



NAUTILUSTM
BIOTECHNOLOGY

**Delivering on the Promise
of the Proteome**

OCTOBER 29, 2024

Safe harbor

This presentation and the accompanying oral presentation contain forward-looking statements within the meaning of the Private Securities Litigation Reform Act of 1995, including, among others, statements regarding the size and growth of the protein analysis market; Nautilus Biotechnology's anticipated total addressable market; the performance, value and enabling nature of Nautilus Biotechnology's proteomics and proteoform analysis technology platform; statements regarding Nautilus Biotechnology's future development milestones and timing; statements regarding the timing and nature of Nautilus Biotechnology's potential engagements with partners in proteoform analysis; Nautilus Biotechnology's business and operational strategy and financial targets; Nautilus Biotechnology's prospective products; Nautilus Biotechnology's business development plans and opportunities; Nautilus Biotechnology's anticipated customer mix and collaborations plans; and objectives of management for future operations are forward looking statements. Forward-looking statements are neither historical facts nor assurances of future performance. Instead, they are based on our current expectations and projections about future events and financial trends that we believe may affect our financial condition, results of operations, business strategy, and financial needs. All statements other than statements of historical facts contained in this presentation, including, without limitation, statements regarding our future performance and our market opportunity, could be deemed forward-looking statements. The words "may," "will," "expect," "anticipate," "aim," "estimate," "intend," "plan," "believe," "is/are likely to," "potential," "continue" and other similar expressions are intended to identify forward-looking statements, although not all forward-looking statements contain these identifying words.

Forward-looking statements are subject to numerous risks and uncertainties that could cause actual results to differ materially from currently anticipated results, including but not limited to risks relating to the development and commercialization of our Nautilus platform; macroeconomic conditions; regional conflicts; Nautilus Biotechnology's dependence on certain sole and single source suppliers; competition; market acceptance of Nautilus Biotechnology's current and potential products; Nautilus Biotechnology's ability to manage the growth and complexity of its organization; Nautilus Biotechnology's ability to maintain, protect and enhance its intellectual property; and Nautilus Biotechnology's ability to continue to stay in compliance with its material contractual obligations, applicable laws and regulations. Information on these and additional risks and uncertainties and other information affecting Nautilus Biotechnology's business and operating results is contained in Nautilus Biotechnology's Annual Report for the year ending December 31, 2023, filed February 28, 2024, and in its other filings with the Securities and Exchange Commission. These forward-looking statements speak only as of the date hereof. Except as required by applicable law, Nautilus Biotechnology does not plan to publicly update or revise any forward-looking statements contained herein, whether as a result of any new information, future events, changed circumstances or otherwise. No representations or warranties (expressed or implied) are made about the accuracy of any such forward-looking statements.

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Nautilus seeks to revolutionize biomedicine

Single-molecule
proteome analysis
platform



with integrated machine
learning designed to
enable unprecedented
sensitivity and scale

Potential to unlock
a massive market



\$55+ Billion
opportunity across
proteomics and
adjacent markets
by 2027
(Source: BCC Research)

Research
collaborations



Genentech
A Member of the Roche Group

AMGEN

THE UNIVERSITY OF TEXAS
MDAnderson
Cancer Center

tgen 
part of City of Hope

Defining a new gold standard for single-molecule protein analysis

Proteins are key drivers of biology

nature COMMUNICATIONS

ARTICLE <https://doi.org/10.1038/s41467-021-28124-0> OPEN [Check for updates](#)

Proteomic analysis of archival breast cancer clinical specimens identifies biological subtypes with distinct survival outcomes

Karama Asleh^{1,2,9}, Gian Luca Negri^{1,3,9}, Sandra E. Spencer Miko¹, Shane Colborne³, Christopher S. Hughes⁴, Xiu Q. Wang¹, Dongxia Gao¹, C. Blake Gilks^{5,6}, Stephen K. L. Chia⁷, Torsten O. Nielsen^{1,5} & Gregg B. Morin^{1,3,9*}

nature neuroscience RESOURCE <https://doi.org/10.1038/s41593-021-00999-y> [Check for updates](#)

OPEN

Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level

Erik C. B. Johnson^{1,2,16,52}, E. Kathleen Carter^{1,2,16}, Eric B. Dammer^{1,3,16}, Duc M. Duong^{1,3}, Ekaterina S. Gerasimov^{1,2}, Yue Liu⁴, Jiaqi Liu⁴, Ranjita Betarbet^{1,2}, Lingyan Ping^{1,2,3}, Luming Yin¹, Geidy E. Serrano⁵, Thomas G. Beach¹, Junmin Peng^{1,6,7}, Philip L. De Jager^{1,8}, Vahram Haroutunian^{1,9,10}, Bin Zhang¹¹, Chris Gaiteri¹², David A. Bennett¹³, Marla Gearing^{1,2,13}, Thomas S. Wingo^{1,2,4}, Aliza P. Wingo^{1,3,4,5}, James J. Lah^{1,5}, Allan I. Levey^{1,2,5} and Nicholas T. Seyfried^{1,2,3,52}

CellPress OPEN ACCESS **Cell**

Resource

Proteogenomic analysis of chemo-refractory high-grade serous ovarian cancer

Shrabanti Chowdhury,^{1,2} Jacob J. Kennedy,^{3,4} Richard G. Ivey,^{5,6} Oscar D. Murillo,^{1,2,6} Noshad Hosseini,^{1,2,6} Xiaoyu Song,^{1,2,7} Francesca Petralia,^{1,2,7} Anna Calinawan,^{1,2,7} Sara R. Savage,^{1,2,7} Anna B. Berry,¹ Boris Reva,¹ Ulmut Ozbek,¹ Azra Krek,¹ Weiping Ma,¹ Felipe da Veiga Lopevost,¹ Jiayi Ji,¹ Seungyeul Yoo,¹ Chenwei Lin,¹ Uliana J. Voytovich,¹ Yajuo Huang,¹ Sun-Hoe Lee,¹ Lindsay Bergan,¹ Travis D. Lorenzen,¹ Mehdi Mesri,^{1,8} Henry Rodriguez,^{1,9} Andrew N. Hootmagie,¹⁰ Zachary T. Herbert,¹¹ Alexey I. Nesvizhskii,¹² Bing Zhang.¹³

nature Article | Published: 24 January 2022

Clonally expanded B cells in multiple sclerosis bind EBV EBNA1 and GlialCAM

Tobias V. Lanz, R. Camille Brewer, Peggy P. Ho, Jae-Seung Moon, Kevin M. Jude, Daniel Fernandez, Ricardo A. Fernandes, Alejandro M. Gomez, Gabriel-Stefan Nadi, Christopher M. Bartley, Ryan D. Schubert, Isabel A. Hawes, Sara E. Vazquez, Manasi Iyer, J. Bradley Zuchero, Bianca Teegen, Jeffrey E. Dunn, Christopher B. Lock, Lucas B. Kipp, Victoria C. Cotham, Beatriz M. Ueberheide, Blake T. Aftab, Mark S. Anderson, Joseph L. DeRisi, ... William H. Robinson [✉](#) [+ Show authors](#)

Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities **Cell**

Sahas Vasakar,^{1,2,14} Chen Huang,^{1,2,14} Xiaojing Wang,^{1,2,14,15} Vladislav A. Petyuk,^{1,14} Sara R. Savage,^{1,14} Bo Wen,^{1,2} Yongchao Dou,^{1,2} Yun Zhang,¹ Zhaio Shi,^{1,2} Osama A. Anshad,¹ Marina A. Gritsenko,¹ Lisa J. Zimmerman,¹ Jason E. McDermott,¹ Theresa R. Clauss,¹ Ronald J. Moore,¹ Rui Zhao,¹ Matthew E. Monroe,¹ Yi-Ting Wang,¹ Matthew C. Chambers,¹ Robbert J.C. Slebos,¹ Ken S. Lau,¹ Qianxing Mo,^{1,12} Li Ding,¹ Matthew Ellis,^{1,7} Mathang Theagarajan,¹ Christopher R. Kinsinger,¹⁰ Henry Rodriguez,¹⁰ Richard D. Smith,¹ Karin D. Rodland,^{1,11,16*} Daniel C. Leubler,^{1,14} Tao Liu,^{1,15} Bing Zhang,^{1,2,7,16,17} and Clinical Proteomic Tumor Analysis Consortium

nature neuroscience Resource | Published: 08 July 2021

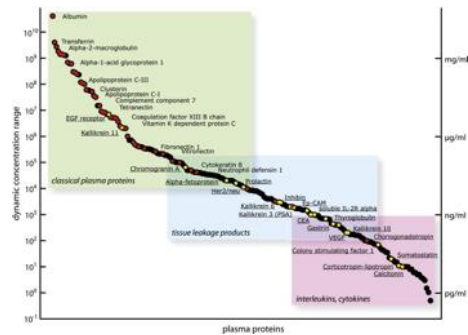
Genomic atlas of the proteome from brain, CSF and plasma prioritizes proteins implicated in neurological disorders

[Chengran Yang](#), [Fabiana H. G. Farias](#), [Laura Ibanez](#), [Adam Suhy](#), [Brooke Sadler](#), [Maria Victoria Fernandez](#), [Fengxian Wang](#), [Joseph L. Bradley](#), [Brett Eiffert](#), [Jorge A. Bahena](#), [John P. Budde](#), [Zeran Li](#), [Umber Dube](#), [Yun Ju Sung](#), [Kathie A. Mihindukulasuriya](#), [John C. Morris](#), [Anne M. Fagan](#), [Richard J. Perrin](#), [Bruno A. Benitez](#), [Herve Rhinn](#), [Oscar Harari](#) & [Carlos Cruchaga](#) [✉](#)

Interrogating the proteome is challenging

Proteins span a **wide dynamic range**

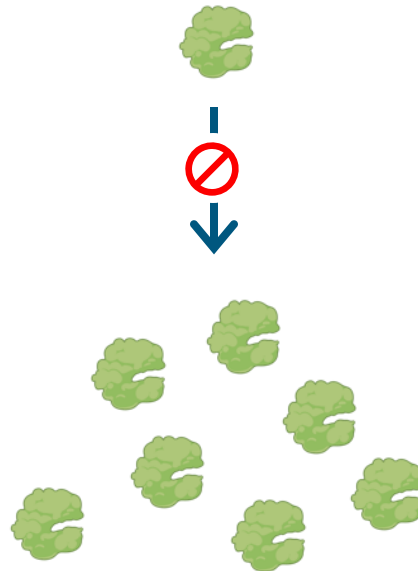
From single-digit numbers of molecules to millions of copies per cell (or drop of blood)



Anderson, N. L. *Molecular & Cellular Proteomics* 1, 845–867 (2002).

