QUANTUM SI™

Quantum Si

Investor & Analyst Day

November 19, 2025

Investor Day Agenda

Jeff Hawkins, CEO	**Tackling the Complexity of the Proteome**	10:00–10:10 AM
Todd Rearick, CTO	**Proteus Program Update and Long-term Technology Roadmap**	10:10–10:40 AM
John Vieceli, CPO	**The Path to Detecting All 20 Amino Acids**	10:40–11:05 AM
Brian Reed, Head of Research	**Post-translational Modification Analysis Solutions**	11:05–11:25 AM
Jeff Hawkins, CEO	**The Road to Proteus Launch**	11:25–11:45 AM
Management	**Q&A Session**	11:45 AM–Noon

Proteins Are the Core of Biological Discoveries Across Many End Markets


Agriculture


Industrial


Pharma + Biotech

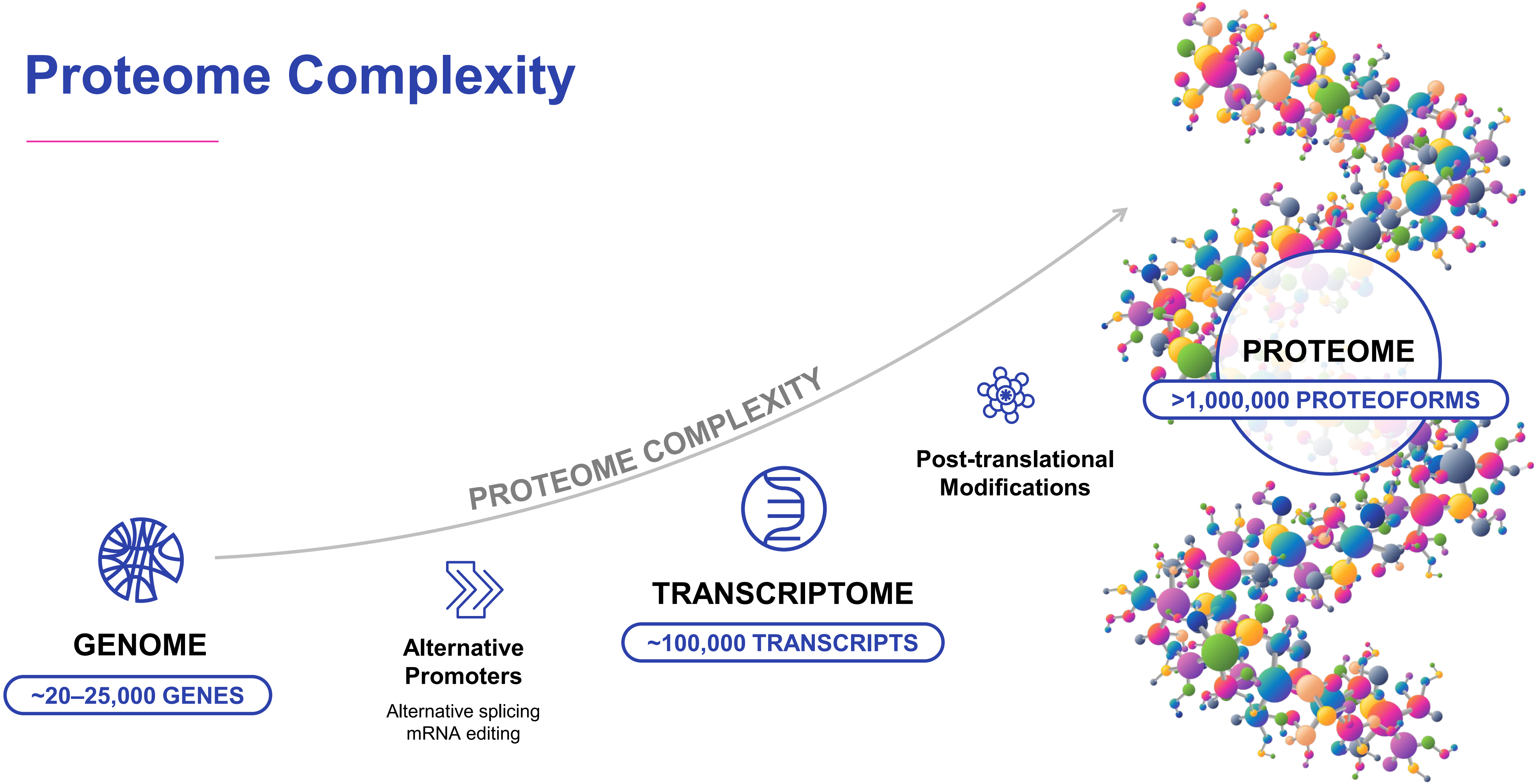

Academic Research


Defense


Clinical Diagnostics


Translational Research

Proteome Complexity



GENOME

~20–25,000 GENES

Alternative Promoters

Alternative splicing
mRNA editing

TRANSCRIPTOME

~100,000 TRANSCRIPTS

Post-translational Modifications

PROTEOME

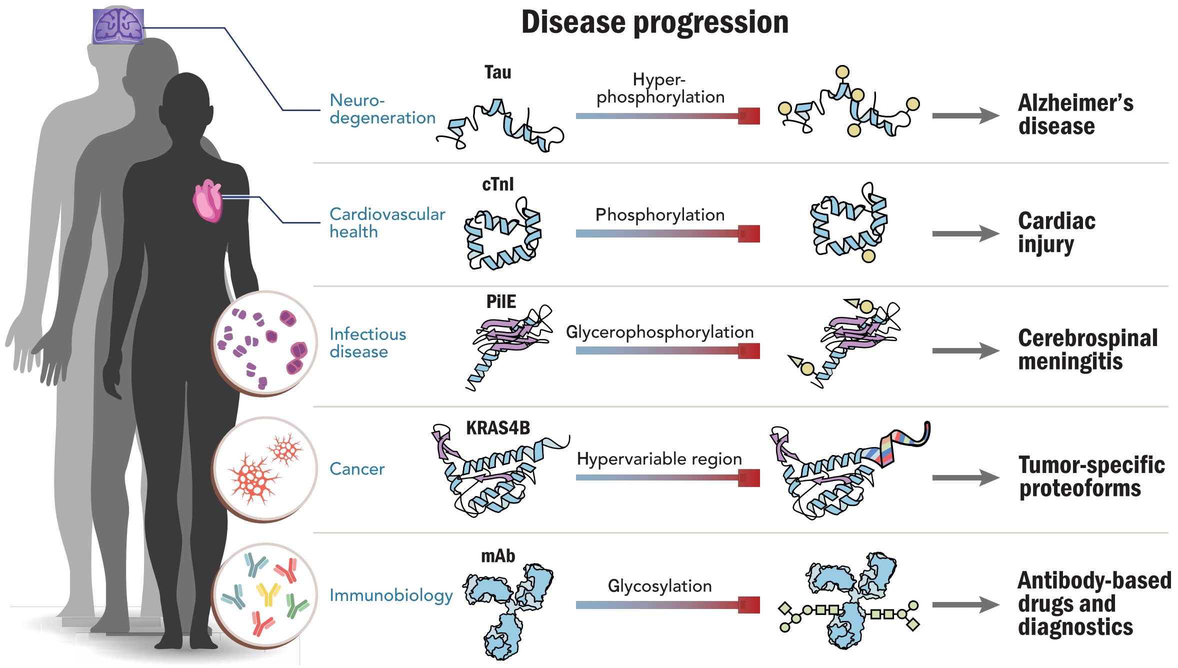
>1,000,000 PROTEOFORMS

The Study of Proteoforms Extends to Many Disease Areas and Thousands of Unique Proteins

Affinity-based methods cannot scale to this complexity

Complete coverage of the proteome would require hundreds of thousands or more unique, site-specific affinity reagents

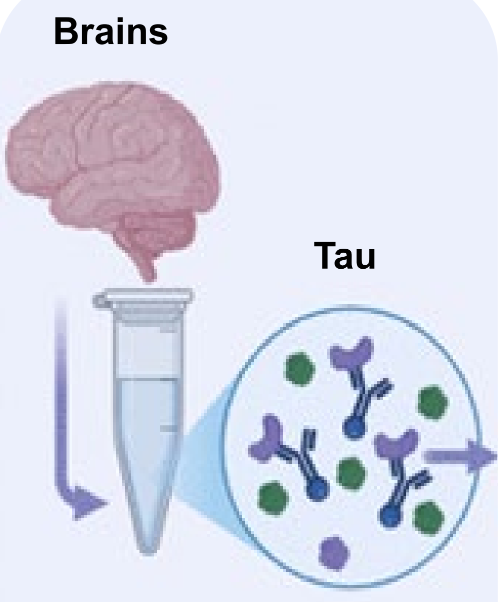
Only single-molecule protein sequencing can tackle this complexity



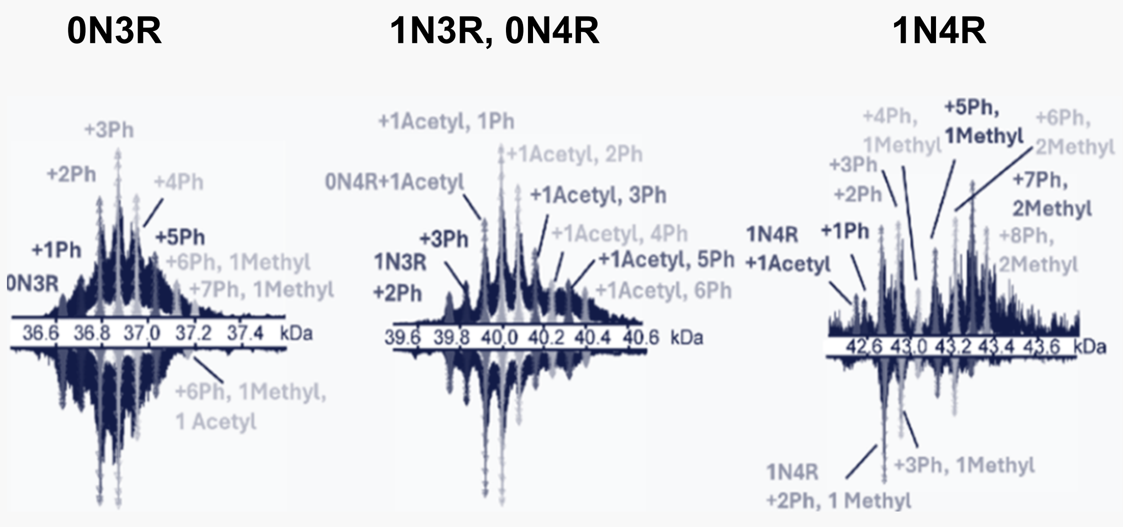
Human Proteoform Project: https://www.science.org/doi/10.1126/sciadv.abk0734

Proteoforms Are Not Limited to a Single PTM Type

They are far more diverse, even within a single protein



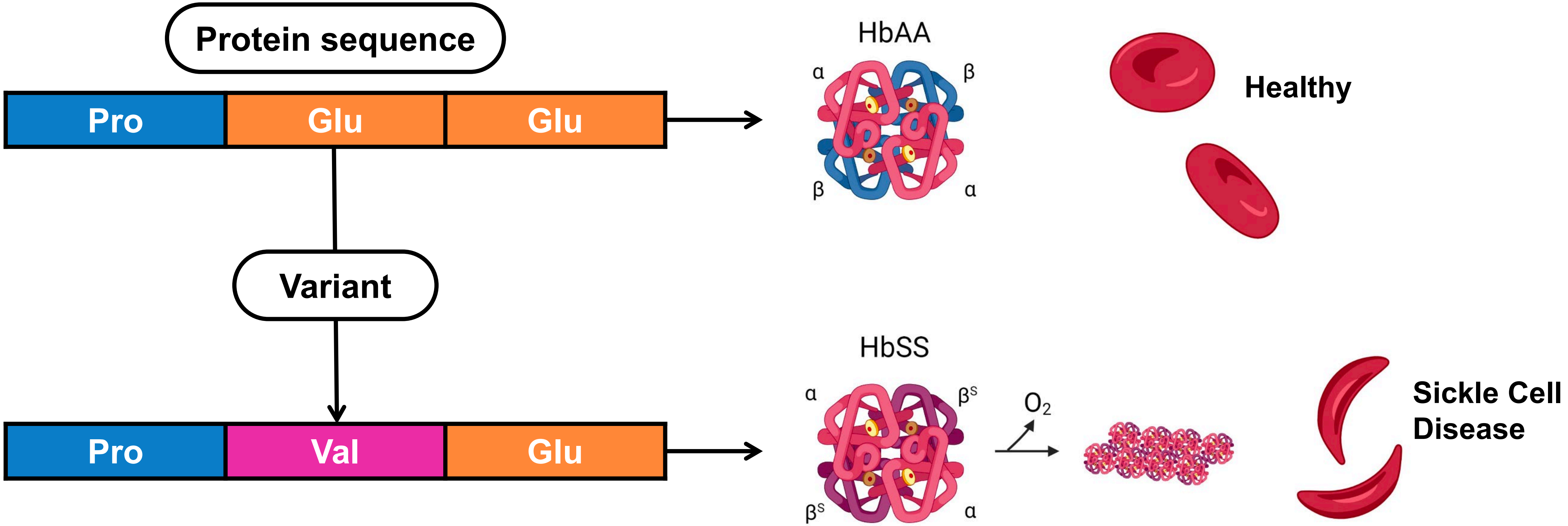
Immunoprecipitation



Intact Tau isoforms/proteoforms

Source: *J. Proteome Res*. 2025, 24, 6, 2916–2925

Proteoforms Also Include Single Amino Acid Variants, Which Can Be Critical to Understanding Disease



Protein sequence

Pro | Glu | Glu

Variant

Pro | Val | Glu

Adapted from Ramadas N and Sparkenbaugh EM (2023). The APC-EPCR-PAR1 axis in sickle cell disease. *Front. Med.* 10:1141020.

Specialized Platforms With High Capital Costs Limit Adoption Outside of Core Labs in Proteomics

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 with the top end instruments costs $1M or more each

Manual laboratory and data analysis workflows limit the number of laboratories capable of performing proteomics

Moving Beyond the Core Lab: Proteus Will Enable Deep Protein Analysis and Accelerate the Field of Proteomics

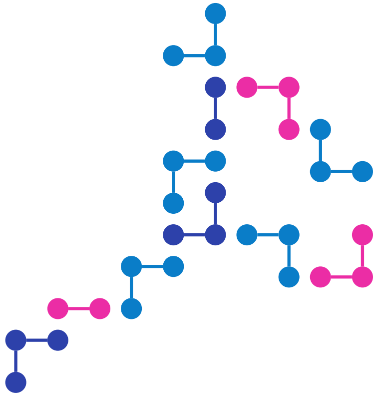
Single-molecule protein sequencing will be the most versatile technology in proteomics — single AA variants, broad PTM coverage, and protein-agnostic

Automation simplifies laboratory workflow, increases throughput, and minimizes the need for specialized staff

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

Themes of Today’s Presentations

Proteus performance data and long-term technology roadmap



The path to detecting all 20 amino acids

A diverse set of tools to enable generalizable PTM analysis

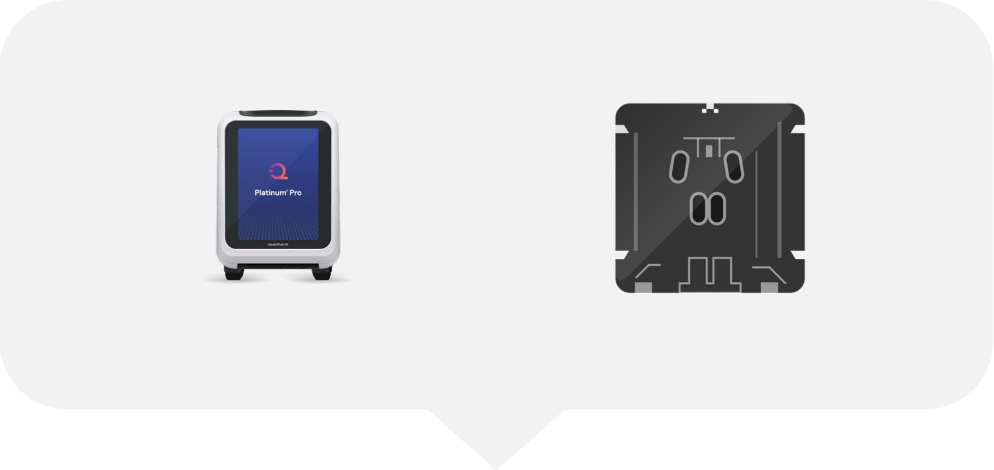
Road to Proteus launch and 2026 milestones

Proteus™ Program Update

Proteus Next-generation Architecture

Platinum® Pro + 2M Chip

- Integrated semiconductor consumable
- Benchtop instrument with manual workflow



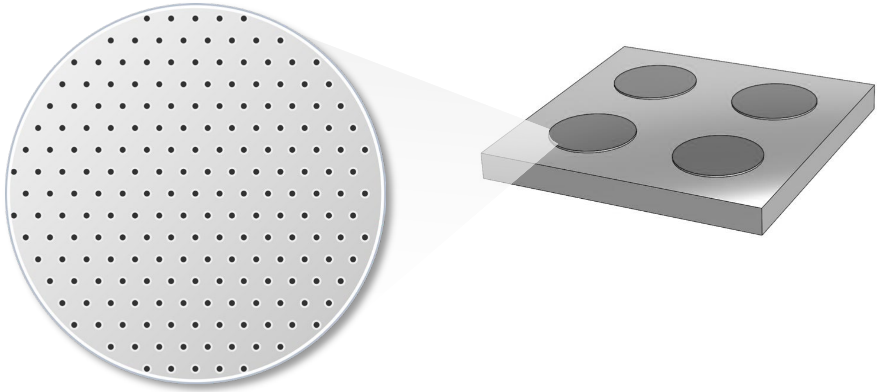
Proteus™ + KinetIQ™ Array

- Simple, passive consumable
- Benchtop instrument with imaging system
- Workflow automation

