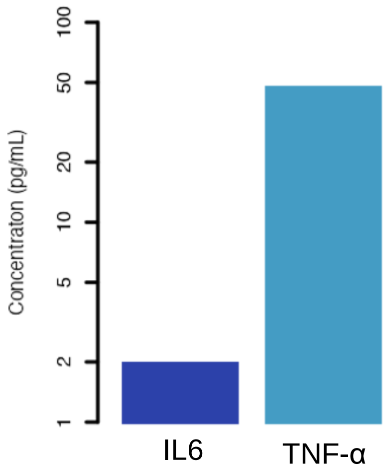


Spike-in titration experiments in serum demonstrate 0.1–1 pg/mL detection (path down to 10 fg/mL with further development)

Multiplexed Ultrasensitive Protein Biomarker Detection

Multiplexed detection of human IL6 and TNF-α





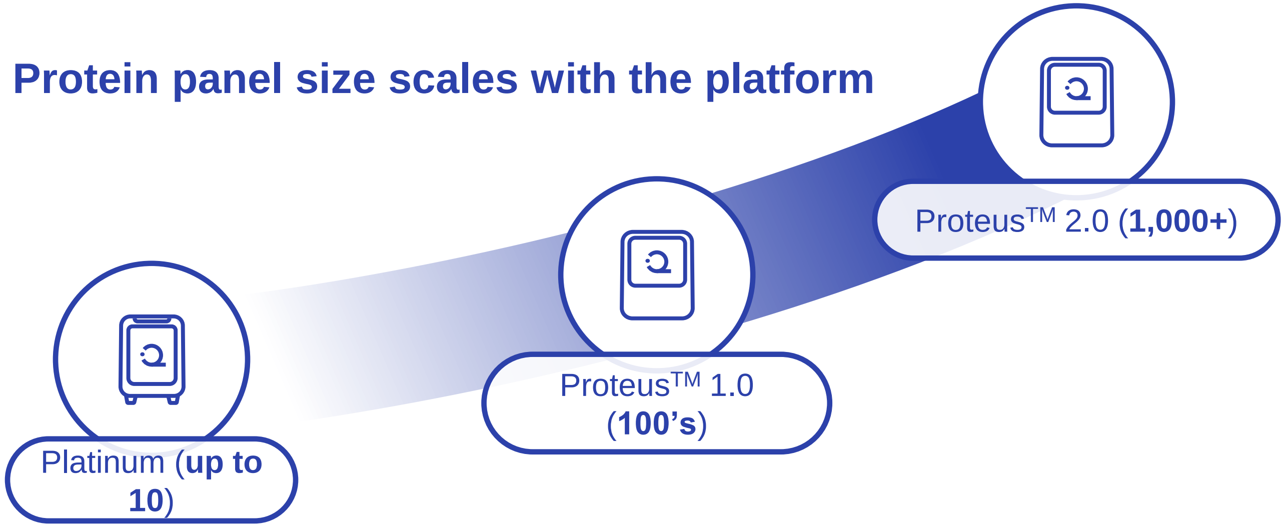
- **Affinity reagents against multiple biomarkers** can be loaded on the chip
- **Dye-cycling approach enables discrimination** of biomarkers by fluorescence and kinetic properties in multiplexed assays, along with PTMs

A Platform for Ultrasensitive Detection of Protein Panels

Multiplexed biomarker detection directly in serum

IL10
IL6
IL2
IL4
TNFα
IFNγ
IL12
:

Protein panel size scales with the platform



Platinum (**up to 10**)

Proteus^{TM} 1.0 (**100's**)

Proteus^{TM} 2.0 (**1,000+**)

- **Sensitivity on Platinum** is suitable for commercialization of panels with up to 10 proteins
- **Panel size scales with the platform**, as well as capacity to multiplex samples
- **Proteins detected directly in serum** on chip, eliminating complex sample prep
- **Sample-to-answer in ~2 hours** with one instrument