There is **no PCR** for proteins

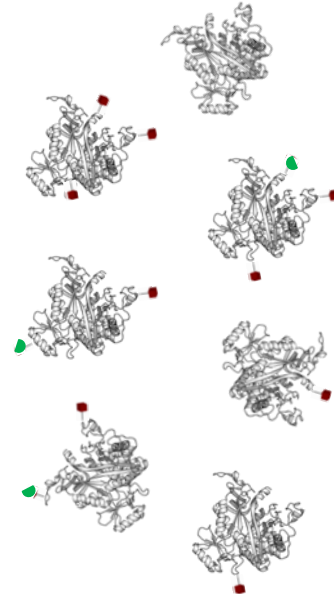
Amplification isn't possible



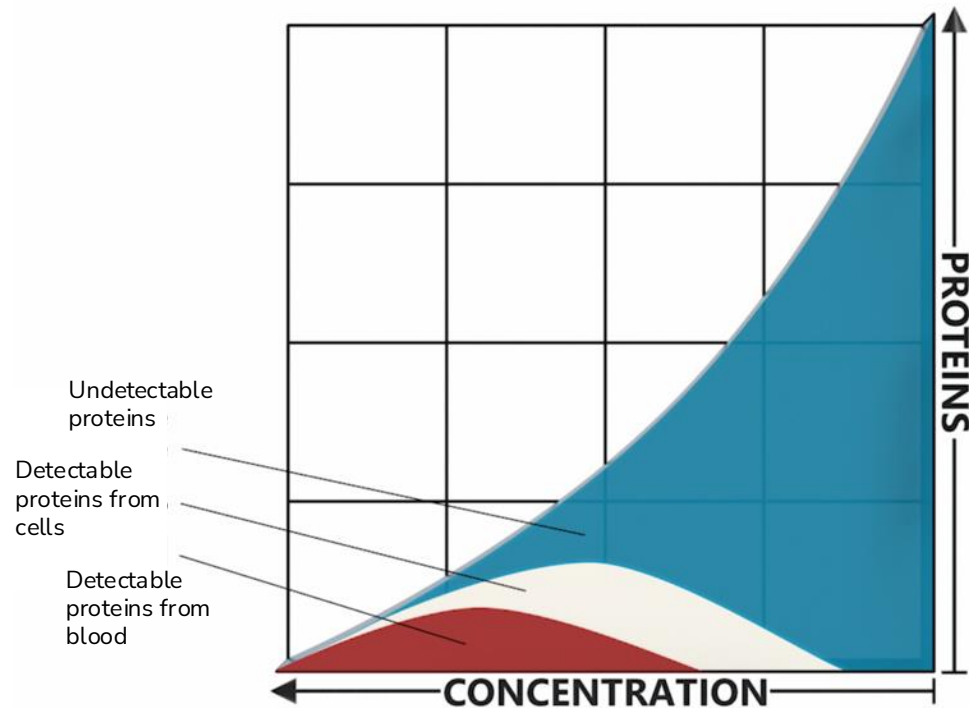
Proteins are biophysically **extremely diverse**



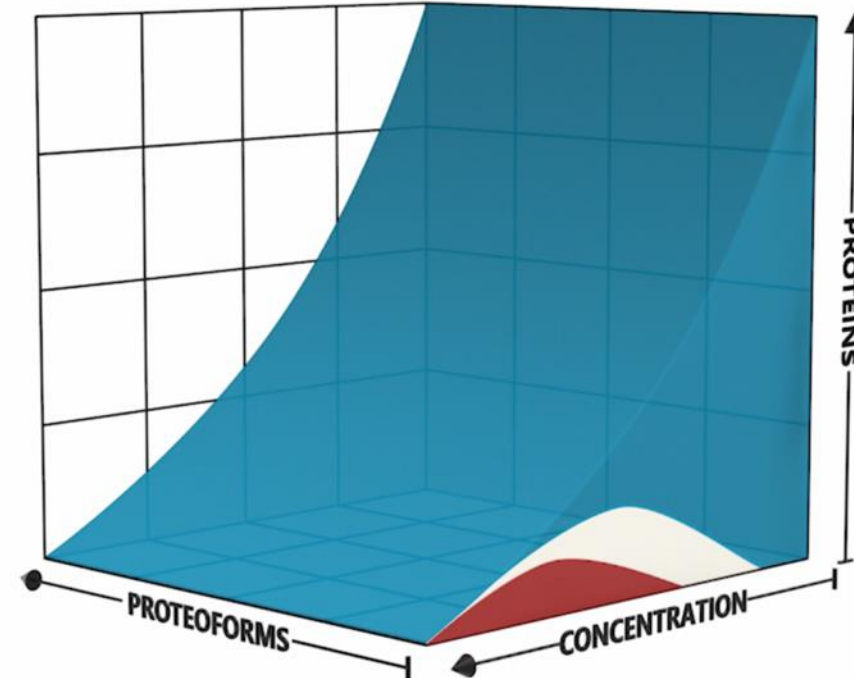
Proteins exist in a **range of modified states (proteoforms)**



Current analysis methods **can't see** most proteins and proteoforms



Mass spec solutions today only capture **a fraction of the proteome** from blood or cells



There is no solution today to **measure and quantify intact proteoforms**

Nautilus is reinventing proteomics from the ground up

What is necessary to **identify** and **quantify** the proteome and proteoforms?

Comprehensive → Measure substantively all the proteins and proteoforms in a sample

Sensitive → Single-molecule detection

Wide dynamic range → Match the scale of the proteome

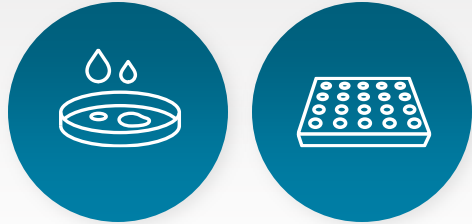
Reproducible and robust → Path to clinical translation of discoveries

Rapid run time → Process a large number of samples

Easy to use → Any lab can run it

Core platform components

Sample Preparation & Single-Molecule Protein Deposition



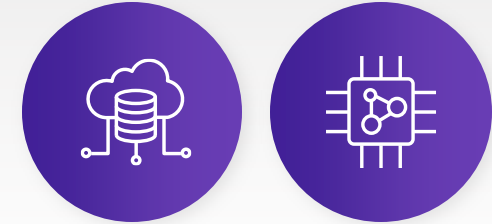
HYPER-DENSE SINGLE MOLECULE ARRAY

Instrumentation and Reagents for Iterative Affinity Reagent Hybridization and Imaging



DIGITAL PROTEOMIC DATA

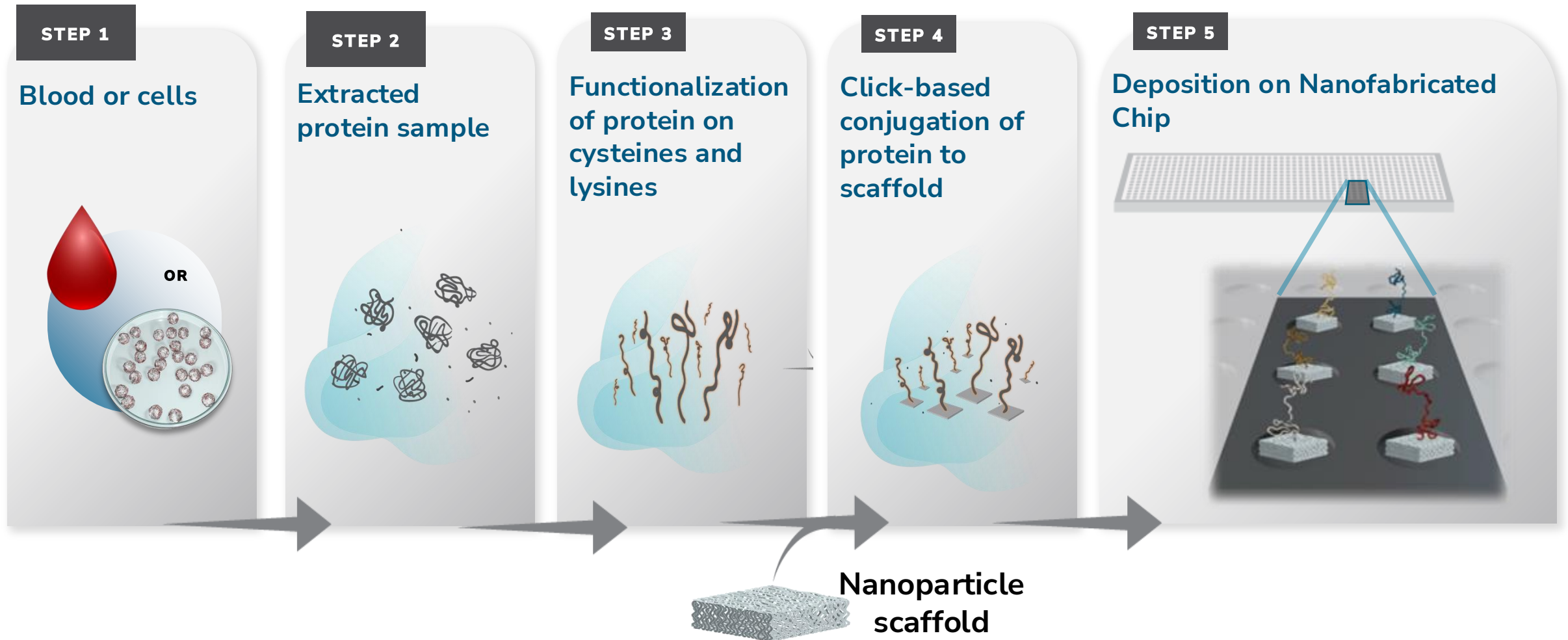
Machine Learning-Based Analysis



PROTEIN DECODING ANALYTICS

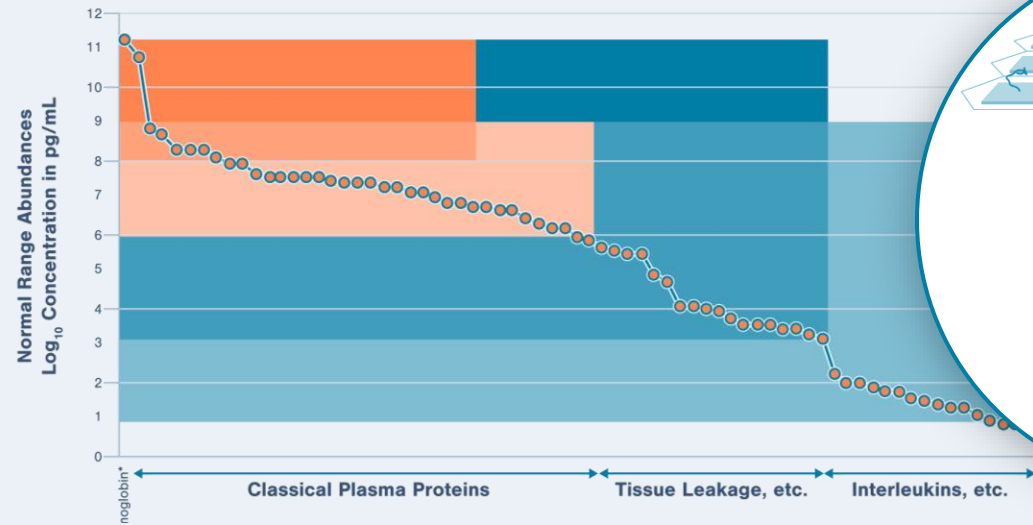
Simple and robust sample preparation workflow