KinetIQ™ Array

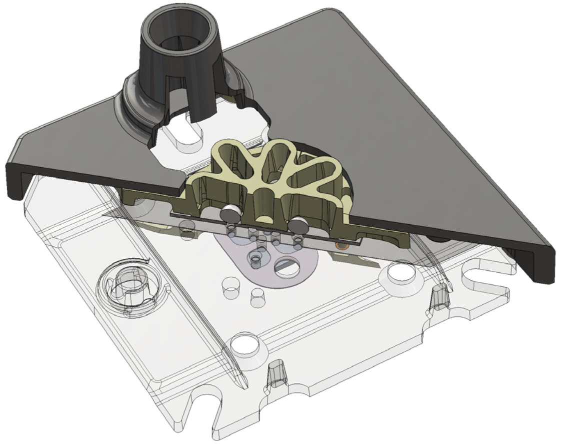
Simple, passive consumable

- Low-cost fused silica die
- 80M wells per device
- Architecture scales to billions of wells

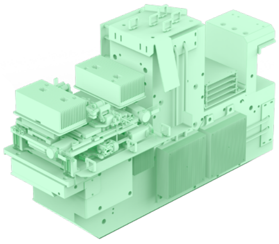


Simple packaging

- Inexpensive plastic assembly
- Four flow cells, each with 20M wells
- Features to support automation

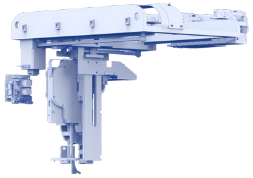


Proteus Instrument



Optical module

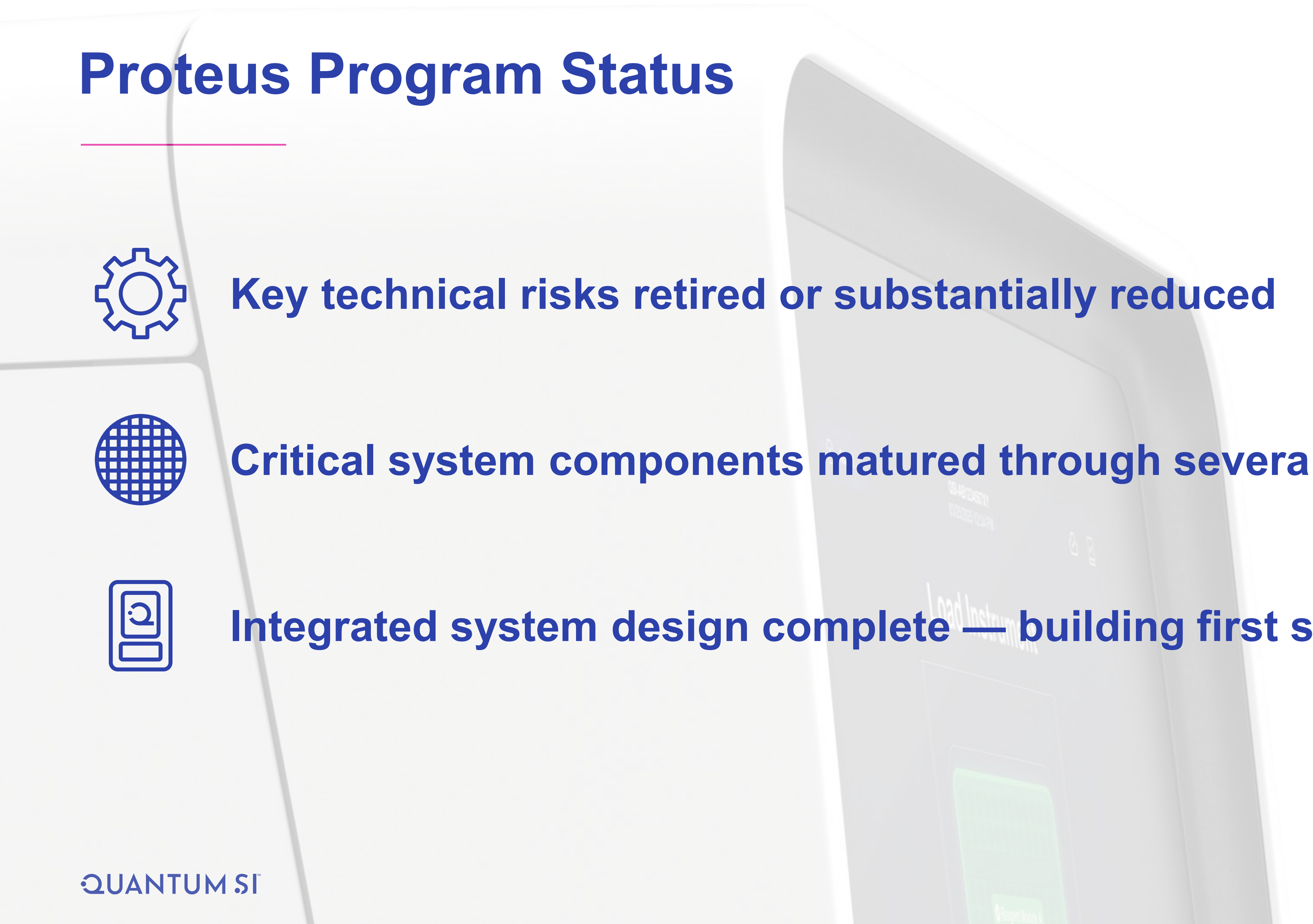
- High-performance custom optical design
- High resolution and large field of view
- Supports simple passive consumable



Liquid handling

- Full workflow automation
- More advanced workflows, deeper insights

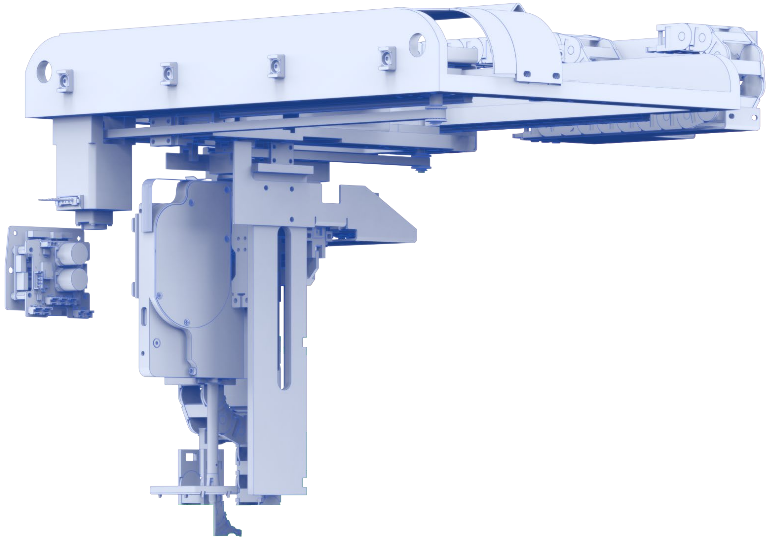
Proteus Program Status



- Key technical risks retired or substantially reduced
- Critical system components matured through several prototypes
- Integrated system design complete — building first systems now

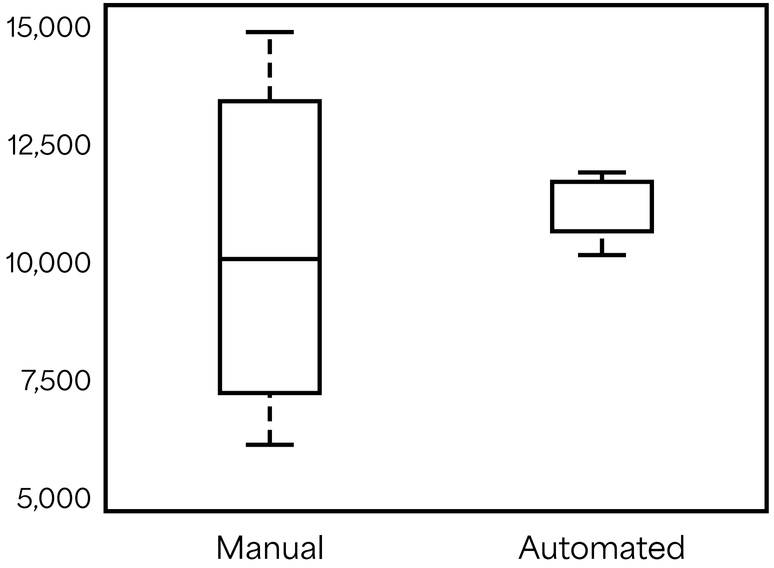
Sequencing Workflow Automation is More Reproducible Than Current Manual Workflow

Integrated System Liquid Handling



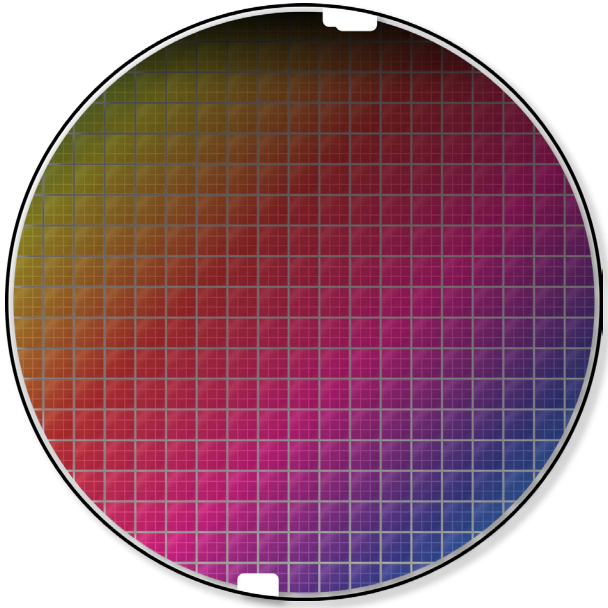
Prototype Liquid Handling Subsystem Data

Automated vs manual workflow alignments



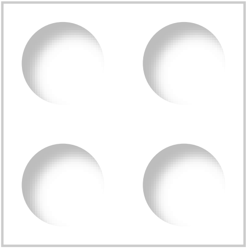
- Same architecture as integrated product design
- Entire sequencing workflow fully automated

KinetIQ Array Fabrication and Post-processing Processes are Established

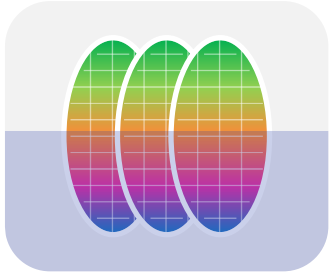


Wafer fabrication
process established

Well structure optimized



Product intent die size + geometry

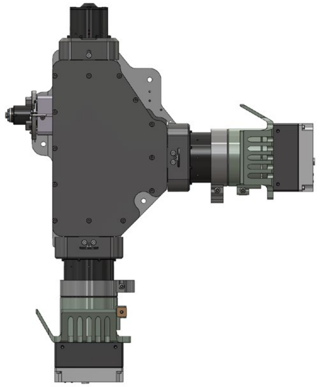


Wafer-scale post-processing

Efficient packaging process

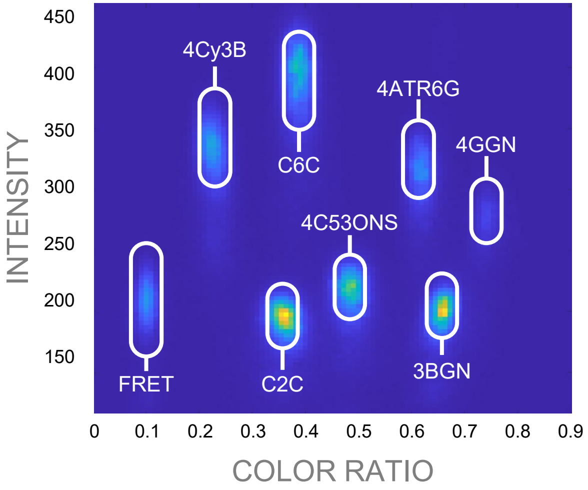
Data from Prototype Imaging System and New Dyes Fully Validates Transition from Lifetime to Color Ratio

Fully Functional Imaging System



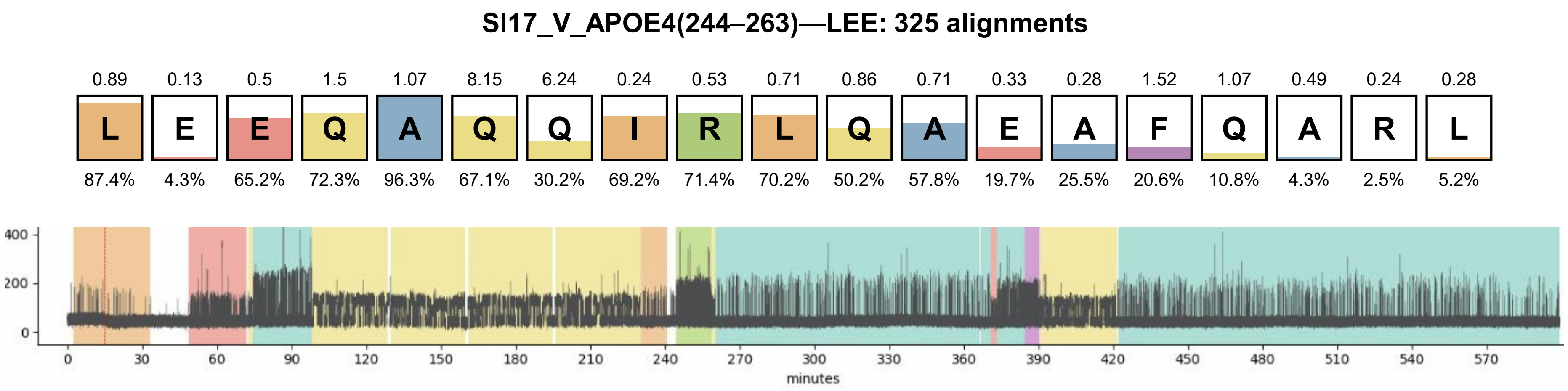
- Same architecture as product design
- Commercial off-the-shelf components
- Product-intent image sensors
- Reduced field of view

Proven Color Channel Detection



- New color-space dye set
- Demonstrated up to 8 dyes
- Room for more if needed

Successful Dynamic Sequencing Runs Completed in Q3



SI17_V_APOE4(244–263)—LEE: 325 alignments

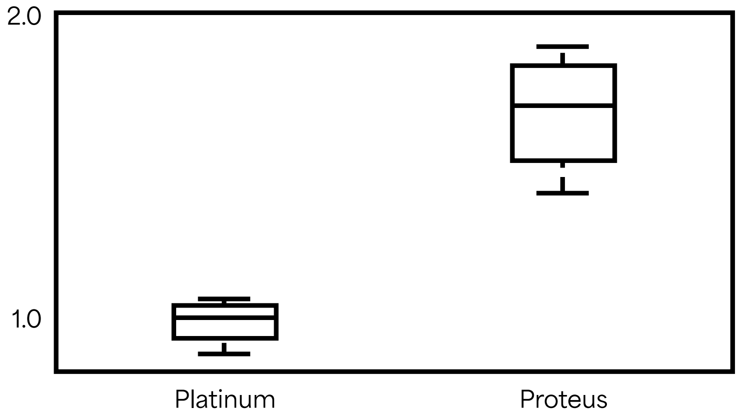
0.89	0.13	0.5	1.5	1.07	8.15	6.24	0.24	0.53	0.71	0.86	0.71	0.33	0.28	1.52	1.07	0.49	0.24	0.28
L	E	E	Q	A	Q	Q	I	R	L	Q	A	E	A	F	Q	A	R	L
87.4%	4.3%	65.2%	72.3%	96.3%	67.1%	30.2%	69.2%	71.4%	70.2%	50.2%	57.8%	19.7%	25.5%	20.6%	10.8%	4.3%	2.5%	5.2%

Substantial de-risking new system elements

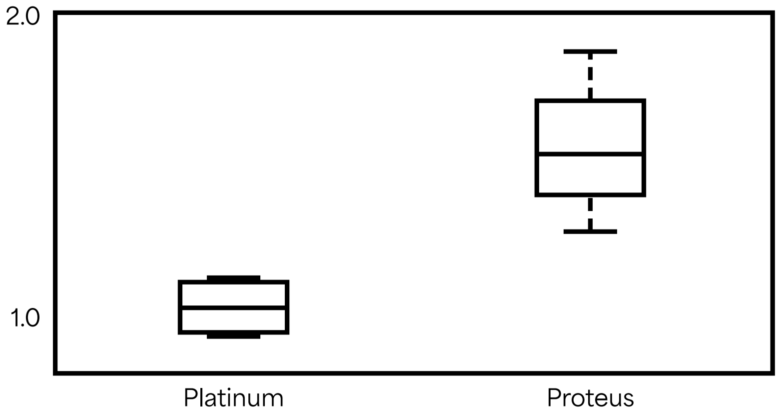
Consumable, dyes, optical system, software