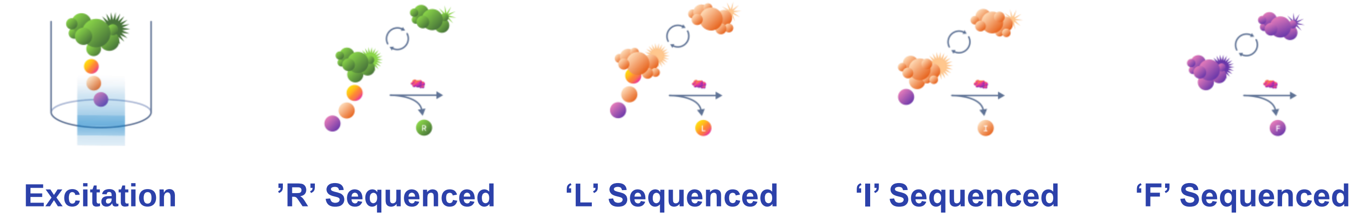
Platform Roadmap

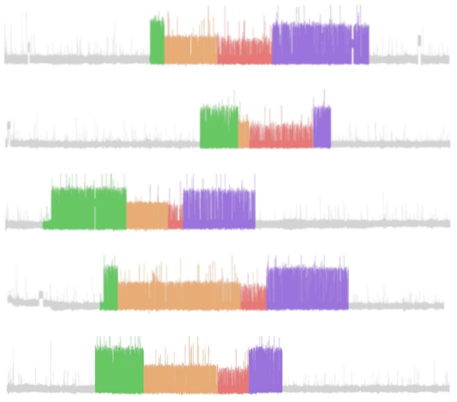
Nov 20, 2024

John Vieceli

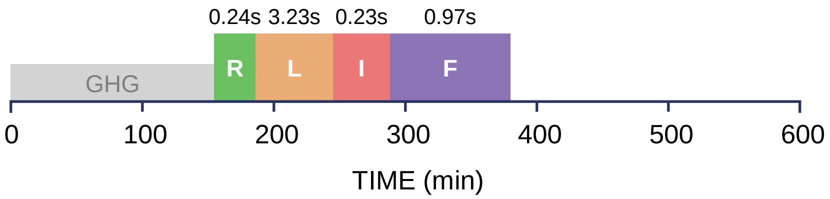
Innovation Pipeline is Robust and Accelerating

Sequencing Analysis Software





Kinetic Signature Plot



Sequence

Measure fluorescence from single molecule binding of N-terminal amino acid recognizers

Pulse Caller

Assign pulses to a recognizer based on fluorescence intensity and lifetime

Analyze

Determine amino acid sequence using kinetic signature

Software Workflows for Next-Gen Protein Sequencing™

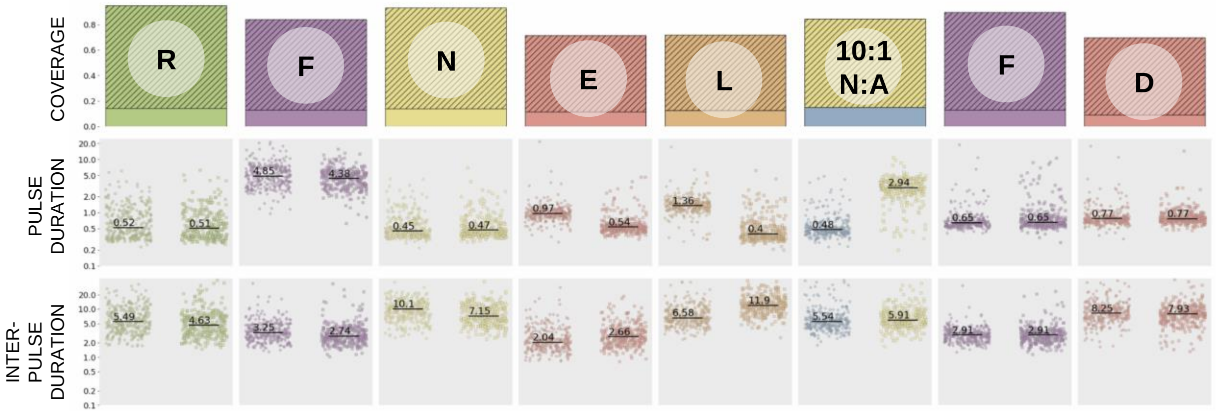
Protein Inference

Kinetic signature enables inference of sample protein from whole human proteome panel