Arraying single protein molecules onto a hyper-dense chip



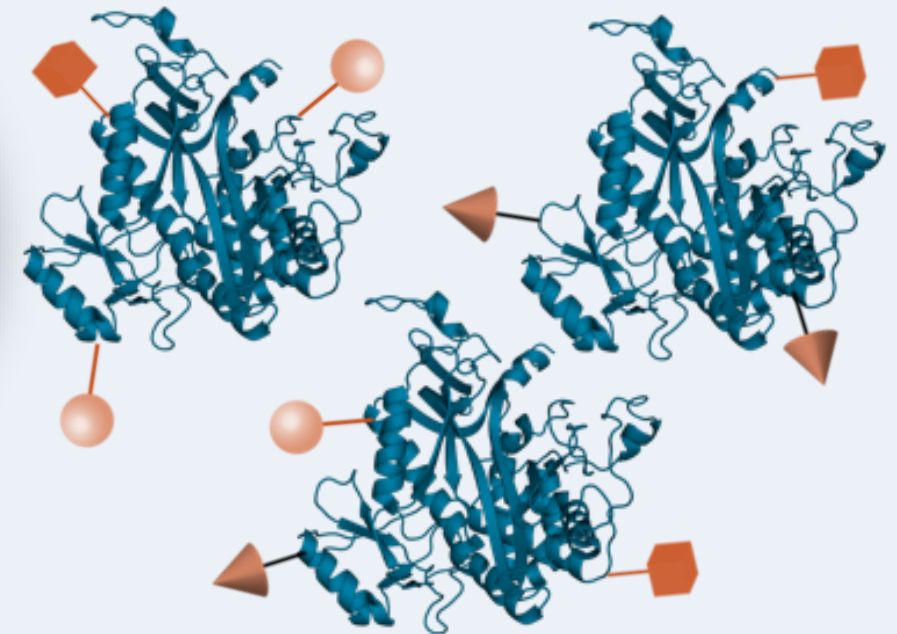
Multiple applications from the same core platform

Broadscale Proteome coverage with wide dynamic range



Protein Identification by Short-epitope Mapping:
Nautilus proprietary reagents designed for comprehensive proteome analysis

Targeted Proteoform High resolution for targets of interest



Off-the-shelf reagents validated for targeted proteoform analysis

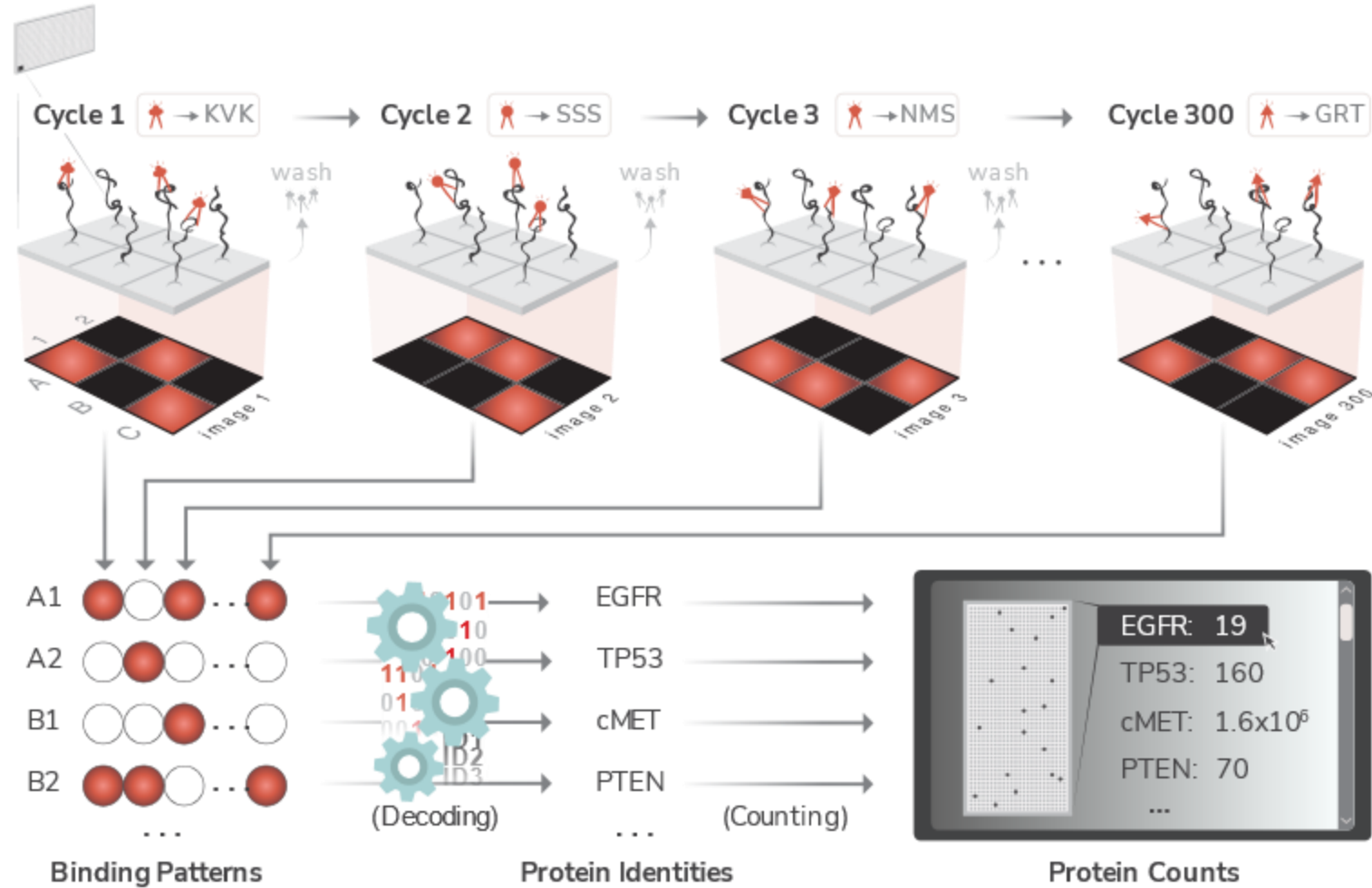
Integration of breakthrough innovations across the platform

Designed to allow access to full resolution digital proteomic data for Broadscale Proteome Analysis

2
Sequential
Affinity Reagent
Hybridization
& Imaging

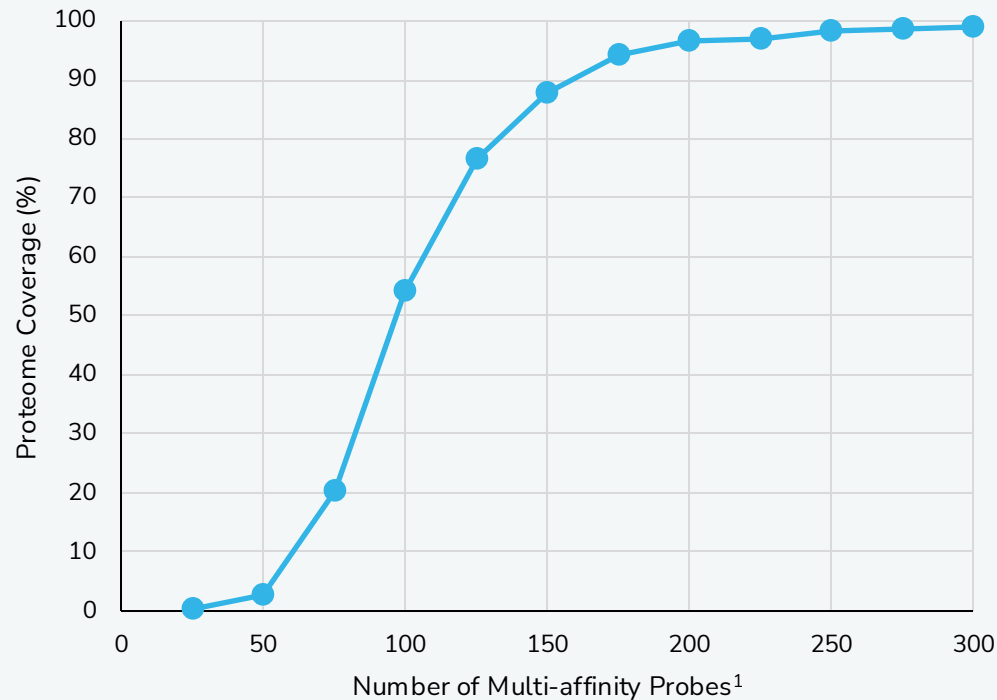


3
Data
Processing



Designed to **comprehensively quantify** the proteome

Human Proteome Coverage Across 300 Unique Multi-affinity Probes

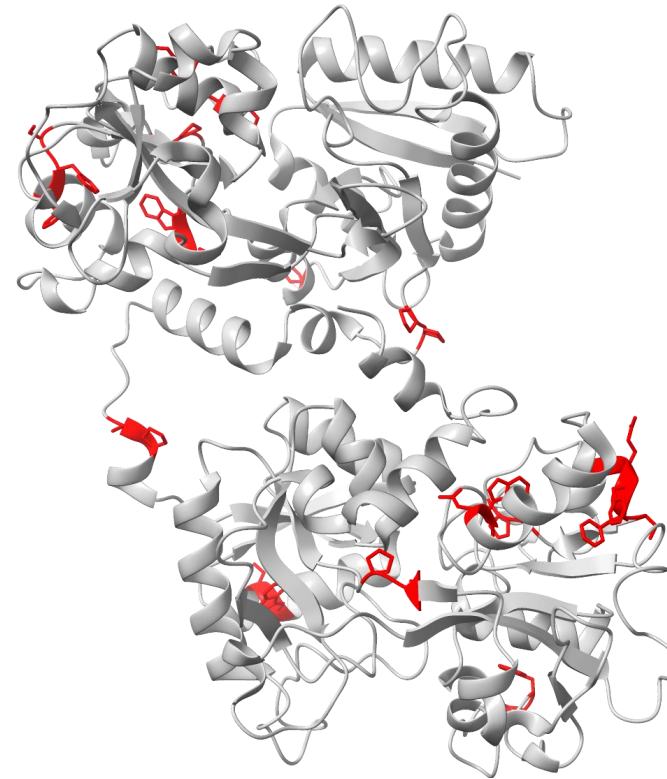


Capable of Achieving
>95%
Proteome
Coverage

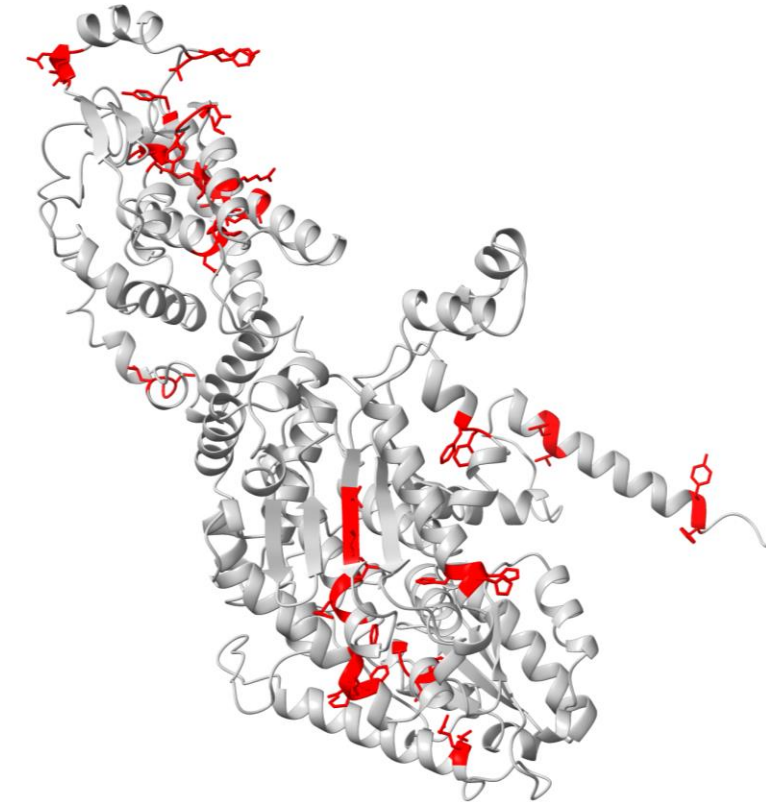
¹Estimates based on Nautilus computational analysis projecting the number of Nautilus designed short epitope probe binding events necessary to identify the SwissProt reference proteome.