Proteus Has Superior Sequencing Output Per Well Compared to Platinum

Alignments per well (normalized to Platinum)



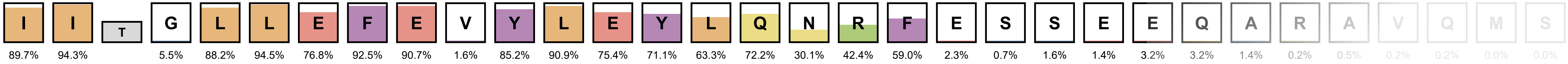
Long-read fraction (normalized to Platinum)



Proteus routinely produces more alignments with the same number of wells

Proteus produces more long alignments compared to Platinum

Proteus Consistently Sequences Deep into Peptides


SI19_V_IL6(87–120)—IIT: 439 alignments

Unique capability for long-range structural information

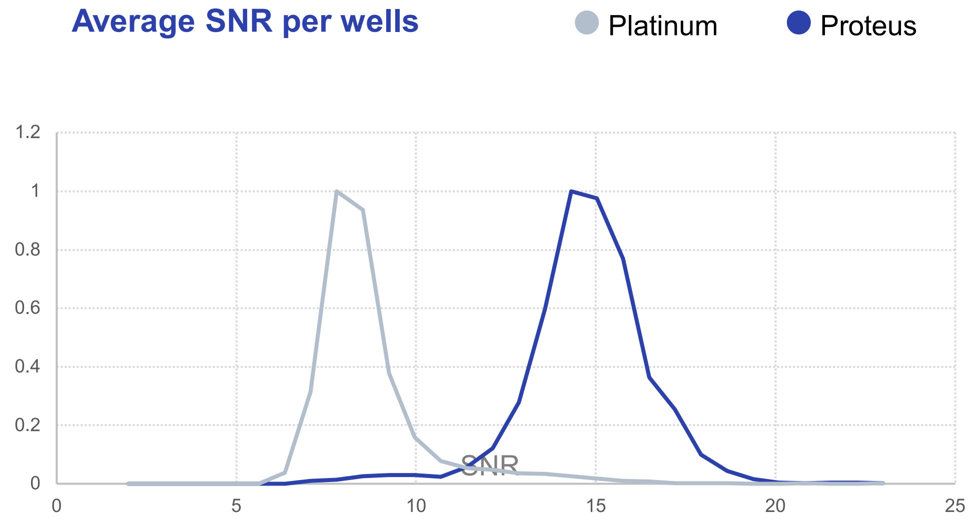
Access to PTMs and variants deep into reads

Sequencing depth expected to continue to improve with increased coverage and further optimization

Proteus Has Superior SNR and Short Pulse Detection Compared to Platinum

Better SNR

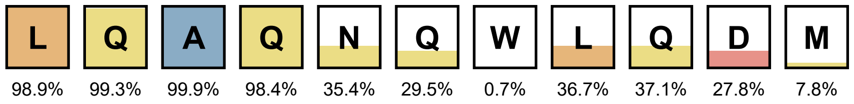
- More high-quality alignments
- Better accuracy
- More sensitive for PTMs and variants



More sensitive short pulse detection

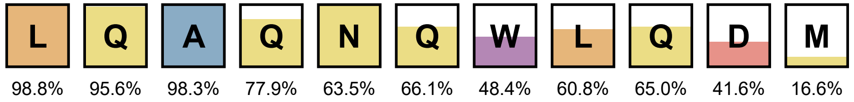
- Increased motif coverage with the same binders
- Software not optimized for improved data

Platinum



L	Q	A	Q	N	Q	W	L	Q	D	M
98.9%	99.3%	99.9%	98.4%	35.4%	29.5%	0.7%	36.7%	37.1%	27.8%	7.8%

Proteus



L	Q	A	Q	N	Q	W	L	Q	D	M
98.8%	95.6%	98.3%	77.9%	63.5%	66.1%	48.4%	60.8%	65.0%	41.6%	16.6%

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Proteus Sequencing Performance is on Track to Far Exceed Platinum at Launch

Proteus data is already superior to Platinum data

Data generated to date is without optimization

Current algorithms | Current V4 binder set | Current cutters and chemistry

Additional improvements expected before launch

Integrated System in Development

First Integrated System Expected 1Q26

- Full integration of imaging and workflow automation
- Product-like consumables
- Full field of view supporting 20M wells

Proteus Program Summary

**Transition to new architecture is proven —
team is executing towards product launch for YE2026**

**Proteus architecture shows significant improvement
over Platinum in the quantity and quality of sequencing output**

**Platform launch is aligned with improvements in biochemistry
and library prep that will drive additional performance gains**

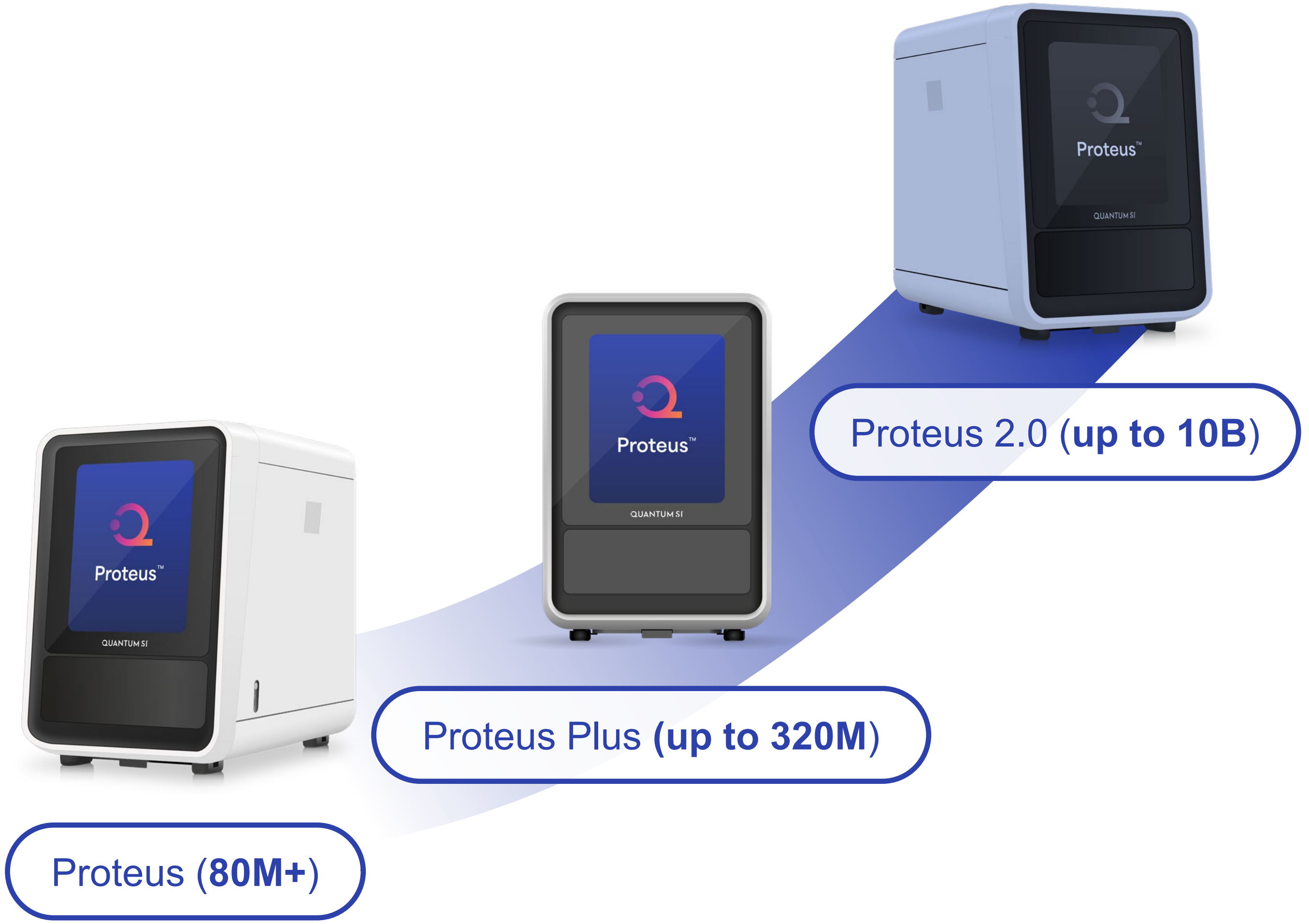
Long-term Technology Roadmap

Proteus Architecture Supports Our Long-term Platform Roadmap Requirements

Consumable architecture
scales to billions of wells

10× scaling from assay
improvements alone

Future instruments
capable of up to 10B reads

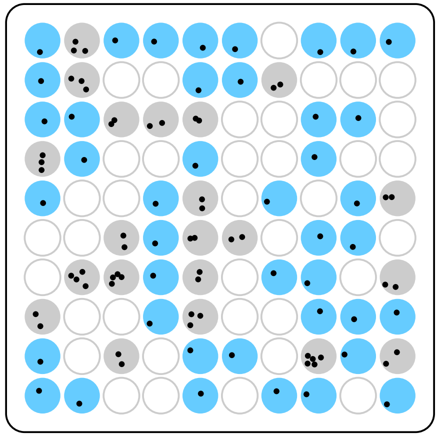


Proteus (**80M+**)

Proteus Plus (**up to 320M**)

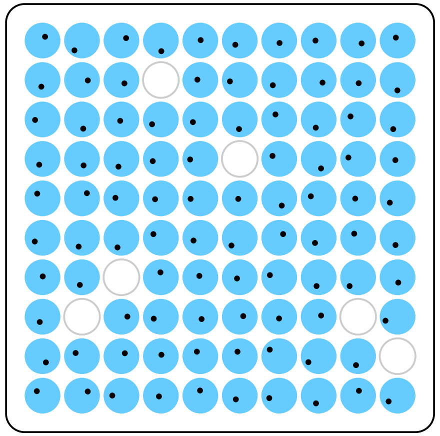
Proteus 2.0 (**up to 10B**)

Super Poisson Loading Increases Sequencing Output per Run by Approximately 3×



Poisson Loading

- Peptides randomly loaded into wells
- Maximum single-molecule loading ~36%
- 64% of wells are empty or multiply-loaded



Super Poisson Loading

- Peptides are loaded in a way that prevents multiple loading
- Only one peptide can be loaded in most wells

Faster Sequencing Roadmap + Field Upgrades Could Drive Output Up to 320M and Increase Samples per Run

Proteus (**80M**)

160M

320M

Proteus Plus **(up to 320M)**

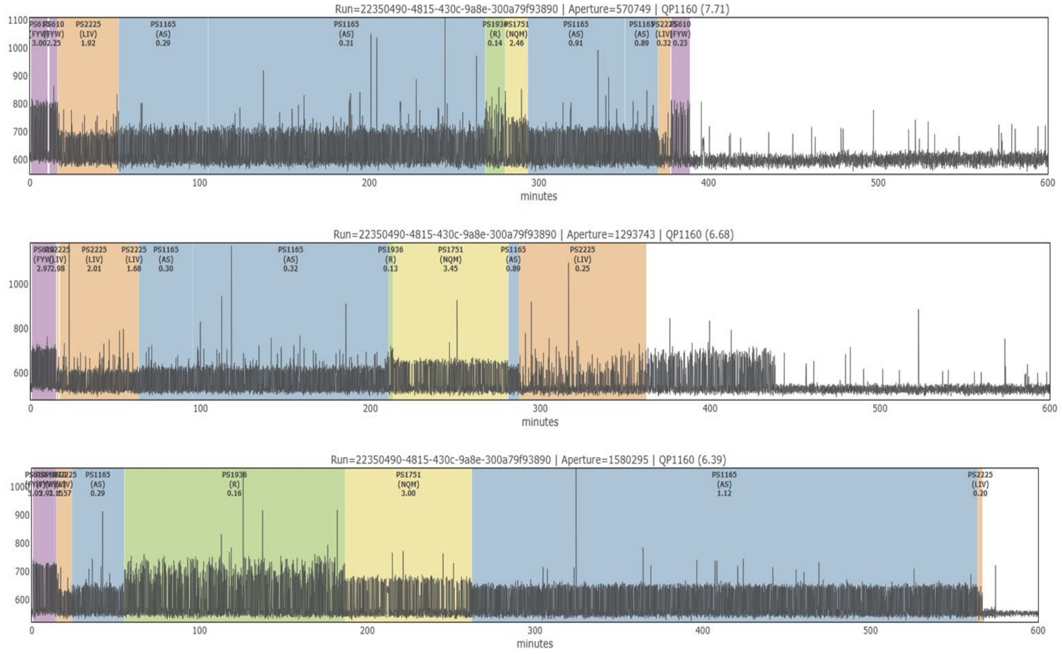
Sequencing time reductions allow more chips to be run in same timeframe as original 80M

Upgrade to drawer/stage and consumable to increase chips/run

The Path to Billions of Reads Requires Controlled Cutting

- **Cutting happens randomly**
- **Residue duration is not uniform**
- **Time/residue is slower on average**
- **Controlled cutting would define the amino acid boundaries + enable a scanning system**

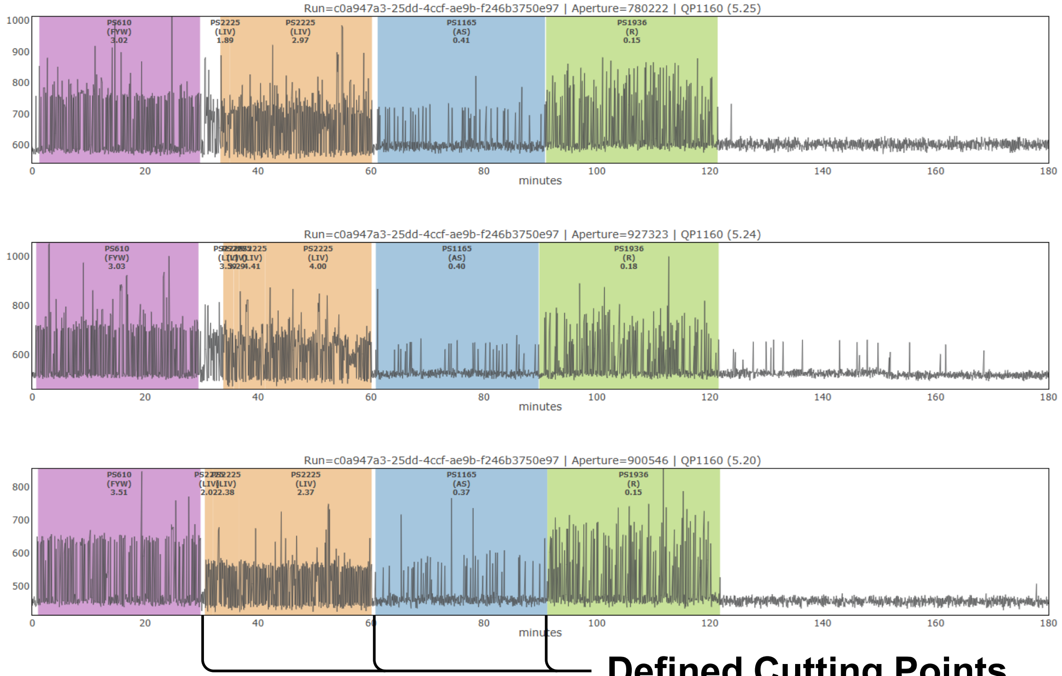
Current Sequencing Chemistry



We Have Successfully Demonstrated a Controlled Cleavage Version of Our Sequencing Chemistry

- **Enables scanning system**
- **Amino acid boundaries are known**
- **Residue duration is controlled and uniform**
- **Time/residue is much faster on average**

Controlled Cleavage Chemistry



Defined Cutting Points

Combining Controlled Cleavage with High-speed Scanning Scales the Architecture to Billions of Reads

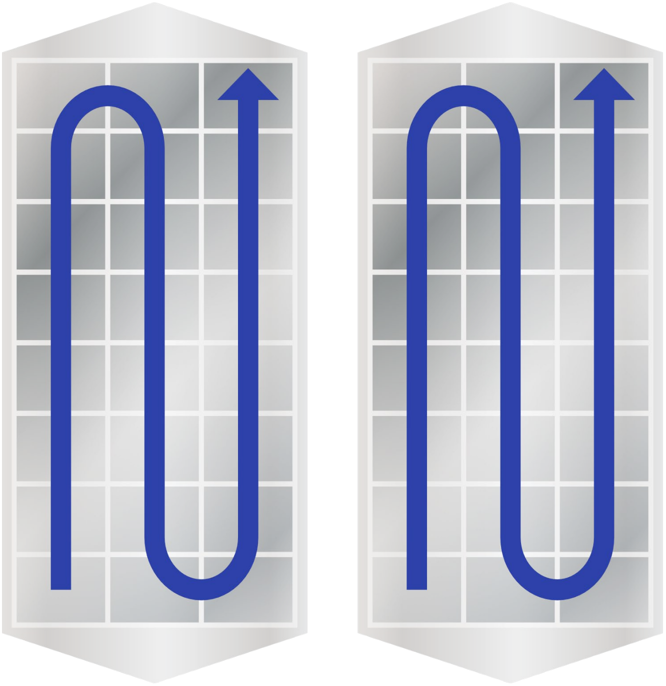
Proteus 2.0 can incorporate high-speed scanning and microfluidic delivery system