Rank		Inferred Protein	Score	Likelihood	Mass (kDa)	Length
1	**IL4**	splP04112lIL4_HUMAN	11.035496	99.99%	17	153
2		splP06127lCD5_HUMAN	0.593929	44.78%	55	495
3		splQ15208lSTK38_HUMAN	0.582068	44.12%	54	465
4		splQ96LQ0lPPR36_HUMAN	0.506878	39.76%	49	422
5		splQ81WR1lTRI59_HUMAN	0.440162	35.6%	47	403
6		splQ9UMR3lTBX20_HUMAN	0.428596	34.85%	49	447
7		splQ96EU6lRRP36_HUMAN	0.403635	33.21%	30	259
8		splQ9H2F9lCCD68_HUMAN	0.371386	31.02%	39	335
9		splQ8IVI9lNOSTN_HUMAN	0.365859	30.63%	58	506
10		splO9BZ81lMAGB5_HUMAN	0.310895	26.72%	32	275

ProteoVue™ Variant Calling

Kinetic signature enables differentiation of protein variations at the single amino acid level



QUANTUM SI

Artificial Intelligence

N-terminal Amino Acid Recognizer Development

FYW **LIV** **R**

***Science* Publication**

Oct 2022

AS **NQ**

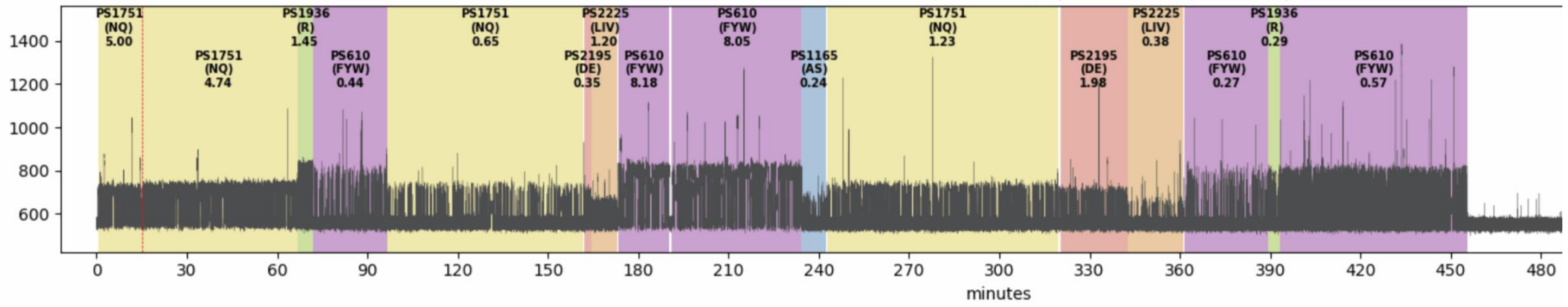
Version 1 Kit

Mar 2023

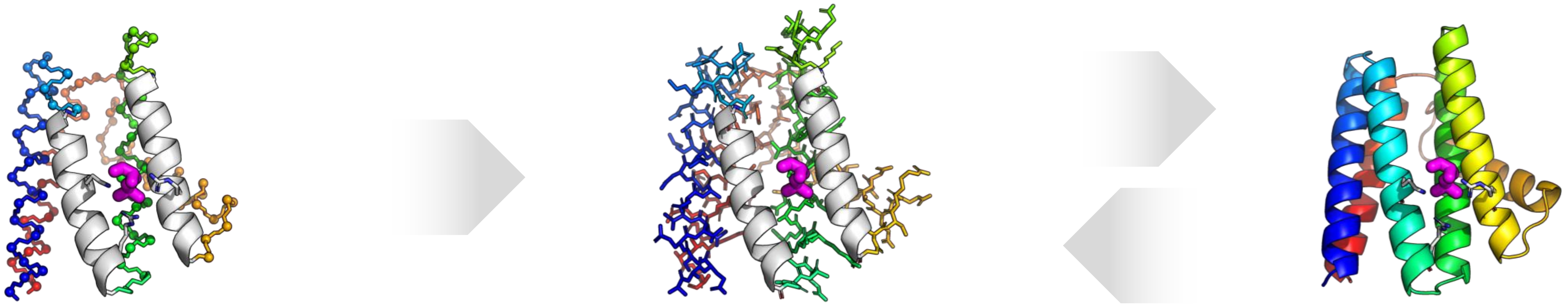
DE

Version 2/3 Kit

Jan/July 2024