Multi-affinity probes bind to buried/structured regions in denatured proteins

- Binding of a multi-affinity probe to its intended peptide target is required
- Multi-affinity probes must also be able to bind to short epitopes in denatured, full-length proteins
- We have demonstrated binding to short epitopes in internal portions of denatured, but full-length proteins (red) using both aptamer- and antibody-based multi-affinity probes



Transferrin



G6PI

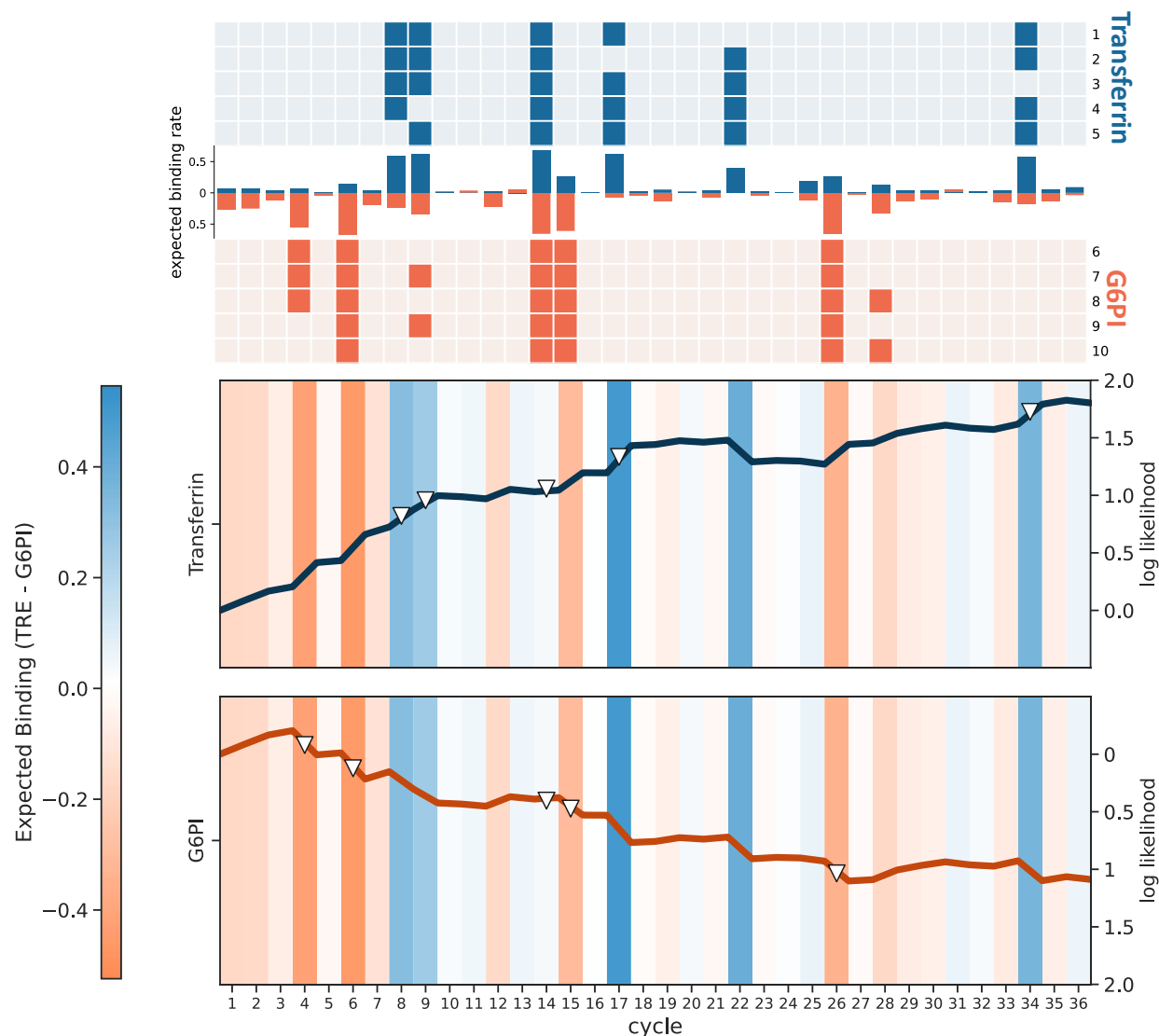
Binding patterns to transferrin and G6PI at single-molecule resolution

Samples consisting of transferrin (TRFE), glucose 6 phosphate (G6PI), pyruvate kinase M2 (PKM2), a model protein, no protein (negative control) or mixtures thereof were deposited into flowcell lanes for PrISM analysis.

Shown top are the 5 most prevalent binding patterns from these experiments for transferrin and G6PI.

From these binding patterns, machine learning tools identify each molecule. Each additional cycle builds additional information about protein identity as transferrin and G6PI have different binding patterns, indicated by the triangles.

The resulting difference in probability between the best-matching protein, and the next best protein in the database leads to confident protein identifications.



Ultra-sensitive quantification of transferrin

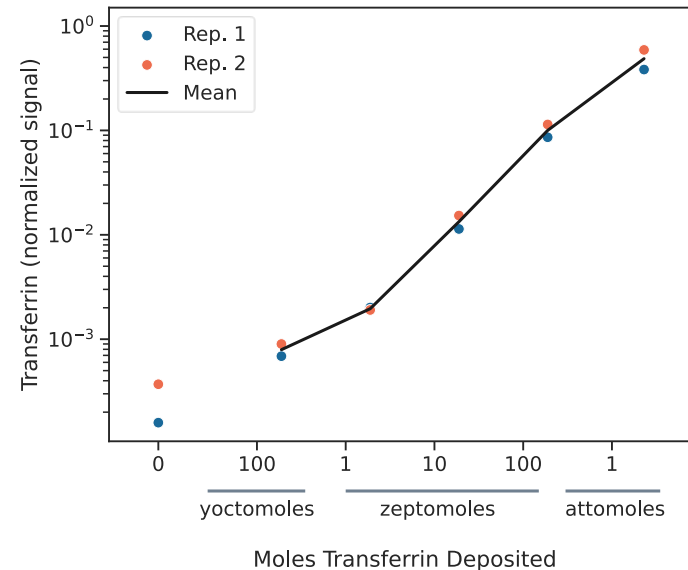
(LEFT) Sensitive single-molecule measurements: Lower limit of detection in the high-yocto to low-zeptomole range

Reproducible single-molecule measurements: The highest abundance Transferrin measurement (2 attomoles) was repeated 7 times across 4 days and 7 flow cells with a CV of 7.7%

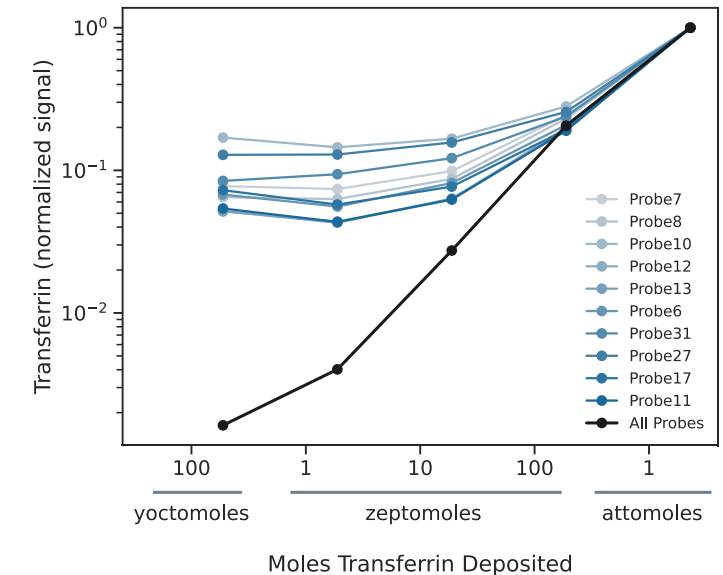
(RIGHT) High fidelity quantification: Multi-cycle decoding data is significantly more sensitive and error tolerant than achievable with any one multi-affinity probe alone

This improvement arises from the ability of the machine learning software to better identify proteins whose identifications were derived from either false positive or false negative bindings

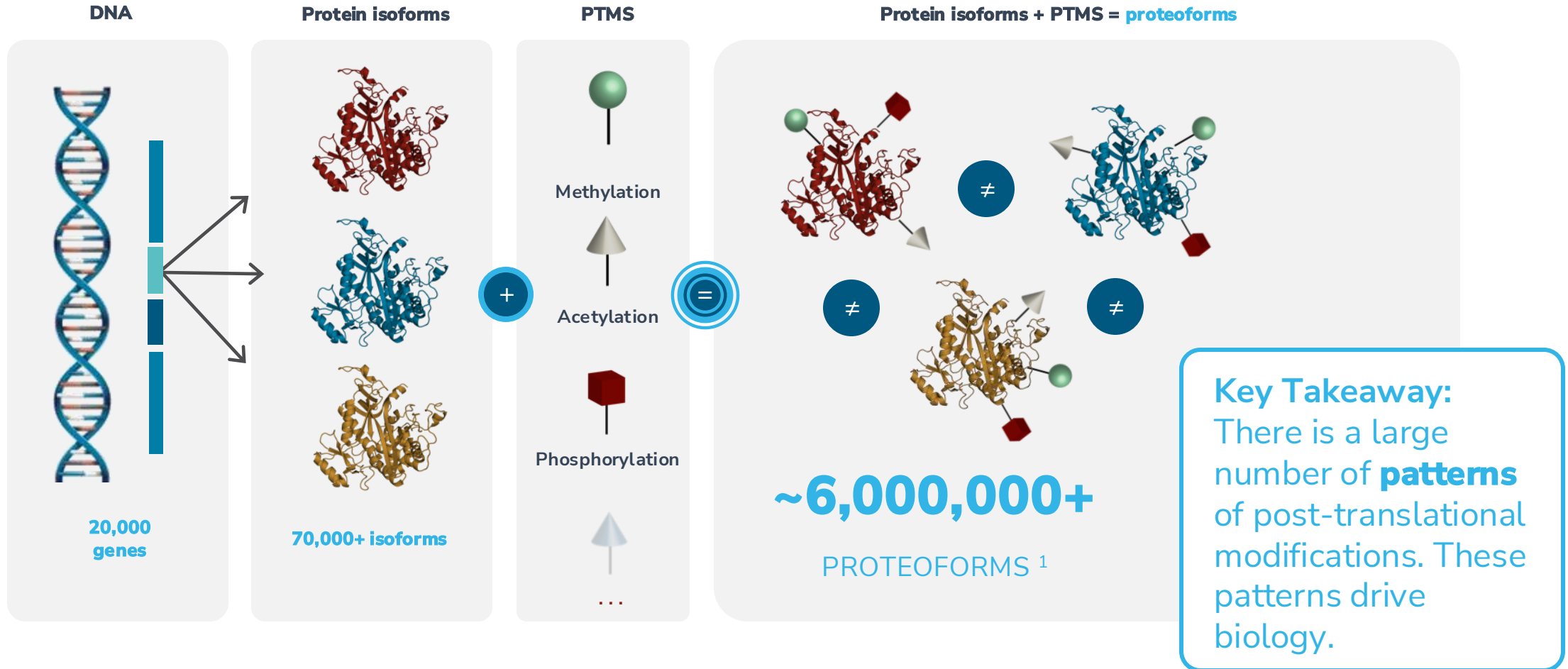
Transferrin dilution series in a background of alternate protein, or null scaffolds