Scanning system enables billions of reads

Multiple imaging locations within one flow cell

Efficient usage of device area

Enabled by controlled cleavage chemistry



Multiple imaging regions per flow cell

The Path to Detecting all 20 Amino Acids

John Vieceli, Chief Product Officer
November 19, 2025

Vision

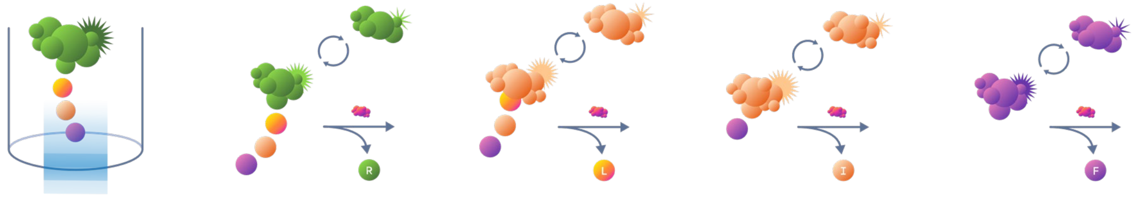
Develop a set of N-terminal amino acid recognizers for twenty canonical amino acids on Proteus™

Recognizer Roadmap

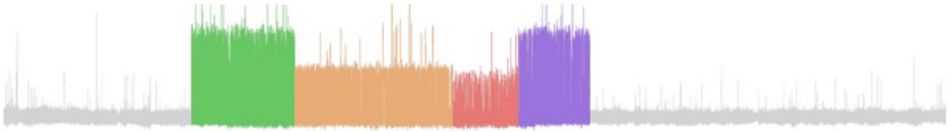
Sequencing Technology Overview

Recognizers bind amino acids in sequence

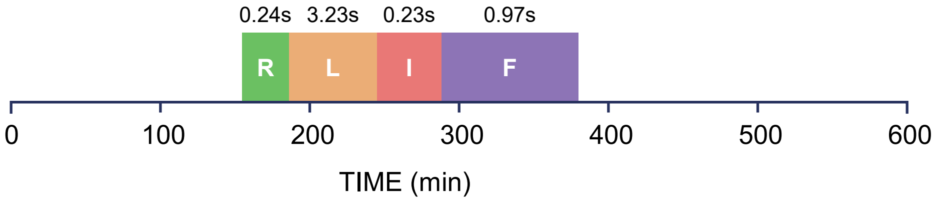
Recognition events produce kinetic signatures



Excitation **'R' Sequenced** **'L' Sequenced** **'I' Sequenced** **'F' Sequenced**



Kinetic signature plot



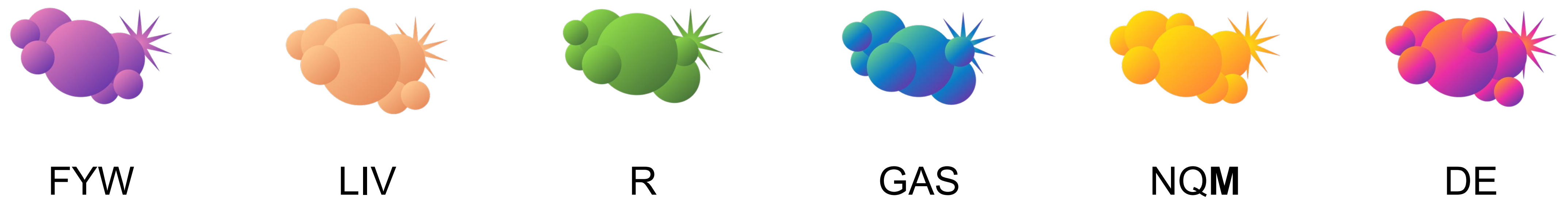
Amino Acid Recognizers in Sequencing Kit V4

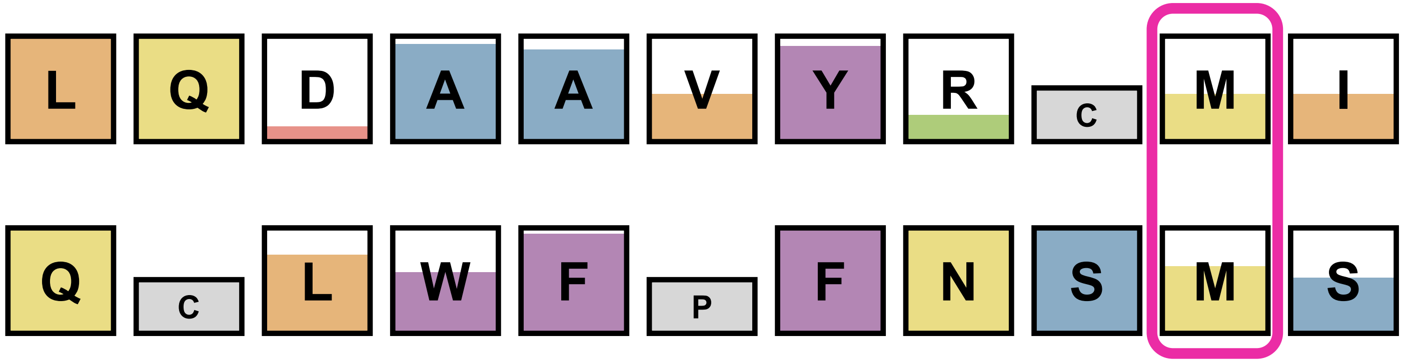
Recognition for 14 of 20 amino acids using 6 recognizers

FYW LIV R GAS NQ DE

Software Improvements Enable More Amino Acids

Q4 software release with Library Prep Kit V3 will increase to 15 amino acids

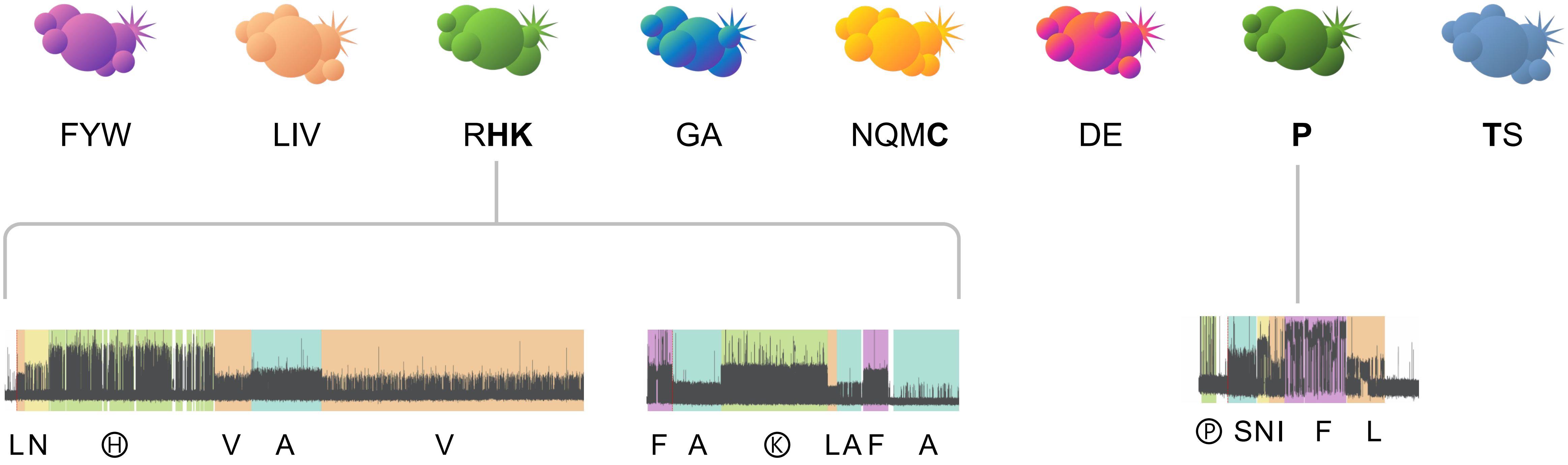




Peptide from **Programmed Death-Ligand 1**	L	Q	D	A	A	V	Y	R	C	M	I
Peptide from **Hepatocyte Growth Factor**	Q	C	L	W	F	P	F	N	S	M	S

Path to 20 Amino Acids with 8 Recognizers

Detection of 18 amino acids demonstrated with campaigns for C and T underway



FYW | LIV | R**HK** | GA | NQM**C** | DE | **P** | **TS**

L N Ⓗ V A V

F A Ⓚ L A F A

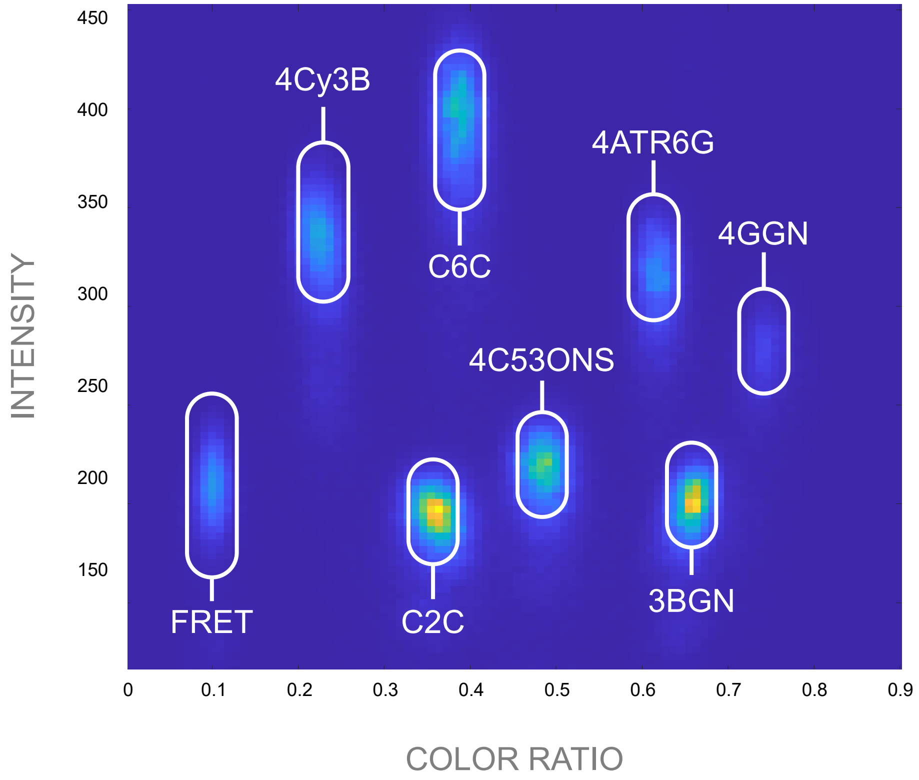
Ⓟ S N I F L

Recognizer Roadmap Supported on Proteus

Intensity and color ratio space supports 8+ dyes

Eight dyes have been demonstrated on Proteus prototype system

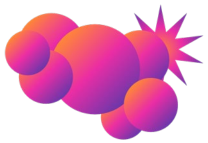
Additional dye space available if necessary



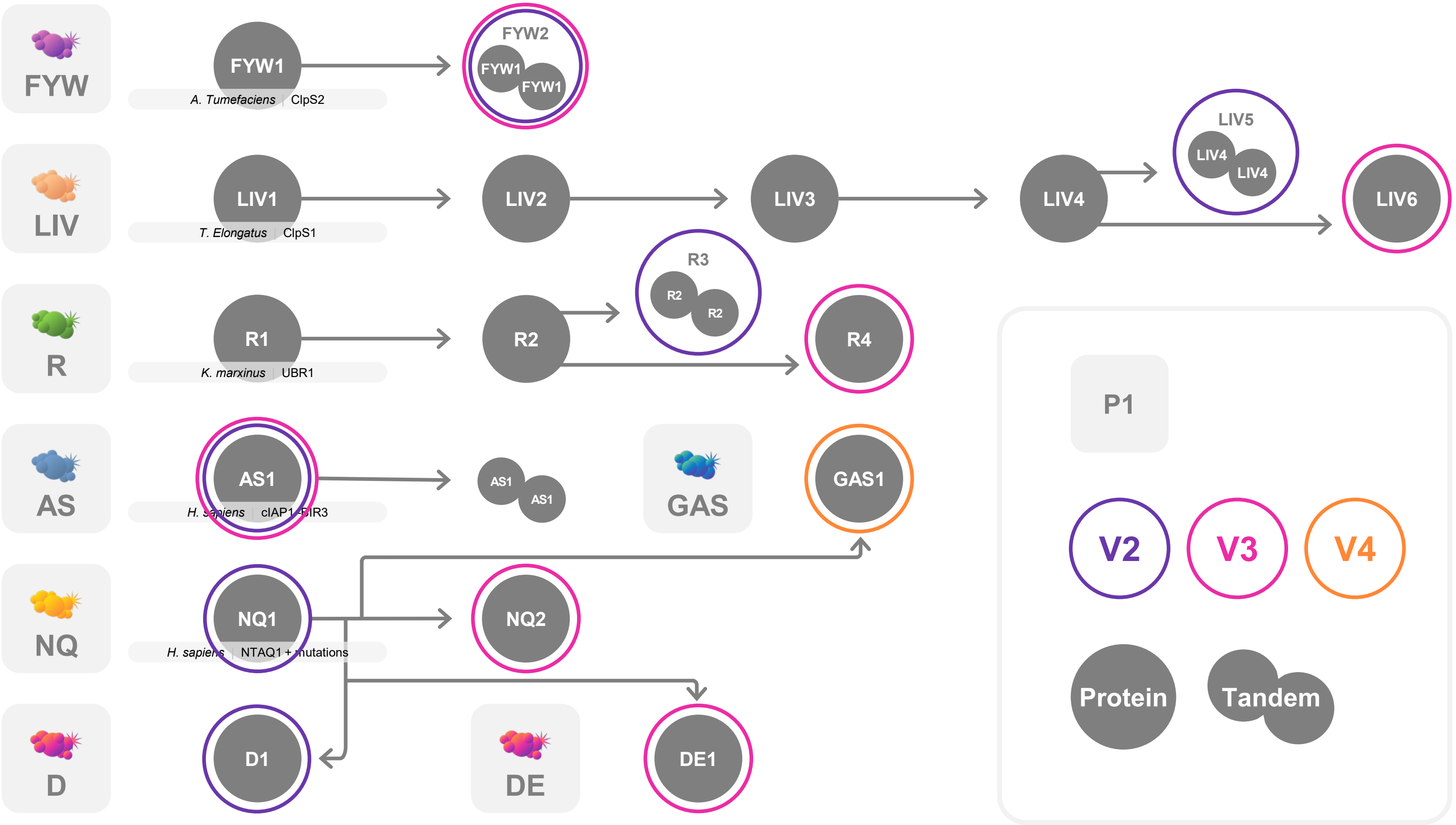
Recognizer Development Pipeline

Recognizer Evolutionary Tree

6 recognizers in Sequencing Kit V4 were derived from 4 starting proteins



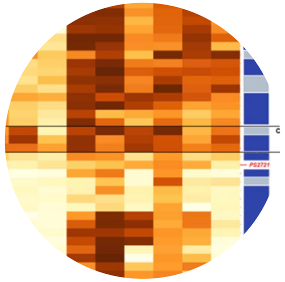
QSI recognizers
protected by 27 granted patents and applications



Quantum-Si N-terminal Amino Acid Recognizer Data

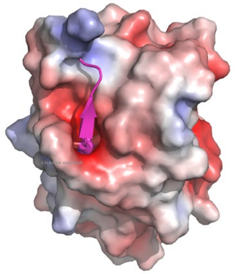
Binding Data

~10^7

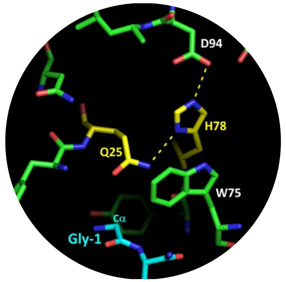


~3,500

Structural Data



~800



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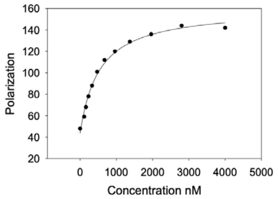
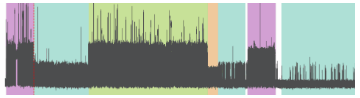
Kinetic Data