Recognizer Protein Design AI



Amino acid recognizer
backbone design

Amino acid recognizer
sequence design

Orthogonal verification
of amino acid recognizer
protein design

Protein design AI leverages **NVIDIA GPUs on-premises and in Amazon Cloud**

Pulse Width Prediction Using Artificial Intelligence

Platinum Sequencing

QSI is continually increasing the size of the training data with more proteins and/or new binders

Pulse Width Prediction AI

Currently predicts ~4.6 million pulse widths used in analysis

Better Performance

Pulse width prediction AI trained with more platinum sequencing data improves protein detection performance

QUANTUM SI™

Platinum® Pro

Platinum® Instrument

Customers identified opportunities to improve workflow and UI/UX

Functionality limited to protein & peptide sequencing

Local analysis enabled by additional server

Introducing Platinum® Pro

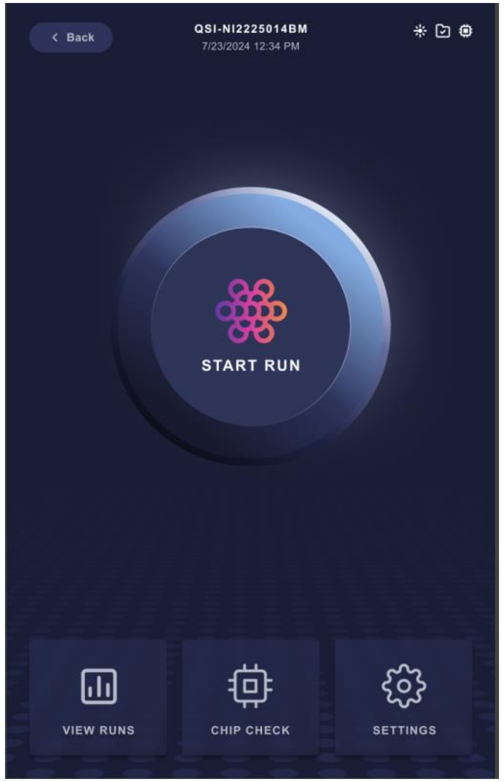
Streamlined workflow
and reduced hands-on time