Multi-probe decode vs single-probe



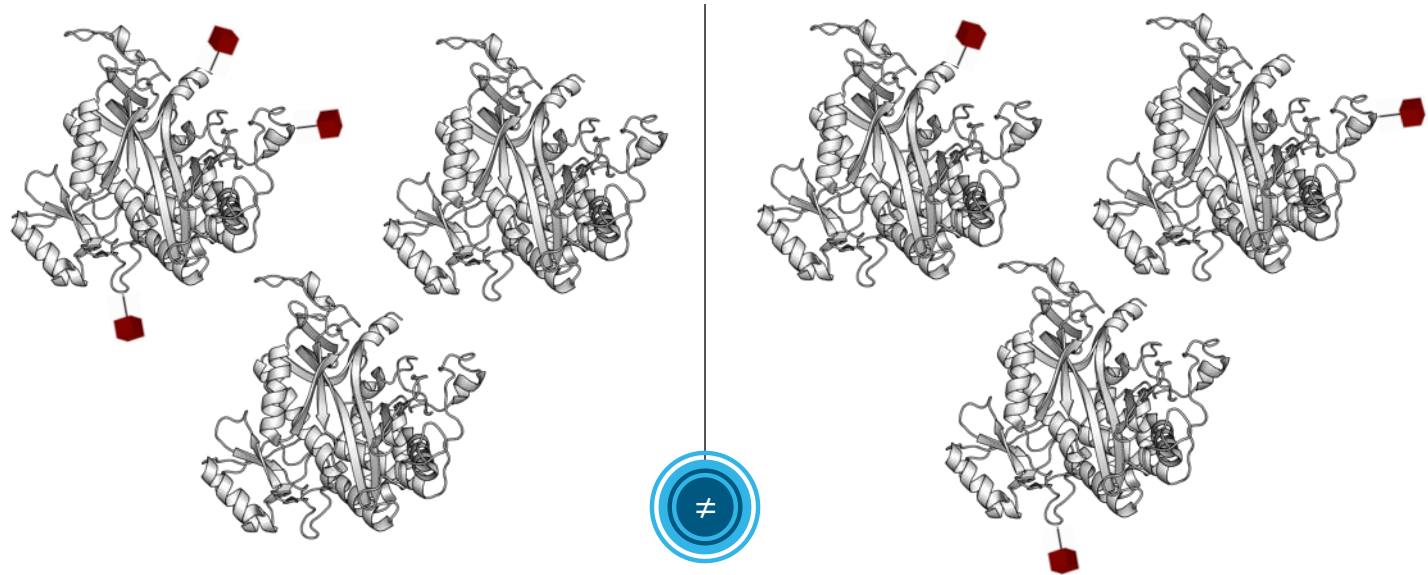
Nautilus: Revealing unseen **proteoforms**



¹International Journal of Analytical Chemistry. 2016; 2016: 7436849. The Size of the Human Proteome: The Width and Depth, Elena A. Ponomarenko et al.

High-resolution proteoform quantitation: a **core** application of Nautilus' platform

Peptide-centric proteomics methods are unable to differentiate mixtures of proteoforms



“ Which drugs work and to what extent is defined not by just the total amount of PTMs and splice forms, but instead by how combinations of specific alterations operate together. Creating a technology to see these PTM patterns, and measure their relationship to one another, has the potential to hugely advance precision medicine. ”

Dr. Ruedi Aebersold, Head of IMSB, Swiss Federal Institute of Technology (ETH) and Nautilus Scientific Advisory Board Member

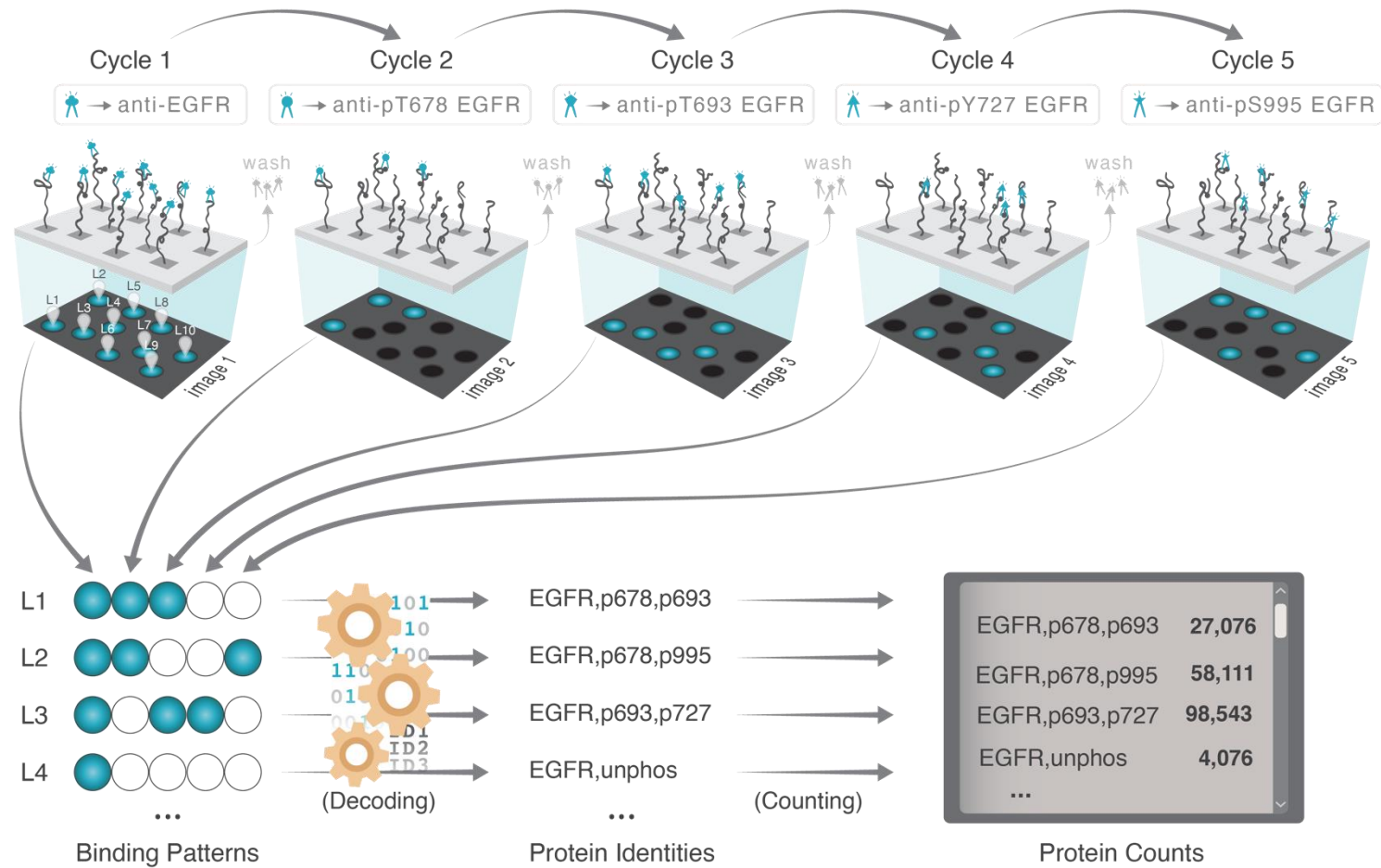
Integration of breakthrough innovations across the platform

Designed to allow access to full resolution digital proteomic data for Proteoform Mapping

2
Sequential
Affinity Reagent
Hybridization
& Imaging



3
Data
Processing

Research collaborations

Genentech

A Member of the Roche Group

- Signed a pilot study Research Collaboration Agreement in **December 2020**.
- Collaborating with Genentech using the Nautilus platform **to analyze and map the proteoform landscape** of a Genentech protein target of interest.

AMGEN

- Signed a pilot study Research Collaboration Agreement in **October 2021**.
- Collaborating with Amgen using the Nautilus platform across **a number of projects to investigate proteins and proteoforms of interest to the company**.

THE UNIVERSITY OF TEXAS MD Anderson Cancer Center

- Signed a Research Agreement in **October 2021**.
- Collaborating with MD Anderson using the Nautilus platform to measure the quantity and patterns of post-translational modifications on **specific oncology protein targets of interest** across different settings.

tgen

part of  City of Hope

- Signed a Research Agreement in **January 2023**.
- Collaborating with TGen using the Nautilus platform to analyze specific protein targets **in diffuse intrinsic pontine glioma (DIPG), a rare and often fatal childhood cancer**.

Sharing insights about our platform...

bioRxiv

A theoretical framework for proteome-scale single-molecule protein identification using multi-affinity protein binding reagents

 Jarrett D. Egerton,  Dan DiPasquo, Alana Killeen,  Vadim Lobanov,  Sujal Patel,  Parag Mallick

doi: <https://doi.org/10.1101/2021.10.11.463967>

This article is a preprint and has not been certified by peer review [what does this mean?].



Abstract

Full Text

Info/History

Metrics

 Preview PDF

Abstract

The proteome is perhaps the most dynamic and valuable source of functional biological insight. Current proteomic techniques are limited in their sensitivity and throughput. A typical single experiment measures no more than 8% of the human proteome from blood or 35% from cells

Key Takeaways:

- 1** Demonstrates the potential to efficiently decode greater than 95% of the proteome.
- 2** Demonstrates potential dynamic range of eleven and a half orders of magnitude in plasma, far exceeding the capabilities of other approaches
- 3** Details the ability of our platform to work across multiple organisms, critical for translational research

The background of the slide is a light blue gradient. In the upper right, there is a detailed 3D ribbon representation of a protein structure. In the lower right, there is a large, semi-transparent grid pattern that tapers towards the top right corner. A solid blue horizontal line is positioned above the text.

Experimental Findings Presented at October 2024 HUPO World Congress

What are the factors that influence the sensitivity and dynamic range in a single molecule assay?