~100



~300

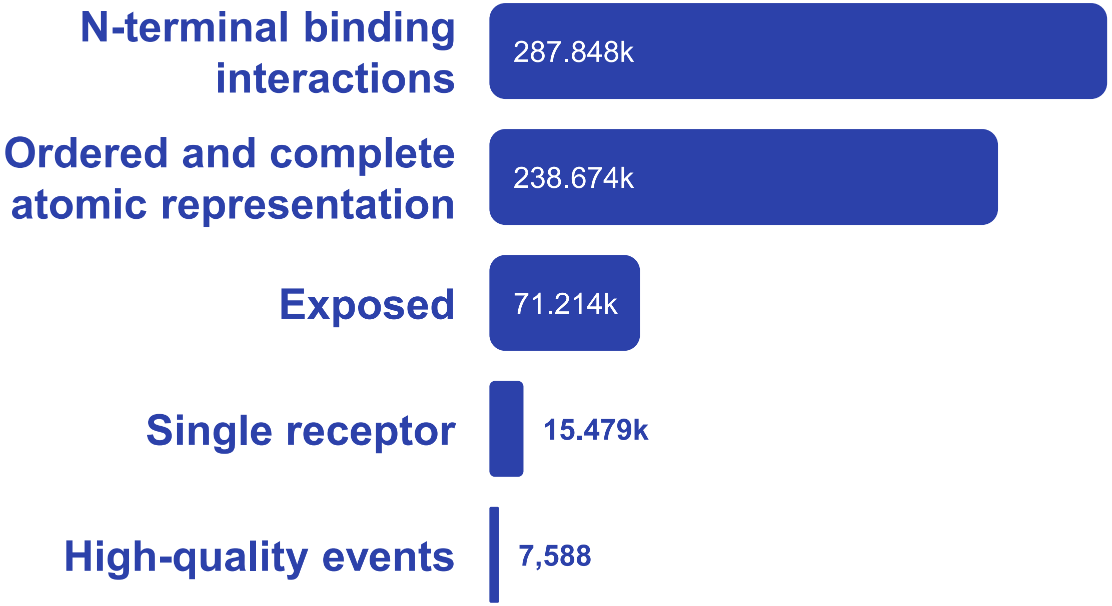
Labeled amino acid sequence data for binding N-terminal amino acids

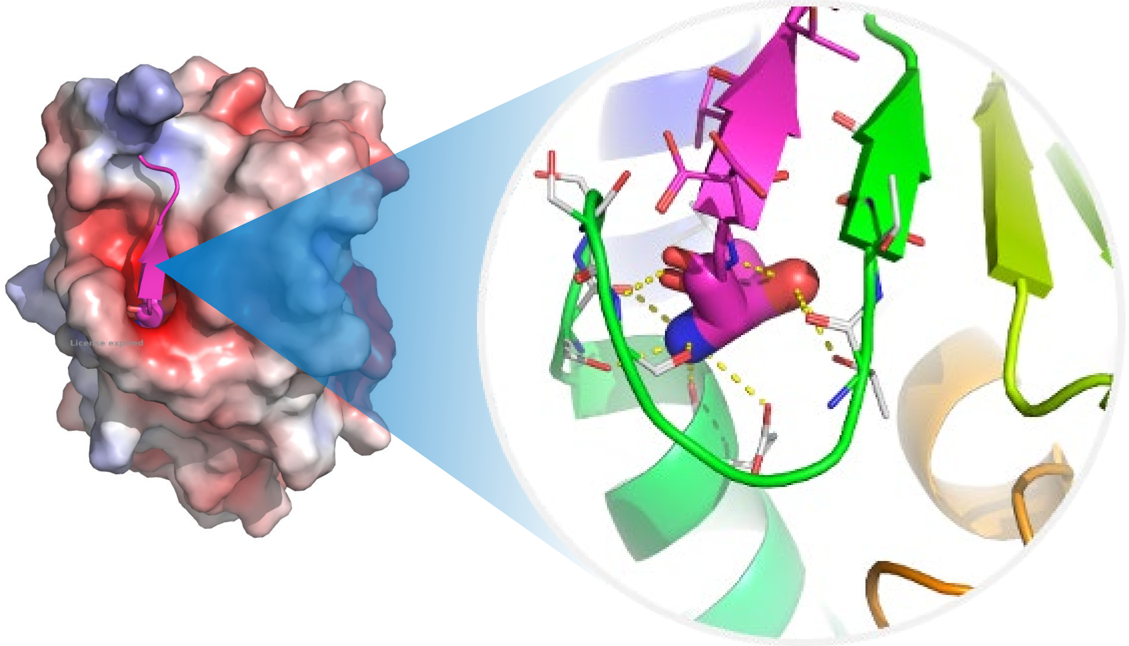
AI model refinement

Predicted N-terminal amino acid binder

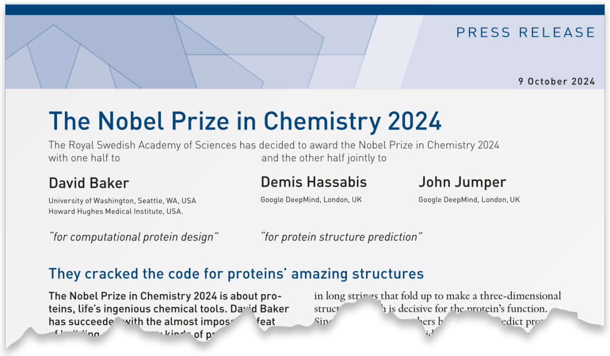
Protein Databank Mining for N-terminal Binders

Used for scaffold generation and model training





AI Model Refinement Enabled By Academia and Industry



PRESS RELEASE

9 October 2024

The Nobel Prize in Chemistry 2024

The Royal Swedish Academy of Sciences has decided to award the Nobel Prize in Chemistry 2024
with one half to

David Baker
University of Washington, Seattle, WA, USA
Howard Hughes Medical Institute, USA.

"for computational protein design"

and the other half jointly to

Demis Hassabis
Google DeepMind, London, UK

John Jumper
Google DeepMind, London, UK

"for protein structure prediction"

They cracked the code for proteins' amazing structures

The Nobel Prize in Chemistry 2024 is about proteins, life's ingenious chemical tools. Da id Baker has succeede with the almost impos feat

in long strings that fold up to make a three-dimensional struc h is decisive for the protein's function.

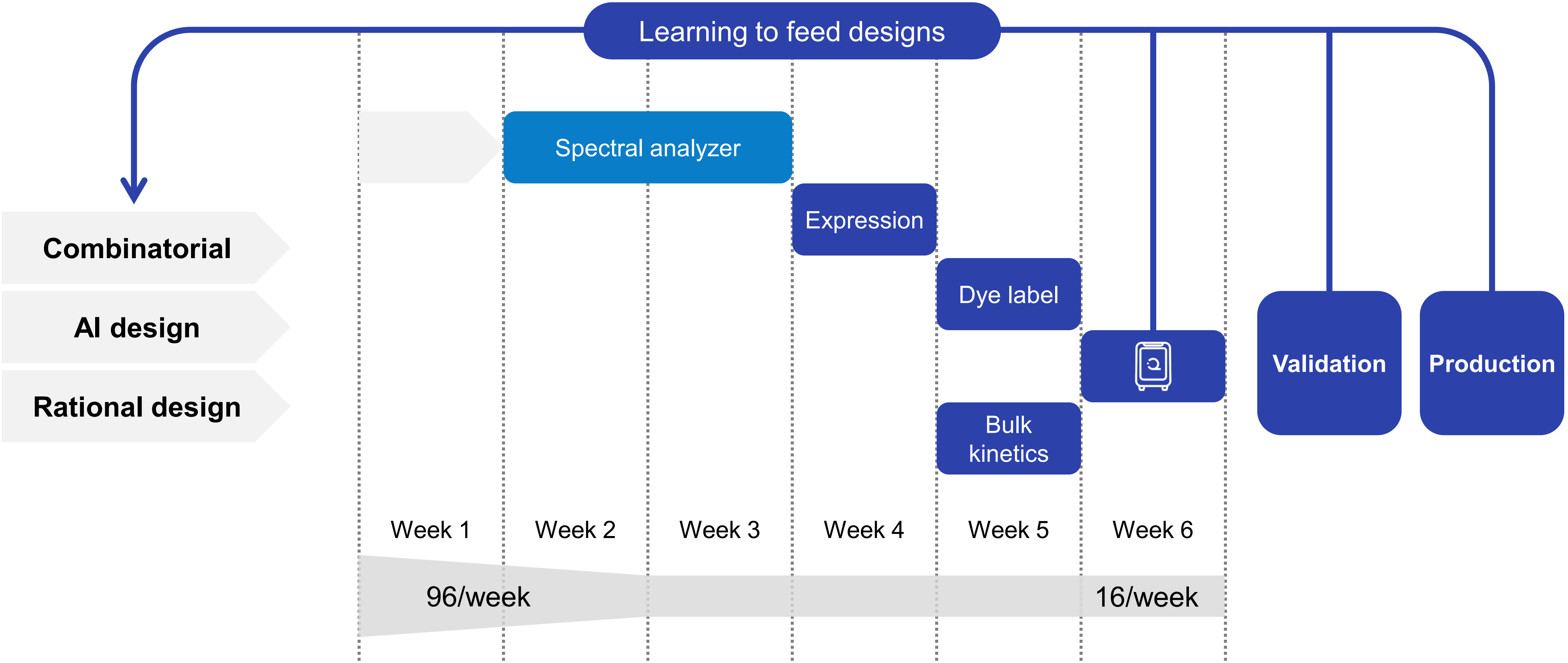
Ligand message-passing neural network

Evolutionary scale modeling

GPU hardware acceleration

4× Scale-up of Recognizer Development Pipeline

Utilize AI, rational, and combinatorial design approaches to generate candidates for screening pipeline



Learning to feed designs

Combinatorial

AI design

Rational design

Spectral analyzer

Expression

Dye label

Bulk kinetics

Validation

Production

Week 1

Week 2

Week 3

Week 4

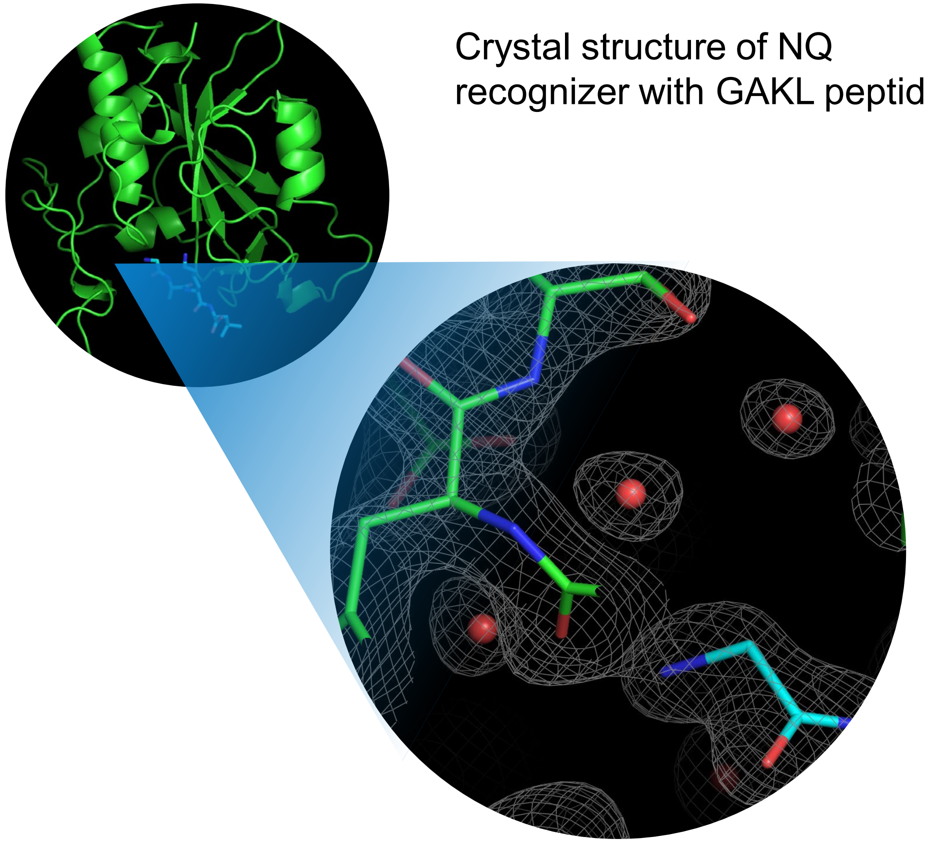
Week 5

Week 6

96/week

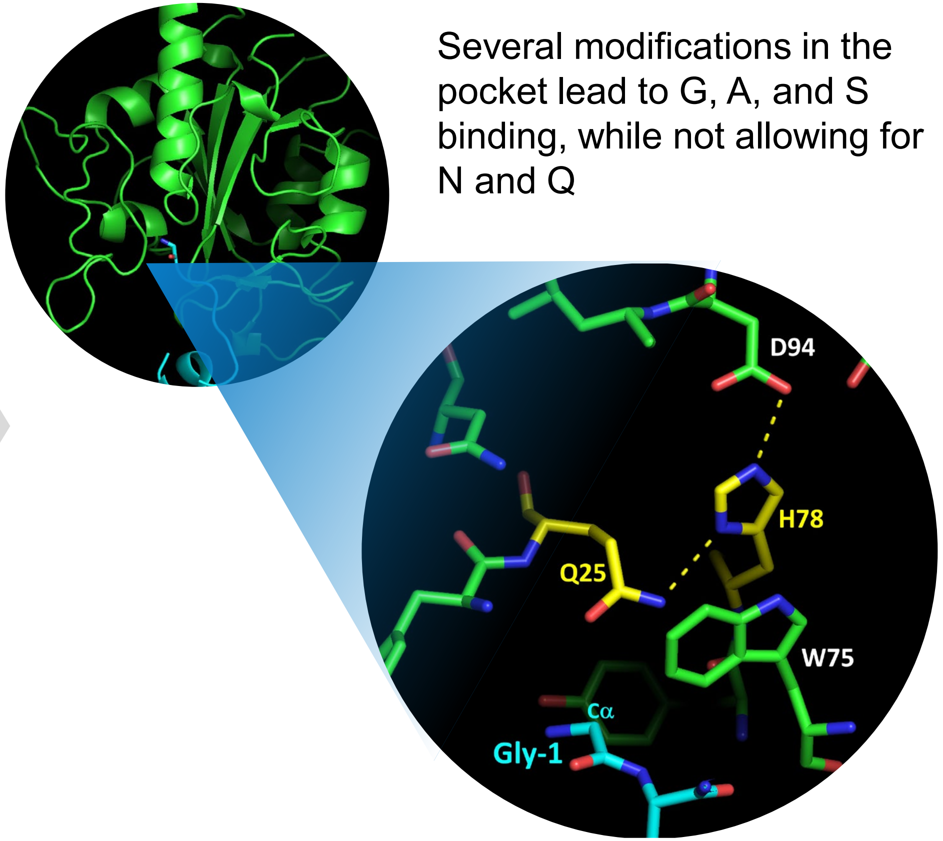
16/week

X-ray Crystallography with Combinatorial and AI Strategies Yielded the GAS Recognizer



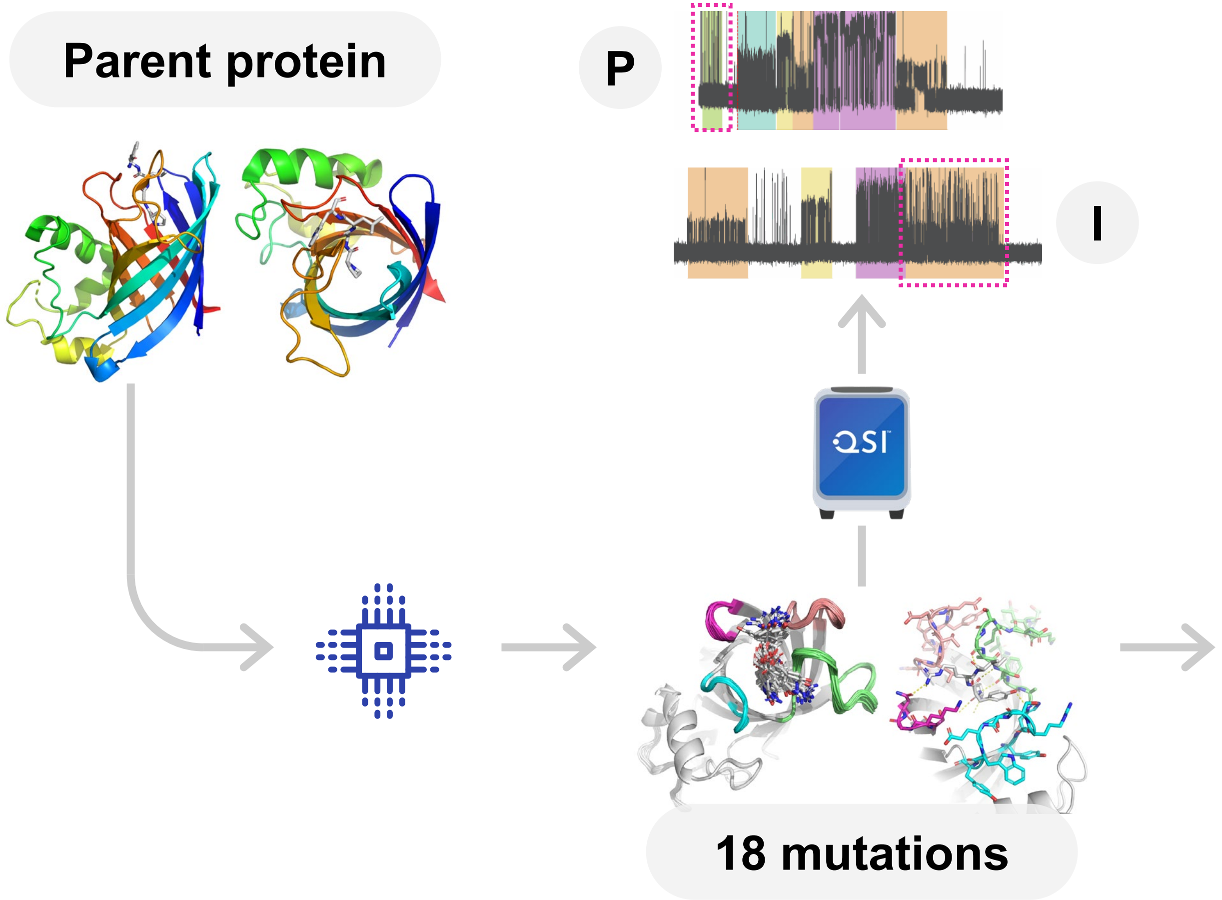
Crystal structure of NQ recognizer with GAKL peptide