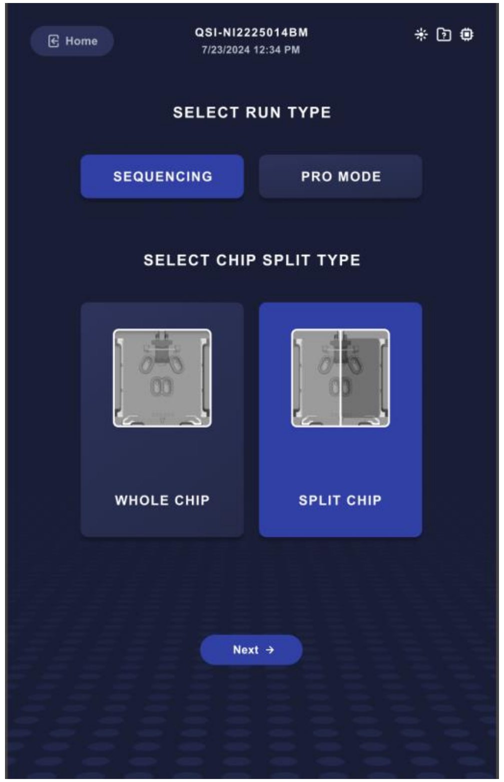
Pro Mode enables new applications

Onboard analysis or via the cloud

Enhanced user interface

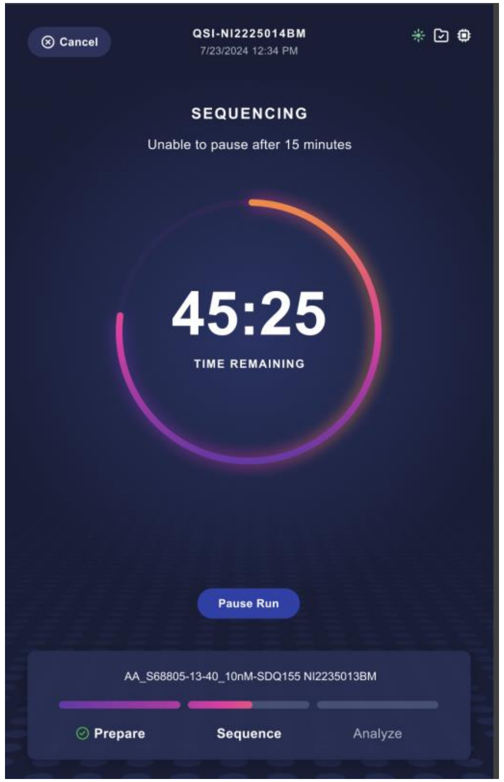
Streamlined Workflow Improves Usability





Open lid, insert chip, and close lid.

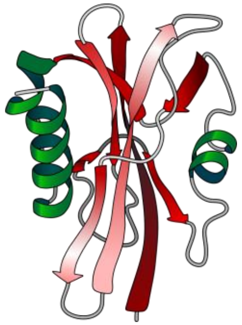
AA_S68805-13-40_10nM-SDQ155 NI2235013BM



Unable to pause after 15 minutes

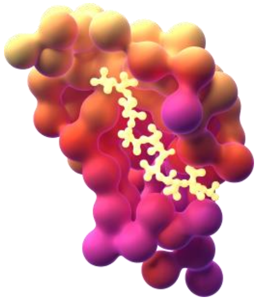
AA_S68805-13-40_10nM-SDQ155 NI2235013BM

Pro Mode Available only on Platinum Pro

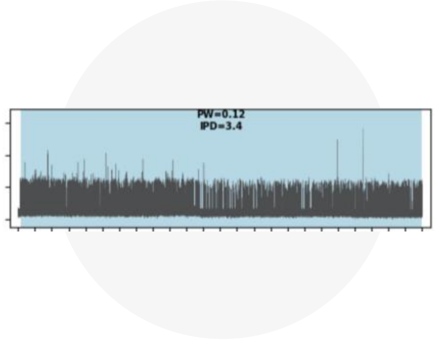


Protein of Interest

Dye-labeling Kit



Protein Binding

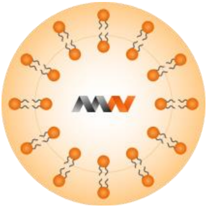


Binding Kinetics

Kit and platform enable detection of **single-molecule protein binding and kinetics**

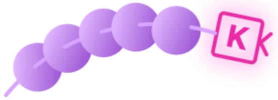
Peptide Barcodes can be Used to Monitor Protein Expression Both *In Vivo* or *In Vitro*

IN VIVO

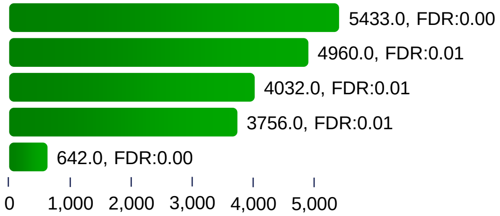


Equimolar 5 barcode mix encoded as mRNA and packaged into LNPs

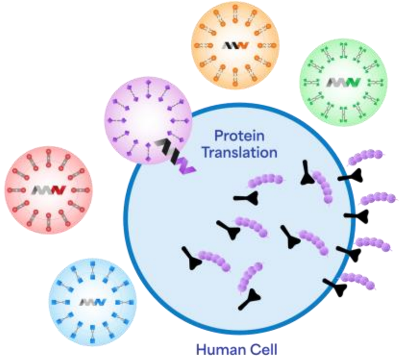
Inject into mouse model; harvest target tissues



Enrich for target protein, functionalize, cleave, and sequence barcodes



IN VITRO



V2 Library Preparation Kit Improvements

Simplified workflow reduces need for buffer exchange

Improved performance with ~80% of proteins successfully inferred

Reduced protein input five-fold

QUANTUM SI™

Proteus™

Proteus^{TM} Increases Throughput + Automation

Switch from semiconductor to optical architecture with patterned array for throughput scalability