Number of molecules measured



In general, the more molecules measured the wider the dynamic range

Peptides vs Proteins



Each protein can give rise to 10s-100s of peptides thus increasing the number of molecules that must be measured to achieve comparable dynamic range

False Positive Rate



The higher the false positive rate the worse the sensitivity and dynamic range

Measurement Time



The longer the measurement time, the longer it takes to measure N molecules, which leads to a trade-off between throughput and dynamic range

Number of measurements required to make a confident identification



The more measurements required to identify a peptide/protein the longer it takes to measure N molecules, which leads to a trade-off between throughput and dynamic range

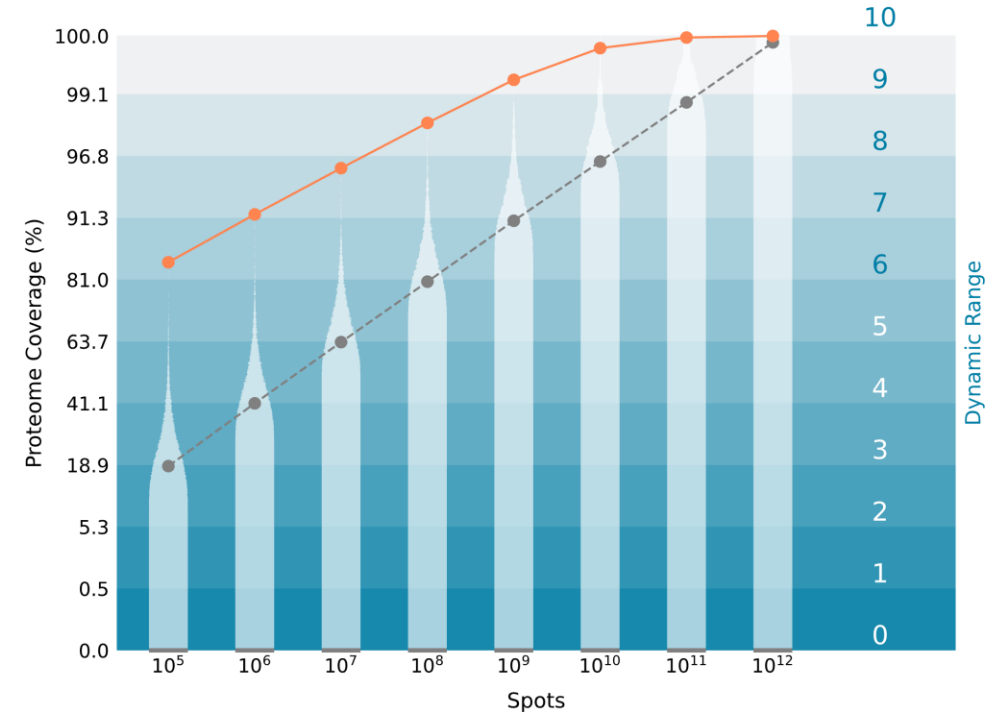
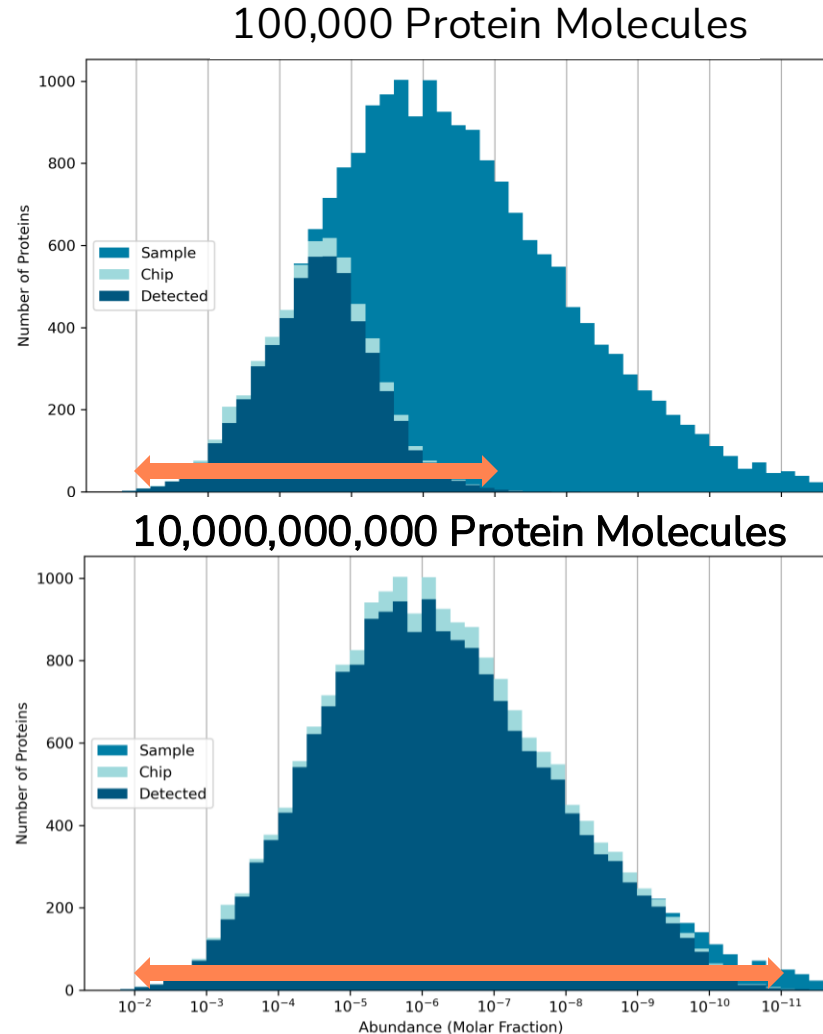
Number of molecules interrogated per measurement



Sparsely patterned molecules require more imaging and longer acquisition times to measure N molecules, which leads to a trade-off between throughput and dynamic range

Scale is critical: dynamic range is directly related to number of molecules measured

- As one increases the number of molecules measured with larger flowcells, one increases the dynamic range of the platform
- (LEFT) In medium blue is the distribution of abundances of proteins in the proteome and in dark blue – the estimate of which of those would get detected if the platform measured either 100,000 or 10,000,000 protein molecules.
- (RIGHT) Modeling the relationship between number of protein molecules measured and dynamic range shows a target of 1-10 billion to be optimal to cover substantially all of the proteome



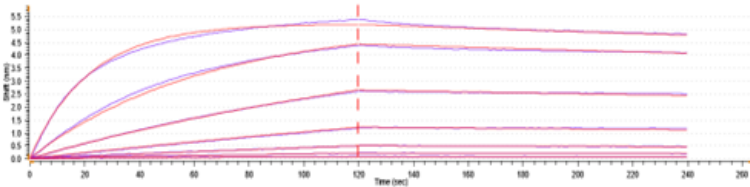
In orange is shown the dynamic range as the difference between the lowest abundance and highest abundance protein.

In grey is shown the dynamic range where greater than 90% of the proteins at a given concentration are measured.

Multi-affinity probes undergo extensive characterization

Candidates are first evaluated for binding to the selection target

Probe raised against epitope WNK. $K_d \sim 1nM$

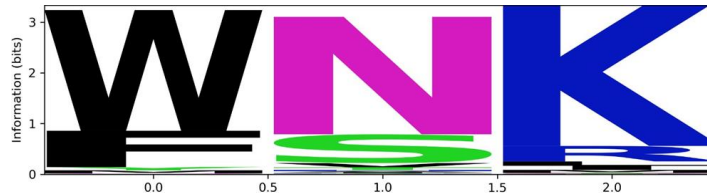


Multi-affinity probe association and dissociation from the panning peptide

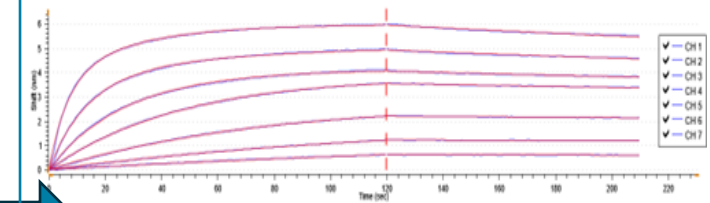
Leads are then tested using millions of peptides to define binding profiles

DCPRYDPRFVGF**WNK**VAHIVELDAQARQARQPLLLCPTLQEYELLVLP
 RFVGF**WNK**VAHIVELDAQEYELLVLEAFTIHLPHAPSLDISRFRSSP
 KQ**FWNK**SAHRPHVVGAKWLECF SKGYMLSEEPYI HANYQPVEI PVSHK
 ERIKNTISYSLQDY IFQSYWGE**WN**SYYSKILGRPTTLCETMGKAEIWLI
 WLDNPER**WNK**VKMVV SREEVE LAYQEAMFNMAT LNR TAAGLMHTFNAHA
WSKVKDKVESDPRYKAVDSS SMREDL FKQYIEKIAKVRSSDVSWSDTRR
 YNHAAANQNSNATS NIRKEFVPK**WNK**PS DVSATERTAKYTMEGKGRAAH
 YRVQWAANYEPYVVVPRDCPRYDPRFVGF**WNK**VAHIVELDAQEYELLV
 WGTPAQNTGTNLPSVE**WNK**LPSNQHSNDSANGNGKFTNGWKSTEEEDQ
 ...

Precise recognition epitopes are defined for each multi-affinity probe



Candidates are next evaluated for binding to epitope-containing proteins



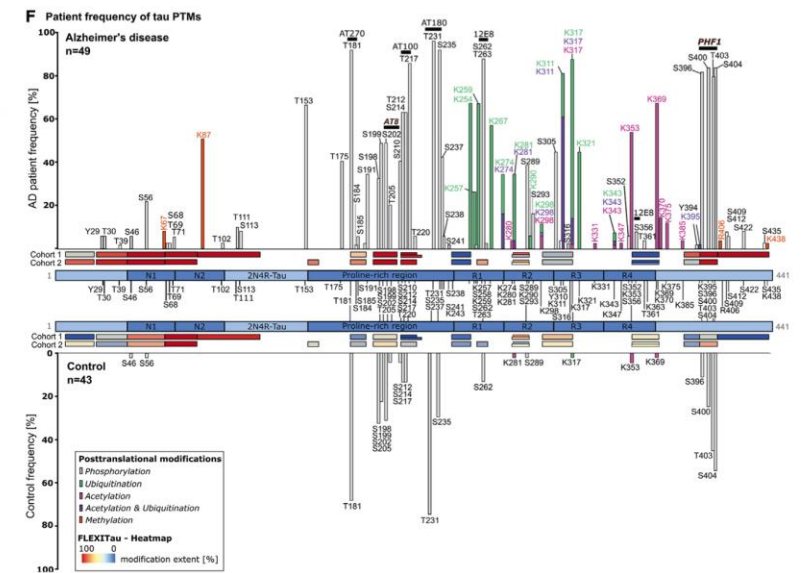
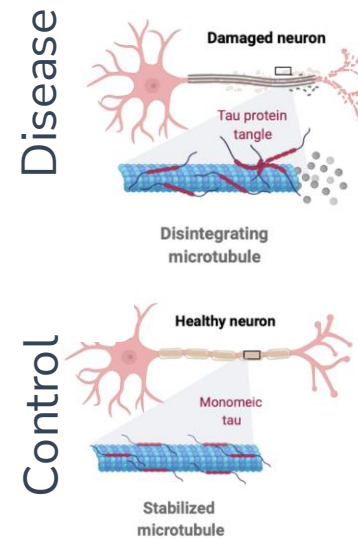
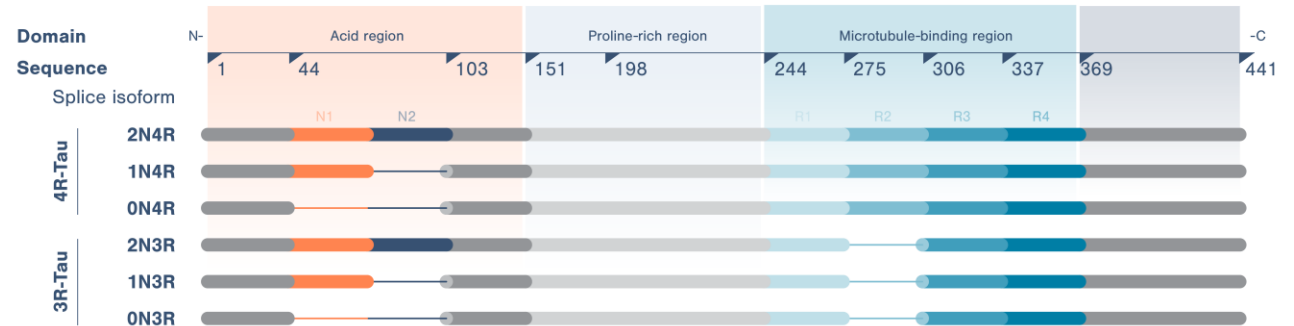
The same probe association and dissociation with the protein PARP-1 in a format used on the platform. Protein $K_d \sim 1nM$