Info from combinatorial screening + AI



Several modifications in the pocket lead to G, A, and S binding, while not allowing for N and Q

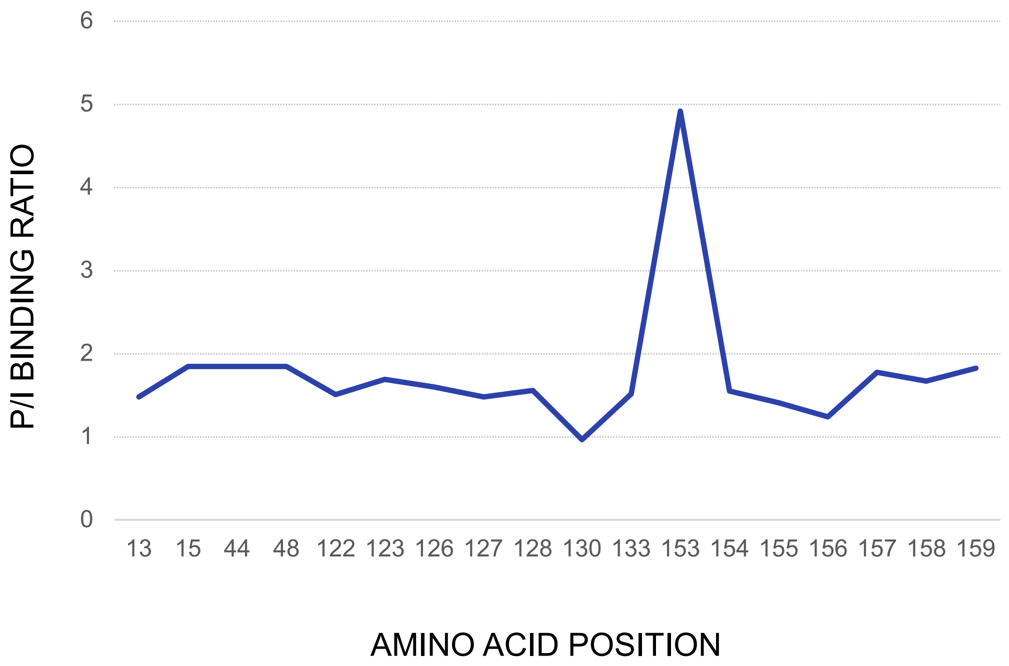
Proline Recognizer from AI and Combinatorial Methods



Parent protein

18 mutations

Single mutant knockouts



Summary of the Path to Twenty Amino Acids

Current recognizer pipeline has candidates to go from 14 amino acids with Sequencing Kit V4 to **18 at Proteus launch in 2026**

Recognizer development program is being scaled **4×** to achieve detection of all canonical amino acids in 2026 and **release on Proteus in 2027**

Efforts in artificial intelligence utilize Quantum-Si screening data to refine deep learning and language models, in conjunction with rational and combinatorial design, to **accelerate the pace of recognizer development**

PTM Analysis Solutions

Brian Reed, PhD

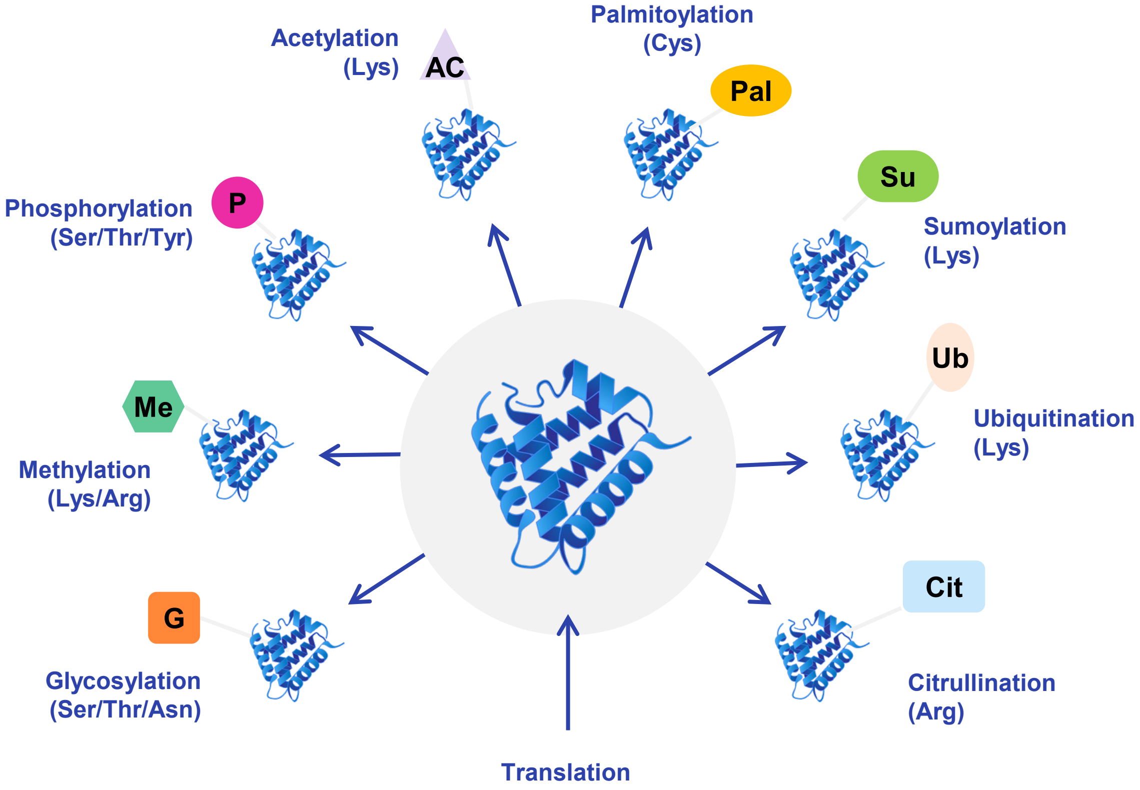
Head of Research

Agenda

PTM Solutions on Proteus

1. **Advantages of single-molecule detection for PTMs**
2. **Broad access to PTMs on Proteus**
3. **PTM applications on the path to Proteus launch**

PTMs and Proteoforms are the Next Frontier in Human Health

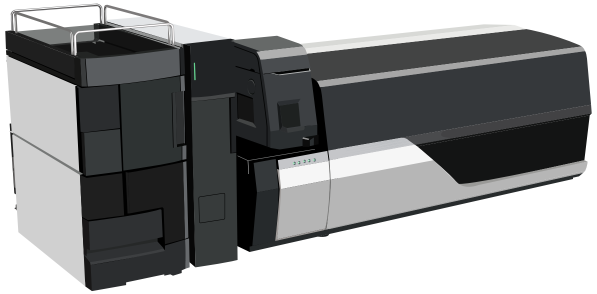


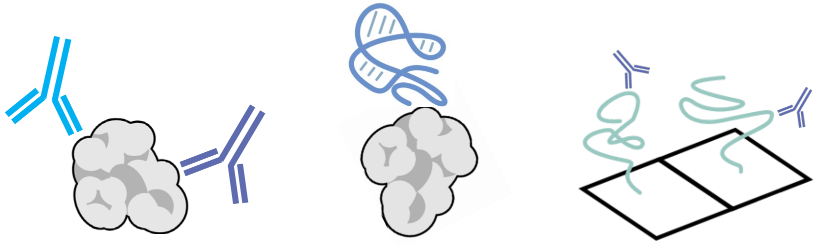
A post-translational modification (PTM) is a chemical change to an amino acid made *after* a protein has been expressed.

There are hundreds of different types of PTMs. A handful are of high interest in the proteomics due to their high abundance and roles in disease pathways. Examples: phosphorylation, glycosylation, ubiquitination.

PTMs determine actual protein function — making them essential for understanding disease mechanisms and therapeutic targets — but have been difficult to study with current proteomics technology.

Challenge to Detecting PTMs With Existing Technologies





Mass spectrometry

- Quantification difficult
- Ambiguity in modification site assignment
- Multi-site combinations extremely challenging
- Workflow and analytical complexity (limits clinical adoption)

Affinity-based platforms

- Detect proteins but provide no proteoform information

OR

- Need costly site-specific affinity reagents for *every* protein

Advantages of Single-molecule Detection for PTMs

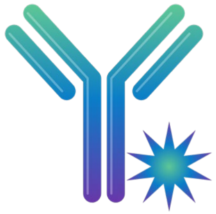
- **Quantitation** straightforward due to direct counting of molecules
- **Direct PTM** site identification
- **Access to multi-site** PTM combinations
- **Simple workflows** for broad PTM proteome coverage; clinical compatibility
- **Universal PTM detection** reagents and assays for ***all*** proteins

Single-molecule Detection Enables Broad PTM Coverage

NGPS unlocks broad and universal access to PTMs with three complimentary approaches | Can be used in combination to address the most challenging needs in PTM detection

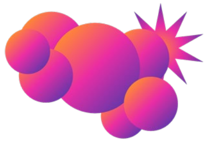
Kinetics

PTM detected via kinetic changes at upstream AAs



Pre-recognition

PTM detected with a PTM binder prior to sequencing



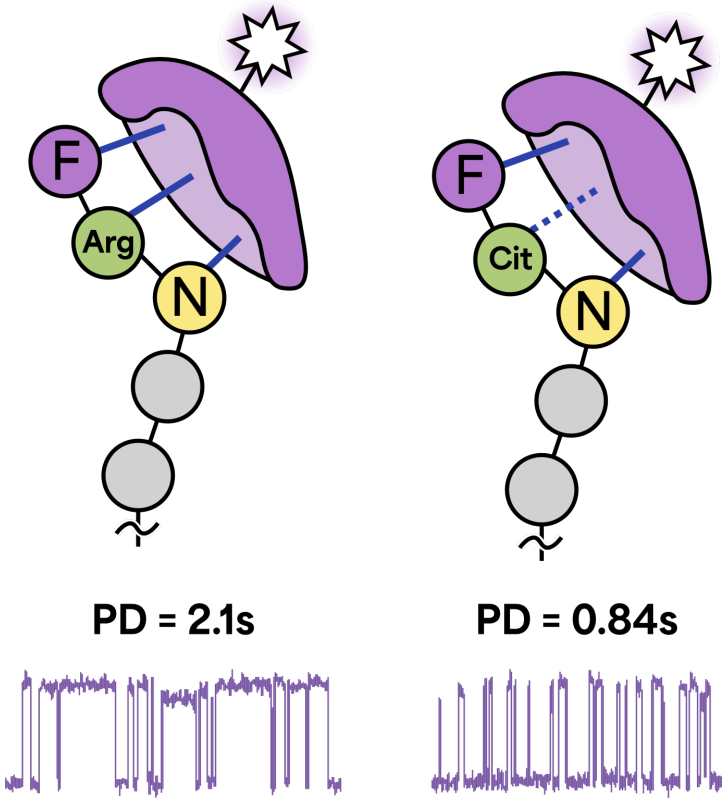
Direct NAA detection

PTM detected with an N-terminal PTM binder during sequencing

Complete AA coverage and deep peptide sequencing will enable very high proteome-wide PTM coverage **on Proteus for all three methods**

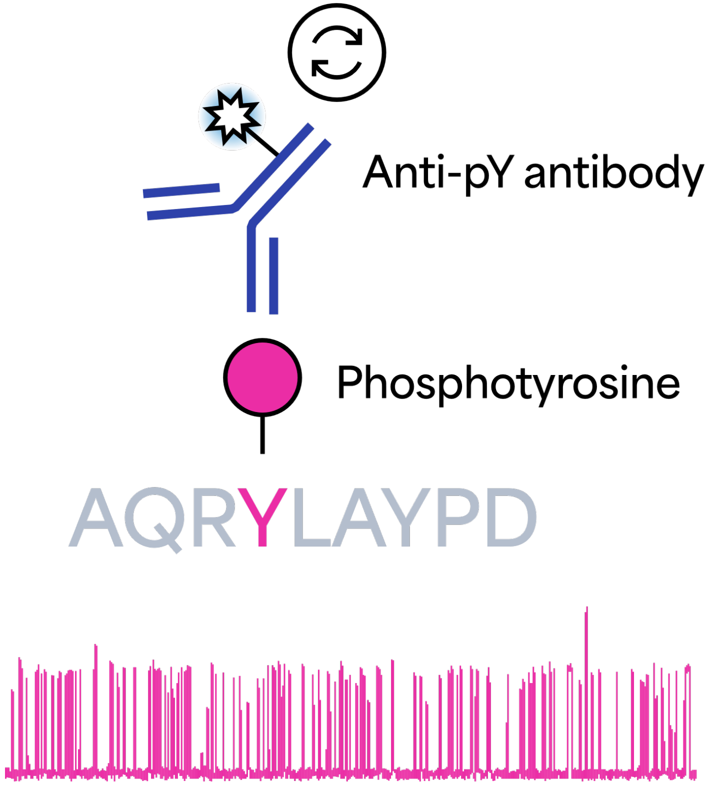
Kinetic Detection of PTMs

- **Kinetic response to PTMs** is a universal feature of NAA recognizers—when the chemical makeup of the peptide changes, the kinetics change. No extra reagents or processing steps needed
- **Examples:** phospho-, methyl-, acetyl-, oxidation, citrullination
- **Customers are using** to dissect complex PTM arrangements that are ambiguous or inaccessible with MS



Pre-recognition of PTMs

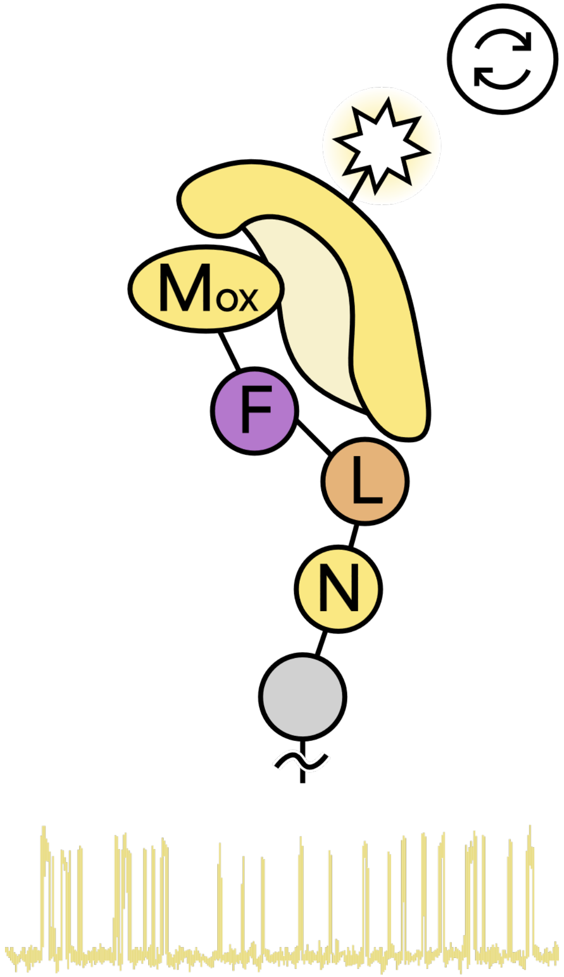
- **PTM detection at any position** regardless of peptide length
- **Parallel detection** of multiple PTMs
- **E.g., Pan-phospho kit:** Comprehensive detection of pS/pT/pY in one assay
- **Extreme sensitivity** to PTM stoichiometry due to the clear pulsing pattern from PTM recognition



Direct N-terminal Detection of PTMs

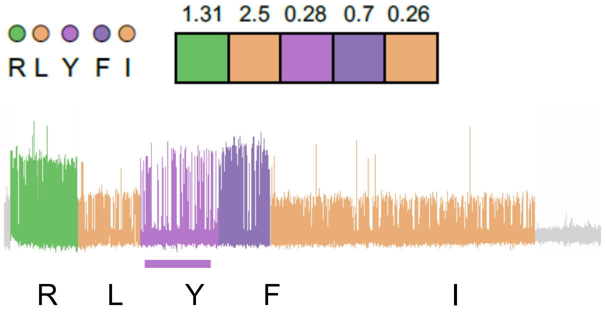
Direct NAA detection

- **N-terminal PTM recognizer** included in sequencing assay
- **Can be standard** NAA recognizer or custom
- **Enables reference-free/*de novo*** PTM discovery
- **Suitable for very complex** sequence contexts and multisite PTM/variant arrangements