Liquid handling automation simplifies workflow and reduces hands-on time

Up to an order of magnitude throughput increase per sample relative to Platinum at initial launch

Proteus^{TM} Increases Number of Samples

Run one or two samples simultaneously

Reagent cartridges with sequencing workflow automation

Run up to 8 samples in one sequencing run

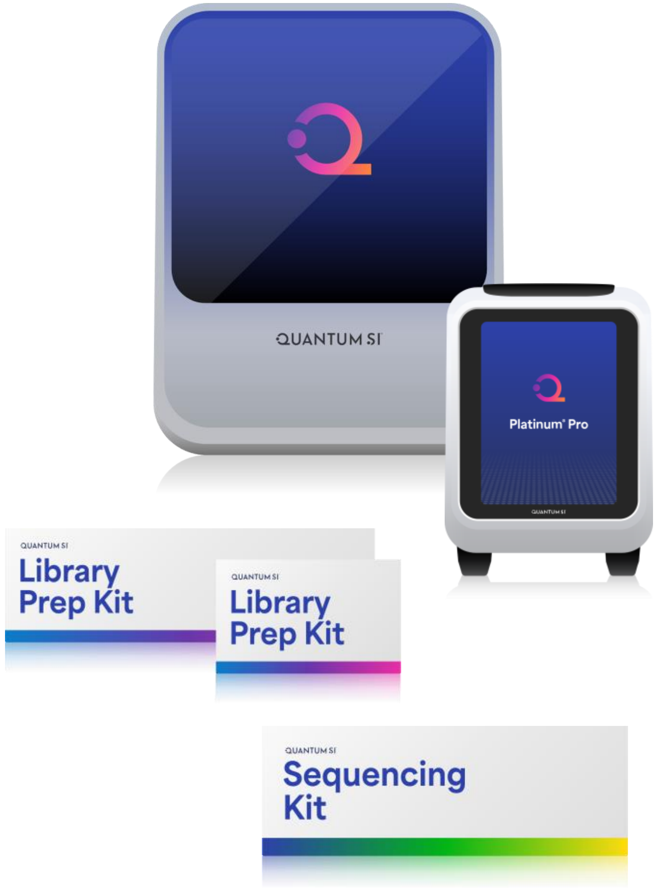
The Proteomics Lab of the Future

QSI's Pipeline is Heavily De-risked Compared to Other Proteomics Companies

Builds upon QSI's existing commercially available technologies

Industry-leading protein and enzyme engineering program operating at scale and with high success rates

Manufacturing infrastructure in place and routinely producing and delivering product to customers today



Strategic Partnerships to Accelerate Commercial Adoption and Deliver on Innovation Roadmap

NVIDIA

avantor™

skywater

Planet Innovation

QSI is Best Positioned to Usher in a New Paradigm in Proteomics

New platform architecture designed so QSI will not be feature limited (can scale to billions of reads)

QSI core technology is the only commercially available tech that can enable single-molecule, top-down, and bottom-up proteomic analysis

QSI ultrarapid sequencing can enable significant increase in sample throughput per day and unlock time-sensitive applications (e.g. clinical diagnostics) in the future

QSI new architecture, combined with other ongoing technology development initiatives, creates clear path to *de novo* sequencing

QSI Near-term Pipeline Will Unlock Opportunities Across All Market Segments

	YE2024	2025	2026	2027+
Clinical Dx	○	○	◔	◕
Production (QC)	◑	◕	●	●
Translational	◑	◕	●	●
Research	◑	◑	●	●
Discovery	○	◔	◑	●

Proteomics Lab Today

Many specialized platforms needed to fully interrogate the proteome

Technical tradeoffs when selecting between the breadth of protein coverage and depth of insights

High capital costs and manual workflows limit the number of laboratories capable of performing proteomics

QSI Will Power the Proteomics Lab of the Future

One platform and core technology capable of addressing the broadest range of proteomics analysis methods

Eliminate technical tradeoffs – single-molecule, amino acids and PTMs, top-down or bottom-up, ultrasensitive, scalable throughput

Affordable and automated, allowing any lab — anywhere — to be a proteomics core lab

Q&A