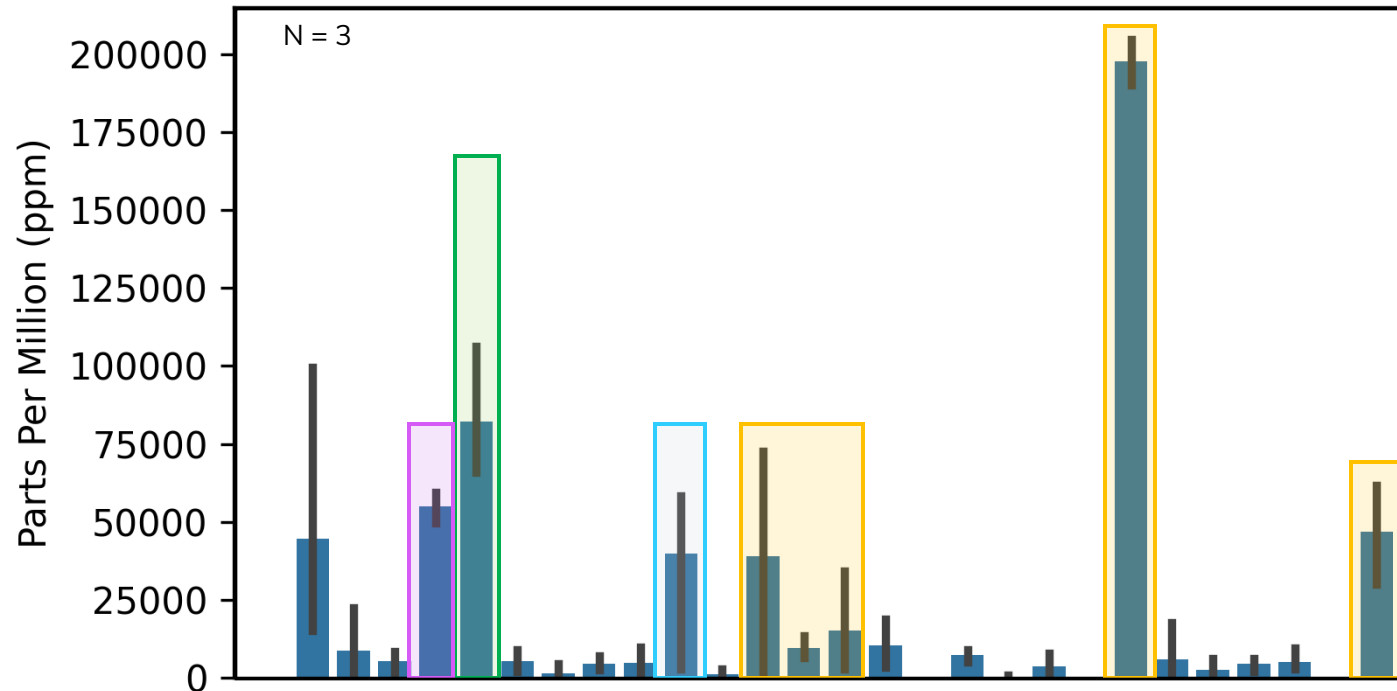
Epitope for this probe in PARP-1 is shown in red

Tau protein exists in many forms

- Tau has multiple functions in a diverse range of molecular pathways including cell signaling, synaptic plasticity, and regulation of genomic stability
- Tau forms a group of six highly soluble protein isoforms and is highly post-translationally modified, which is pivotal in defining and modulating tau localization and its roles in health and disease
- Tau proteoforms are directly linked with Alzheimer's disease (AD) phenotype in addition to contributing to numerous other tauopathies
- The stoichiometries of tau modifications over the course of the development of AD pathology remain uncharacterized
- Technical limitations prohibit the characterization of the co-occurrence of these PTMs on molecules of tau to date

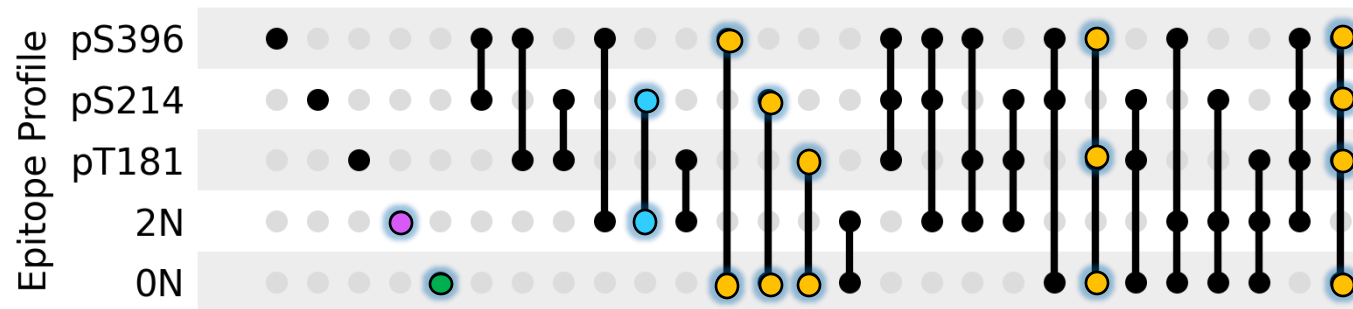


Quantification of mixtures of proteoforms



Tau proteoforms	Molar ratio
0N	25
0N ERK (181 & 396)	50
2N	12.5
2N PKA (214)	12.5

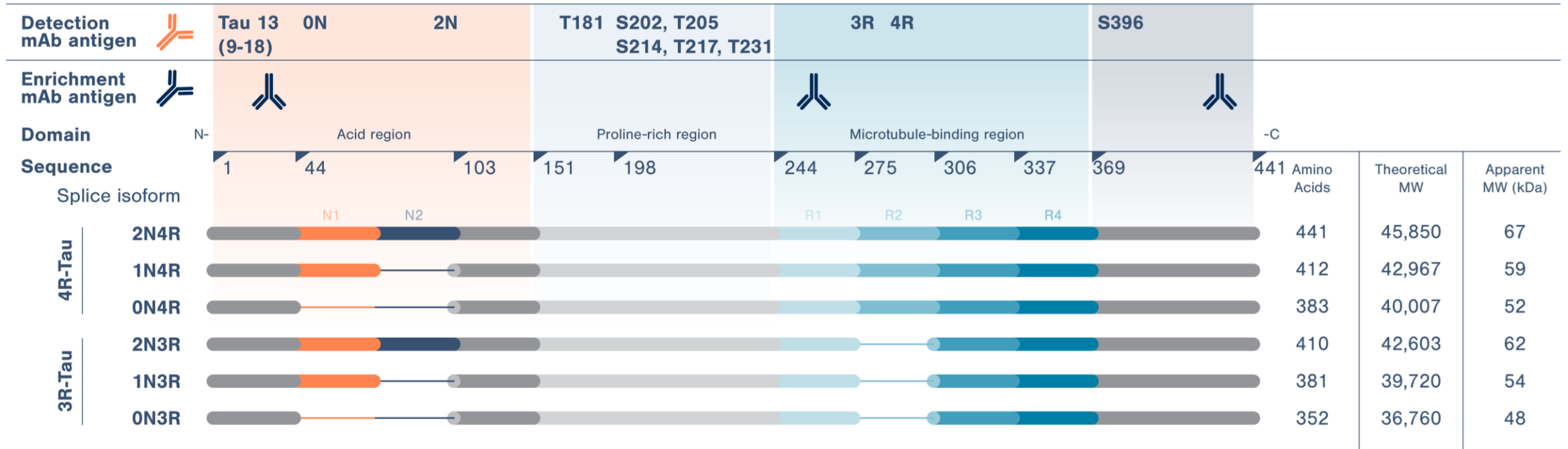
Exploiting the massively parallel nature of our platform, the relative abundances of seven Tau proteoforms were accurately quantified. This measurement is intractable on both traditional and emerging peptide-based platforms.



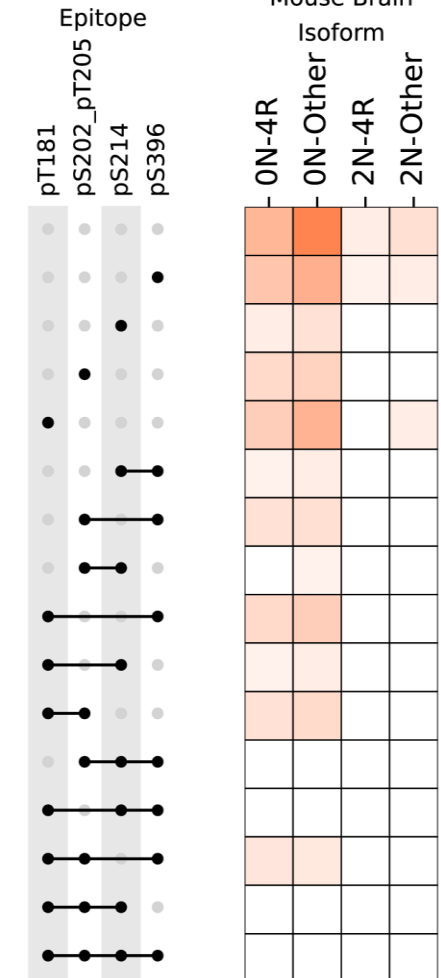
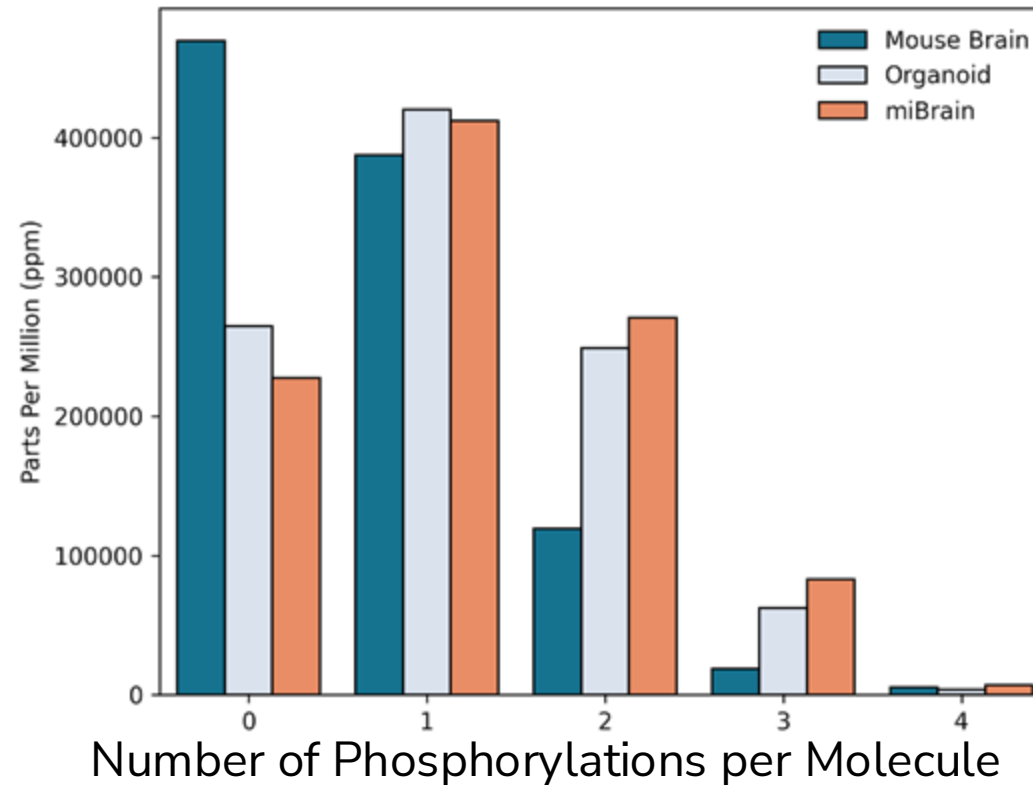
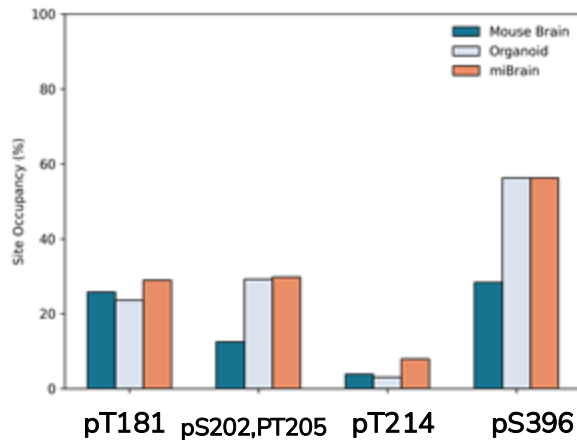
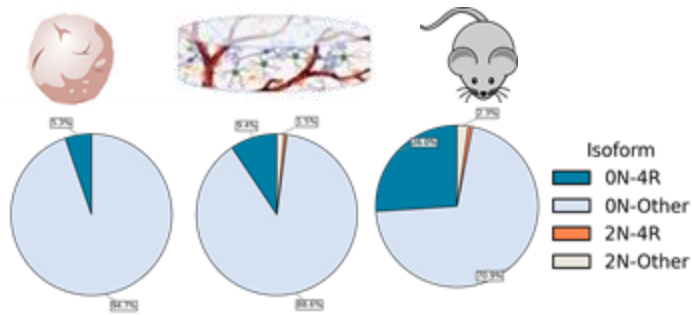
We additionally showed how the platform can be applied to measure Tau proteoforms.