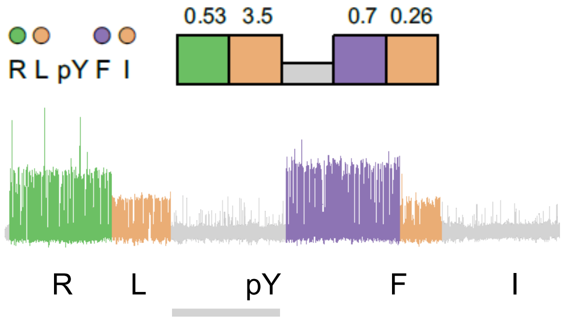


Kinetics: Influence of Downstream pY on NAA Recognizers

Unmodified peptide

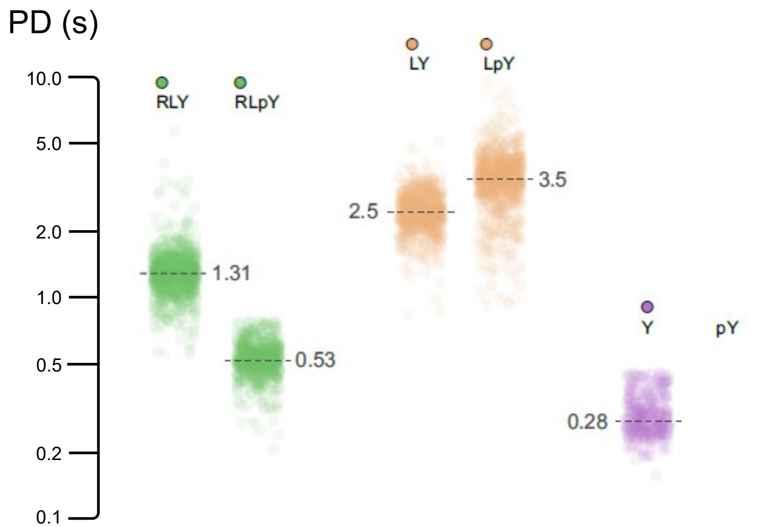


pY modified peptide



How pY influences recognizer kinetics in this peptide

- **R pulse duration** decreases from 1.3 to 0.5 sec.
- **L pulse duration** increases from 2.5 to 3.5 sec.
- **Y** is no longer recognized



Used to detect tropomyosin proteoforms

Journal of proteome research

pubs.acs.org/jpr

Article

Protein Sequencing with Single Amino Acid Resolution Discerns Peptides That Discriminate Tropomyosin Proteoforms

Natchanon Sittipongpittaya,[⊥] Kenneth A. Skinner,[*,⊥] Erin D. Jeffery, Emily F. Watts, and Gloria M. Sheynkman[*]

Cite This: https://doi.org/10.1021/acs.jproteome.4c00978

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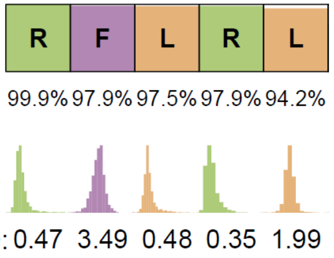
ABSTRACT: Protein variants of the same gene—proteoforms—can have high molecular similarity yet exhibit different biological functions. Thus, the identification of unique peptides that unambiguously map to proteoforms can provide crucial biological insights. In humans, four human tropomyosin (TPM) genes produce similar proteoforms that can be challenging to distinguish with standard proteomics tools. For example, TPM1 and TPM2 share 85% sequence identity with amino acid substitutions that play unique roles in m

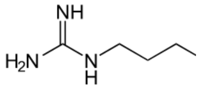
https://pubs.acs.org/doi/pdf/10.1021/acs.jproteome.4c00978

Kinetics: Influence of Citrulline on NAA Recognizers

Arginine citrullination is challenging to detect by mass spec because of the negligible increase in mass (0.984 Da)

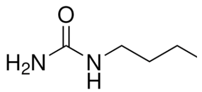
Unmodified peptide



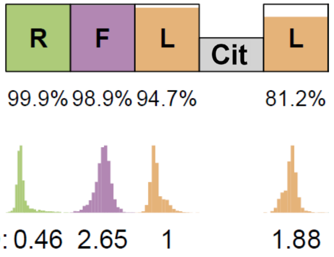


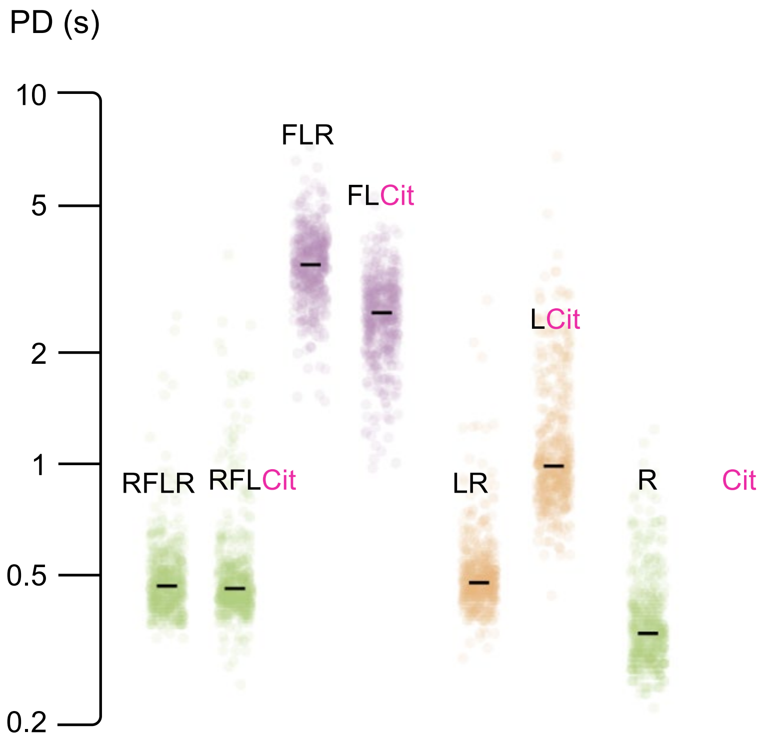
Arginine (R)

Cit-modified peptide



Citrulline (Cit)

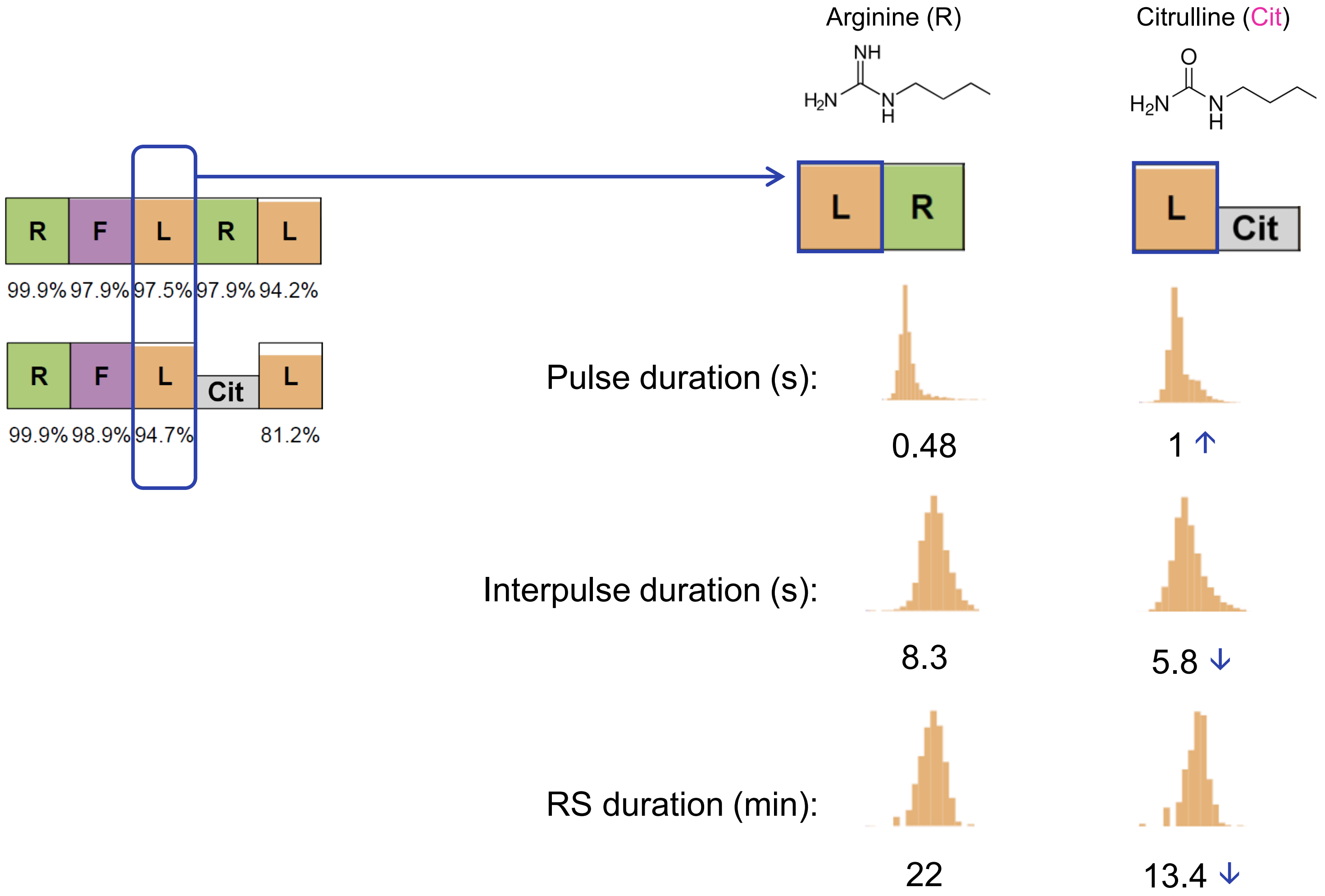




How citrulline influences recognizer kinetics in this peptide

- **F pulse duration** decreases from 3.49 to 2.65 seconds
- **L pulse duration** increases from 0.48 to 1.0 seconds
- **R** is no longer recognized

Kinetics: Multiple Kinetic Parameters Inform PTM Detection



Citrulline and other PTMs influence *multiple* kinetic parameters

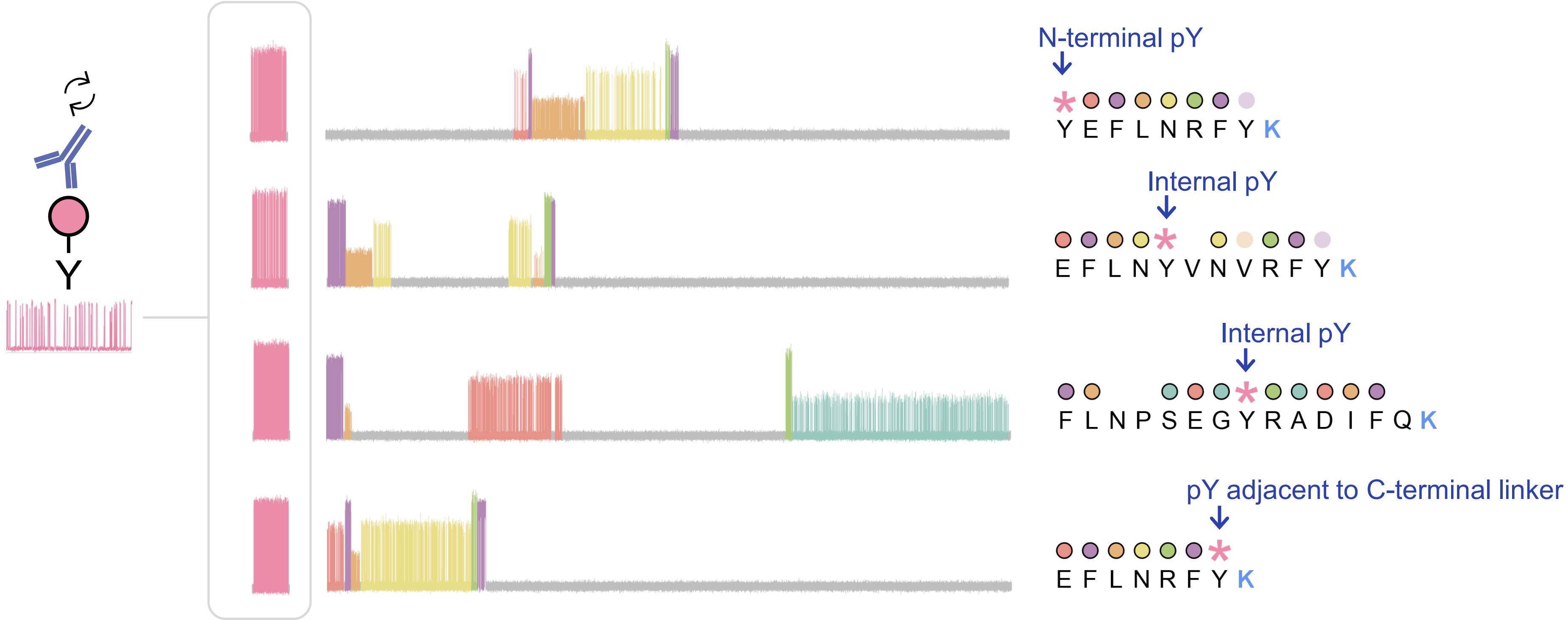
- **Pulse duration:** the lifetime of the recognizer-NAA bound state
- **Interpulse duration:** the time between recognizer binding events
- **Recognition segment (RS) duration:** the time between NAA cleavage events

Pre-recognition: pY Detection at *Any* Peptide Location

An anti-phosphotyrosine antibody detects phosphotyrosine at any peptide location — N-terminal, internal, and C-terminal linker adjacent — independent of sequence context

pY recognition

Sequencing



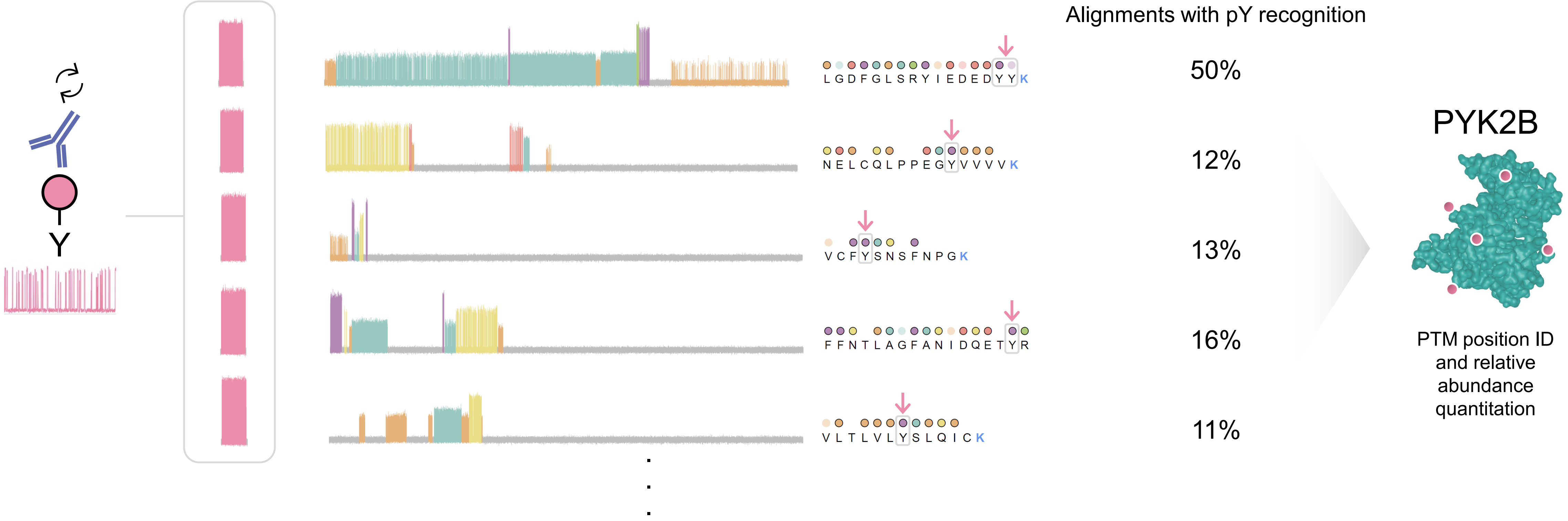
Pre-recognition: Carna Biosciences Kinase Panel

Phosphorylation is a key determinant of activity for protein kinases used in drug discovery applications | Pre-recognition identifies phosphotyrosine in protein-tyrosine kinase 2-beta (PYK2B) and other important kinases

pY recognition

Sequencing

Analysis



	Alignments with pY recognition
LGDFGLSRYIEDEDYYK	50%
NELCQLPPEGYVVVVK	12%
VCFYSNSFNPGK	13%
FFNTLAGFANIDQETYR	16%
VLTLVLYSLQICK	11%