Expanded panel for tau proteoform quantification

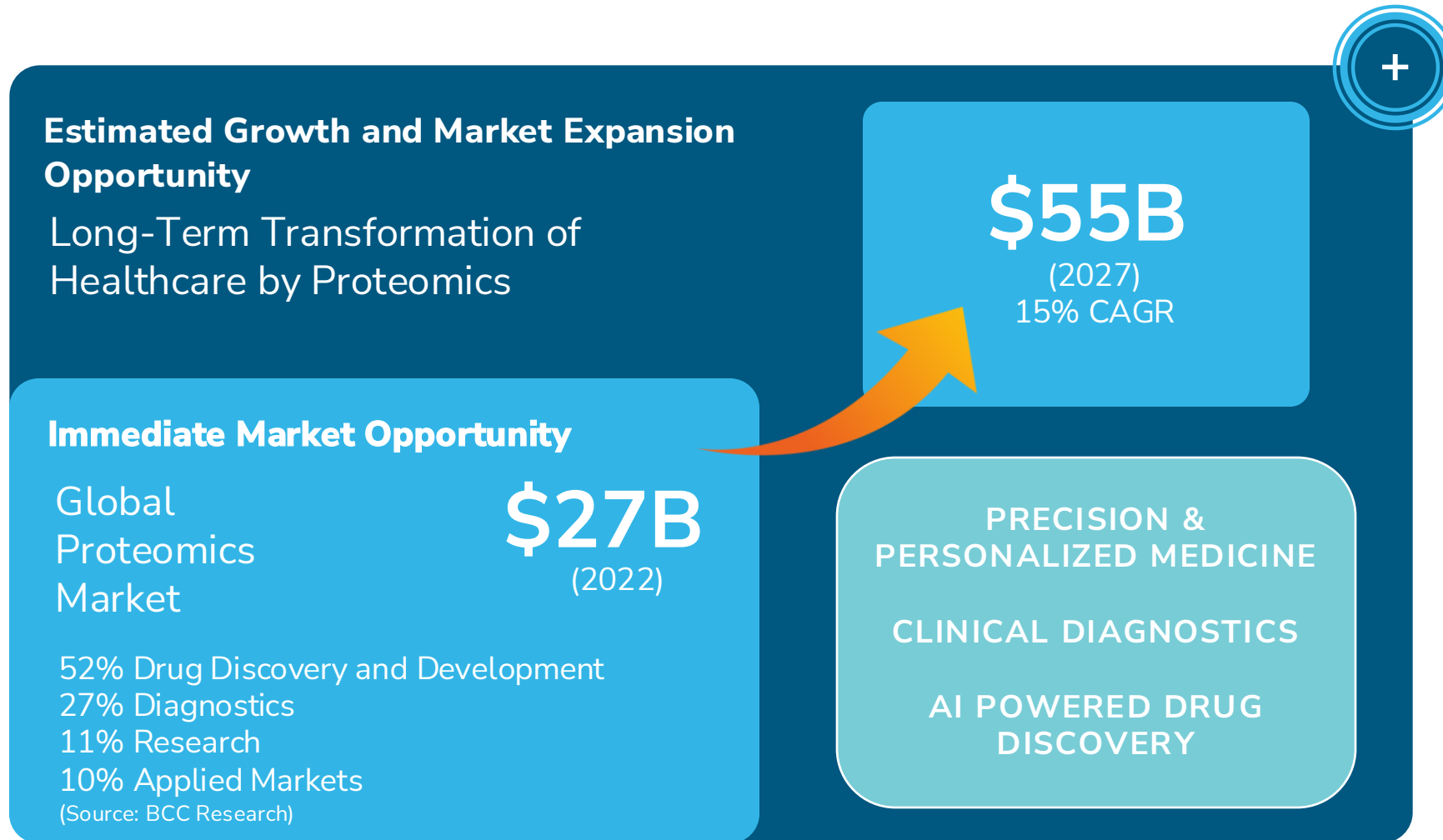
11 reagents enables measurement of 2,048 proteoform groups of tau



New additional detail into the proteoform landscape of model systems enabled by Nautilus Platform



Large market opportunity **ready for disruption**



Addressable markets & applications



Basic Sciences

Multi-Omics &
Systems Biology

Proteoform
Composition
& Landscape

Proteome Profiling
(species agnostic)



Translational Research

Biomarker & Drug
Target Discovery

Mechanism of
Action Studies

Toxicity Profiling
and Prediction



Clinical Research & Development

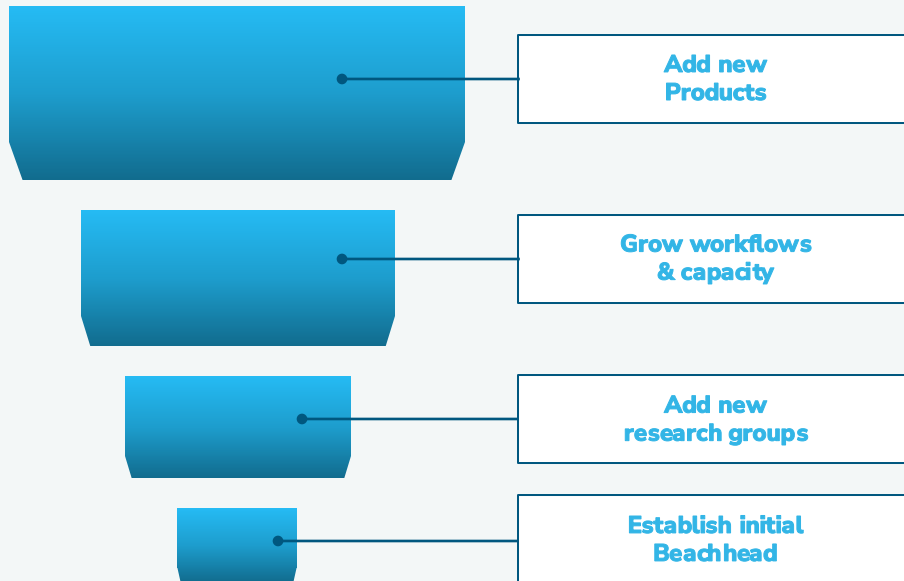
Longitudinal
Monitoring of
Proteome Dynamics

Precision Medicine
Development

Drug Rescue
& Repurposing

Planned sales model and key customer segments

Land and expand sales model



Target customers

- 🎯 Pharmaceutical & Biotech
- 🎯 Academic & Research Community
- 🎯 Large-Scale Omics Core Laboratories
- 🎯 Contract Research Organizations
- 🎯 B2B Diagnostic Service Partnerships

Planned strategic elements of the platform designed to create **competitive advantage** in the field



First to Market with Novel Detection Platform

First mover advantage in a large and expanding market



Highly Disruptive Technology

Unlocks new sources of primary biological information



Immense Data Production Capacity

Drives discovery potential and technology ubiquity
Data is an asset



Proven Commercial Model

Average selling price enables efficient direct sales model (>\$1M ASP)
Start in North America and then start building international footprint with distribution partners



Diversified and Recurring Revenue Sources

Partnerships
Instrumentation
Consumables
Service and support
Software as a service

Phases leading to commercial launch planned for 2025

Every step represents a fundamentally new and unprecedented use of our technology

Today

2025

Note: timeline not to scale

3. Launch of Proteome Analysis Platform (Expected in late 2025)

Shipment of First Instruments & Consumables

Early Access Beta Testing, and Full Commercial Launch

2.b. First Broadscale Proteome Decoding Data

Early Access Program for High-Output Discovery Proteomics

Launch in-house data production facility, support customer proof of concept studies

2.a. Tau Proteoform Data

Collaborations and Partnerships

Accelerate engagements with pharma partners and key academic collaborators using Tau as our first biomarker

1. Leveraging Single-Molecule Multi-Cycle Data Read-out



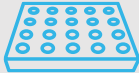








Continue to Establish Collaborations & Partnerships Focused on Targeted Proteomics

Engage early through research collaborations, build a foundation of publications

Patent Portfolio Summary

(as of October 29, 2024)

Overall Process (3 Families)
 3 US Pending 1 PCT
 8 US Granted EP, CN, JP, IN

										
APPLICATIONS & SAMPLE PREP 12 Families	ARRAYS 15 Families	INSTRUMENT HARDWARE 6 Families	PROBES & REAGENTS 17 Families	INSTRUMENT SOFTWARE 2 Families	DECODING & BIOINFORMATICS 6 Families					
12 US Pending 1 US Granted	21 US Pending 8 US Granted	7 US Pending 1 US Granted	24 US Pending 3 US Granted	2 US Pending	6 US Pending 4 US Granted					
4 PCT EP, CA, AU	5 PCT EP,CN, JP, CA, AU, IN, IL	2 PCT EP, CA, AU, HK	5 PCT EP, CN, JP, IN, HK, CA, AU, KR	EP, CA, AU	3 PCT EP, CN, JP, CA, AU, IN, BR, MX, HK, IL, KR, HK					

Why Nautilus?

We believe that humanity needs a dramatic acceleration of drug development and that a bold scientific leap is required to make possible a new world of precision and personalized medicine.

To deliver, we need to radically reinvent proteomics, a large untapped opportunity in biological science today.



Potential for revolutionizing biomedicine



Proven team, driven to win



Significant new potential market opportunity



Designed to address what the market wants – the proteome at single molecule resolution, enabling unprecedented sensitivity and scale

NAUTILUS™

BIOTECHNOLOGY

Corporate Headquarters

2701 Eastlake Avenue, Suite 300
Seattle, WA 98102

Research Headquarters

835 Industrial Rd, Suite 200
San Carlos, CA 94070

 (206) 333-2001  info@nautilus.bio

www.nautilus.bio