PTM position ID and relative abundance quantitation

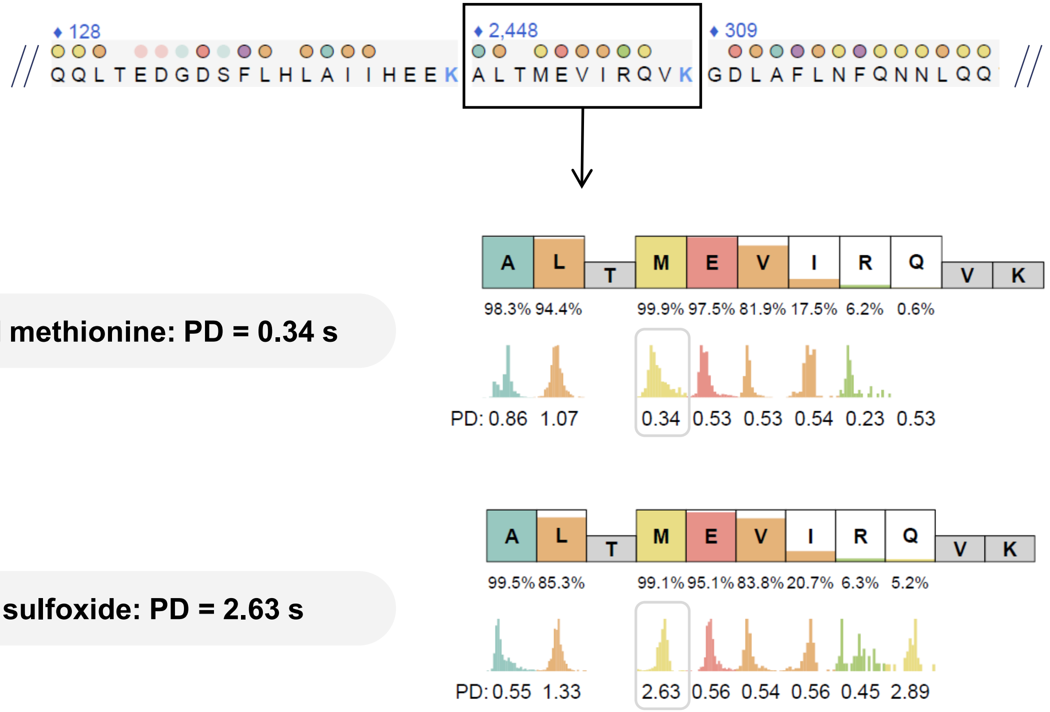
Direct NAA Detection: Methionine Oxidation

The NQM recognizer directly detects N-terminal methionine sulfoxide at position Met91 in IKBA

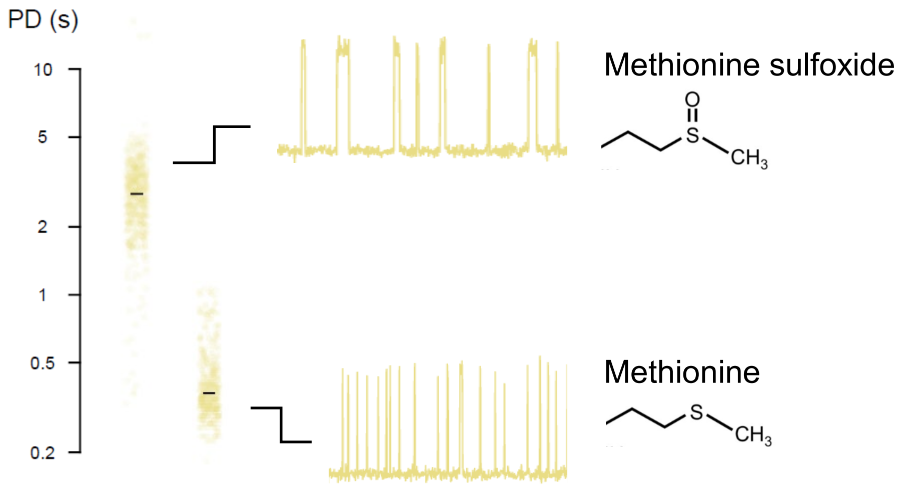
NF-kappa-B inhibitor alpha (IKBA)

Unmodified methionine: PD = 0.34 s

Methionine sulfoxide: PD = 2.63 s



Pulse duration distinguishes the modified and unmodified forms of methionine



We Have a Clear Path to Broad PTM Coverage on Proteus

Recognizer development

Recognizers for all 20 amino acids will ensure maximum protein coverage and kinetic information available for PTM detection with all three methods

Higher output on Proteus

Enables deeper and more sensitive PTM detection and multiplexed panel-based solutions

Artificial intelligence

For data analysis to fully extract the massive volume of kinetic information in our NGPS output for PTM and variant detection and quantitation

PTM access with three methods

Three complimentary approaches that can be used in combination ensure access to the broadest range of PTMs anywhere in the proteome

The Road to Proteus Launch

From Platinum to Proteus — Market Learnings Inform Proteus Requirements and Commercial Strategy

General technology first;
defined applications second

Sample prep-agnostic

Broad marketing to all segments at launch

Defined applications first;
general technology second

***Sample-to-report* workflows** for high-value applications

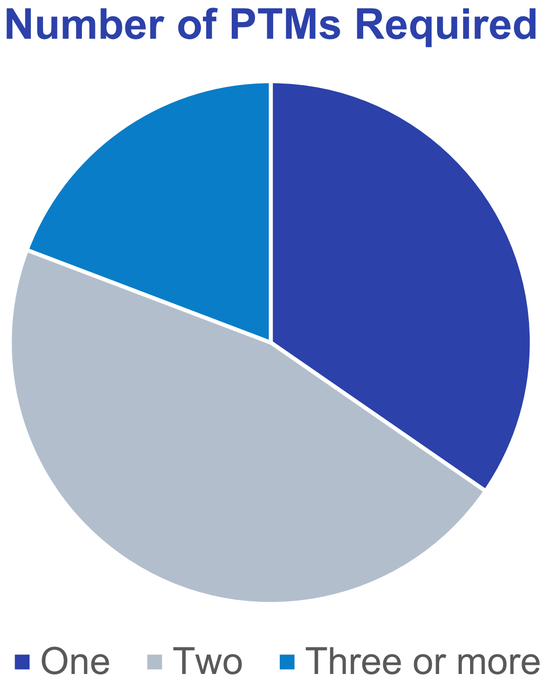
Focused launch — achieve application depth in target segment(s)

Amino acid coverage ▲ **Reliability ▲** **Sample input ▼**

Sequencing output ▲ **Consumable COGs ▼**

The Customer Data is Clear

Researchers need a breadth of capabilities to answer their biological questions

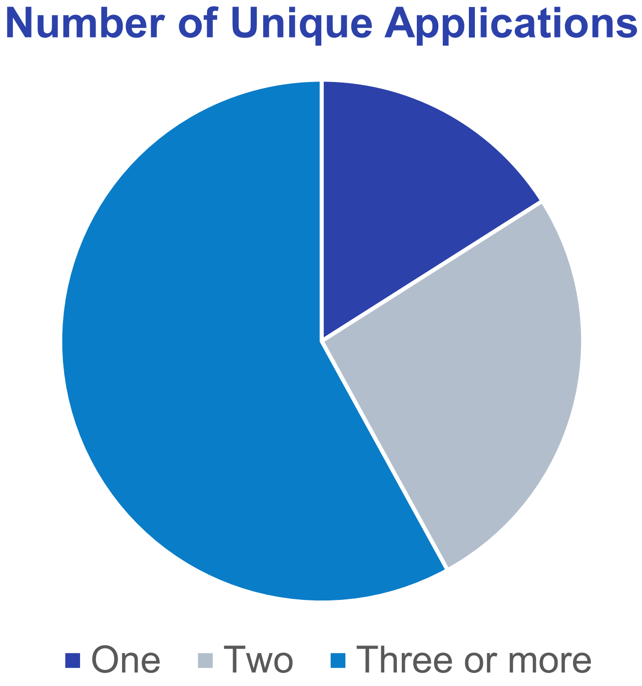


PLATINUM PIONEER GRANT PROGRAM

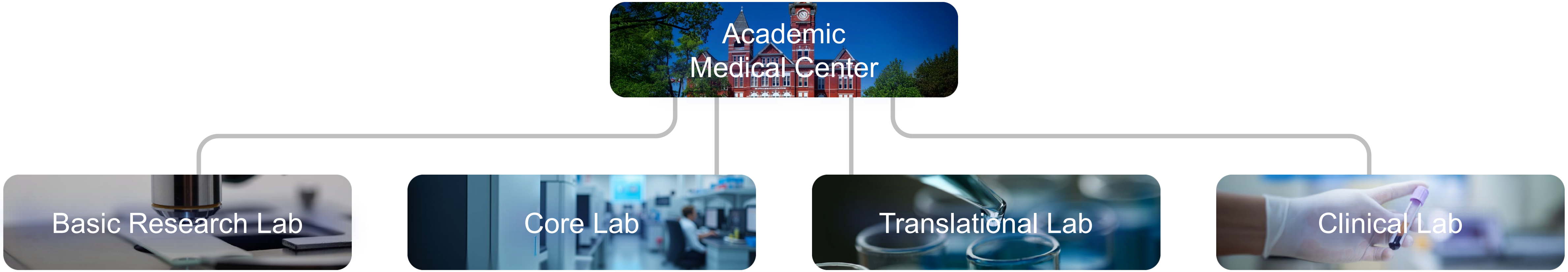
More than 50 detailed study proposals submitted by prospective customers

>50% require three or more types of protein analysis applications

Detection of two or more PTMs is required in >65% of cases



A Look Inside an Academic Medical Center



Academic Medical Center

Basic Research Lab

- Wide range of application interests
- Limited infrastructure
- Lower utilization

Core Lab

- Many technologies in use in one lab
- Significant infrastructure
- High utilization potential

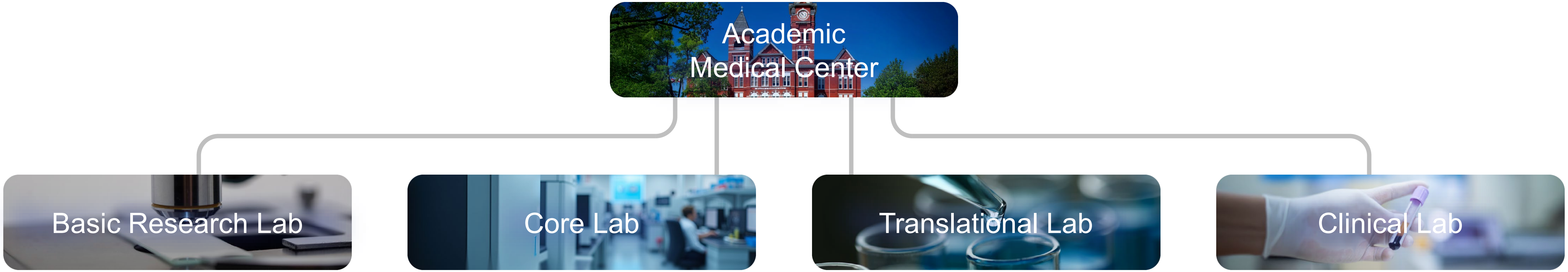
Translational Lab

- Targeted applications; many involve PTMs
- Value automation
- High utilization potential

Clinical Lab

- Defined application content; *sample-to-report* workflows
- Automation is key
- High utilization potential given repeat sample testing

Platinum Case Study — The Academic Medical Center



Academic Medical Center

- Basic Research Lab
- Core Lab
- Translational Lab
- Clinical Lab

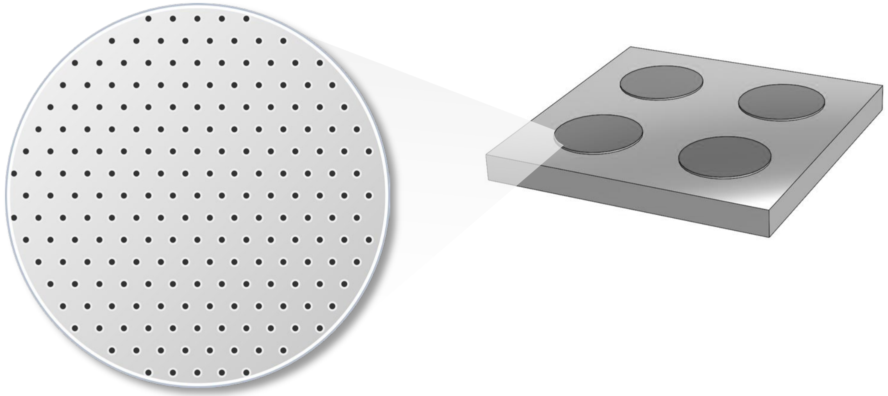
Basic Research Lab	Core Lab	Translational Lab	Clinical Lab
Good value prop but most users are low-utilization	Limited to reflex testing downstream of mass spec	Adoption limited by current technology capabilities	Not accessible with Platinum Pro

The Increased Sequencing Output and Lower Costs of the Nanowell Array is Broadly Enabling

More samples per run with 40× the output per consumable compared to Platinum Pro

Deep analysis of a single sample to address complex mixtures or rare events like variants or PTMs

Multiplexing samples to achieve higher throughput and lower costs per sample for cost sensitive applications like protein ID



Accelerating the Core Sequencing Technology and Analytics to Unlock the Highest-value Applications

Robust PTM detection and multi-PTM profiling

Sequencing of variable regions of antibodies

Single-amino acid variant detection

Biothreat detection and surveillance

Proteus Automation Greatly Simplifies the Sequencing Workflow and Makes New Lab Startup Even Easier

Over 30 individual reagent tubes
to handle to process four samples

Over 100 pipetting steps per sample

A single reagent module per run
— simply unbox and load

Pipette your sample(s) into
the cartridge and hit *Run*

Building a Partner Ecosystem to Accelerate Application Development + Deliver *Sample-to-report* Workflows

Application Development

Sample Prep + Enrichment

Applications of AI for Data Analysis

New Industry Partnerships in PTMs and Ultra-low-abundance Protein Panels

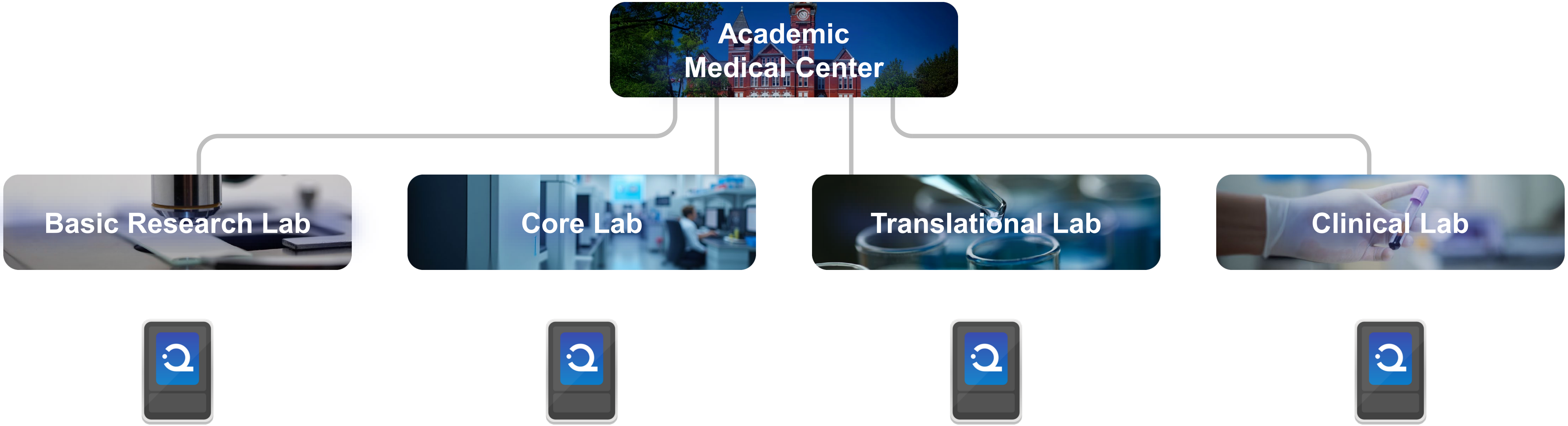
CARNA BIOSCIENCES

- Carna Biosciences is a leading provider of assay-grade kinase proteins to biopharma for drug discovery and profiling
- Carna Biosciences is evaluating the use of QSI technology to assess and validate phosphorylation profiles of kinases
- Collaboration presents the potential to leverage the complementary strengths and global reach of both organizations

SIENA • QUANT™

- Siena Quant™ is a SISCAPA Holdings Company — experts in the field of sample enrichment for proteomics
- Siena Quant is enabling the quantitation of ultra-low-abundance biomarkers that have been historically unreliable to measure
- QSI and Siena Quant will collaborate to develop sample-to-report workflows for customers to accurately measure clinically relevant biomarker panels

Proteus Will Increase the Depth of Penetration in Academic Medical Centers Compared to Platinum



Academic Medical Center

Basic Research Lab

Core Lab

Translational Lab

Clinical Lab

Single-molecule protein sequencing will remain a useful tool for basic research

High-value application capabilities + increased throughput = first-line platform

Expanded PTM capabilities + high-value targeted panels + automation

Automation + sample-to-report workflows opens this lab for Proteus

Proteus Will Enable Single-molecule Protein Sequencing Across a Broad Range of End Markets

Agriculture

Industrial

Pharma + Biotech

Academic Research

Defense

Clinical Diagnostics

Translational Research

Milestones on the Path to Proteus Launch in 2026

Sequencing on Proteus **prototype**

Fully integrated systems **delivered and operational** (Q1)

End-to-end sequencing on fully integrated systems (Q2)

External customer collaborations initiated (summer 2026)

Internal V&V (Q4)

Launch (Q4)

4Q25 | 1Q26 | 2Q26 | 3Q26 | 4Q26

Instrument list price released (Q2)

Platinum upgrade program released (Q3)

Proteus launch capabilities released (Q3)

Demonstration of 20 amino acid detection (Q4)

QUANTUM SI

QSI is Well-positioned to Build Upon Our First-to-market Advantage and Extend Our Leadership into the Future

Grow user base with Platinum Pro and develop the market for Proteus launch

Execute on development roadmap to deliver a compelling Proteus launch

Build a partner ecosystem to accelerate application development + deliver *sample-to-report* workflows

Extend our technology lead through best-in-class R&D innovation + execution