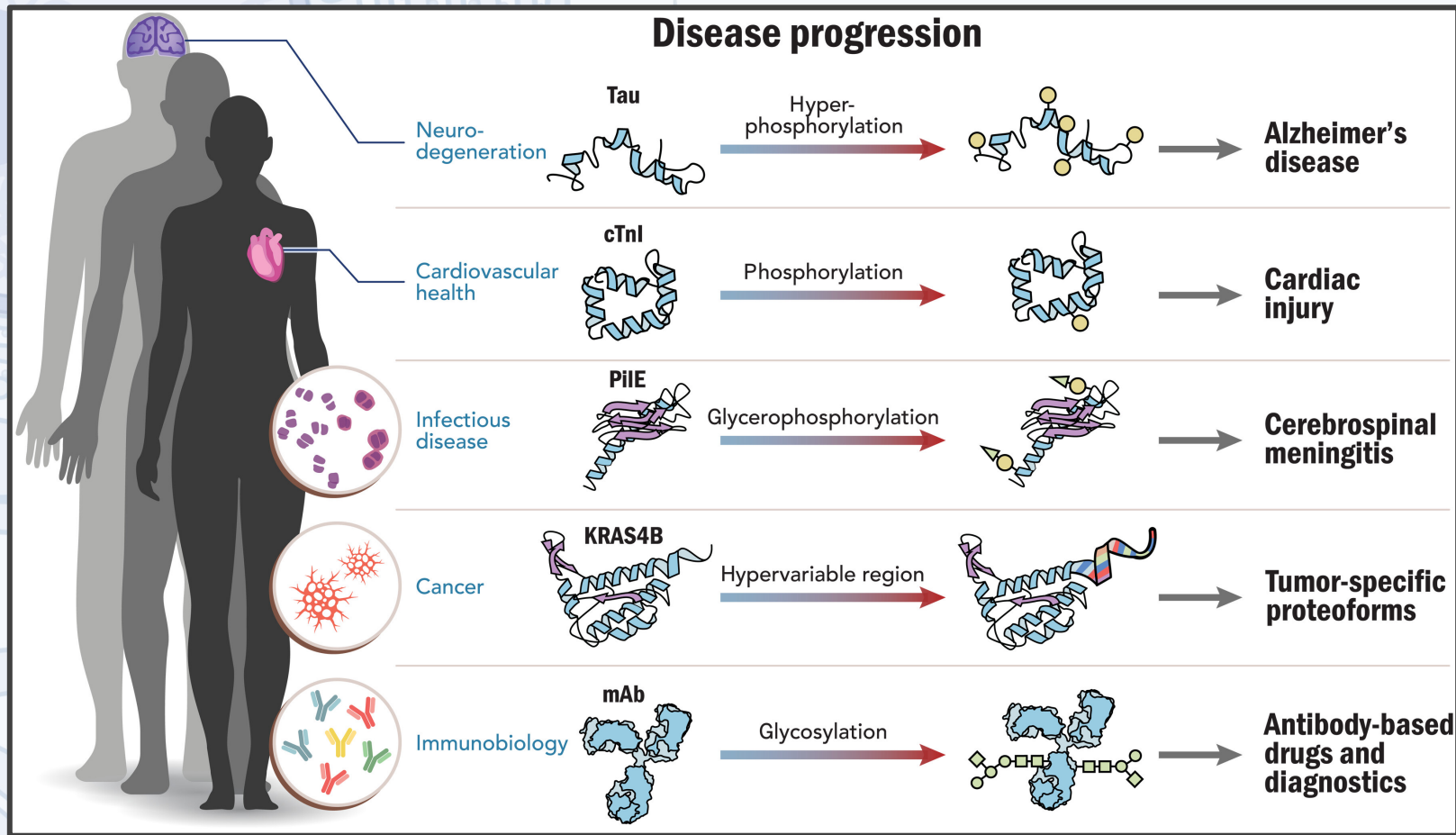




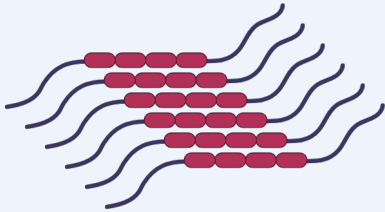
Atomic vibrations → protein sequence
Unlocking the most valuable data in biology

Small protein changes define human health



Current tools barely scratch the surface

Current tools can't scale
beyond DNA and RNA



Affinity reagents



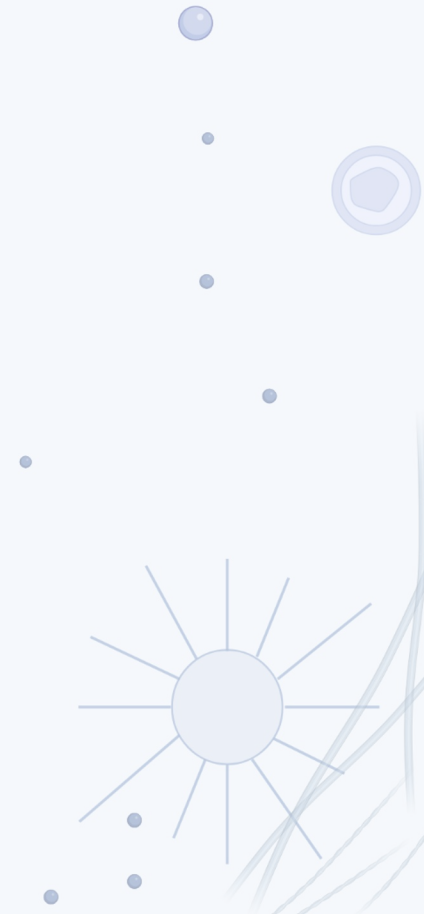
Fluorophore



Nanopore

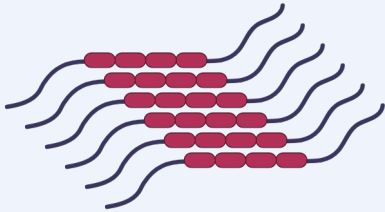


Mass spec



Primary Bioscience reveals the biological reality no one else can see

Current tools can't scale beyond DNA and RNA



Affinity reagents



Fluorophore

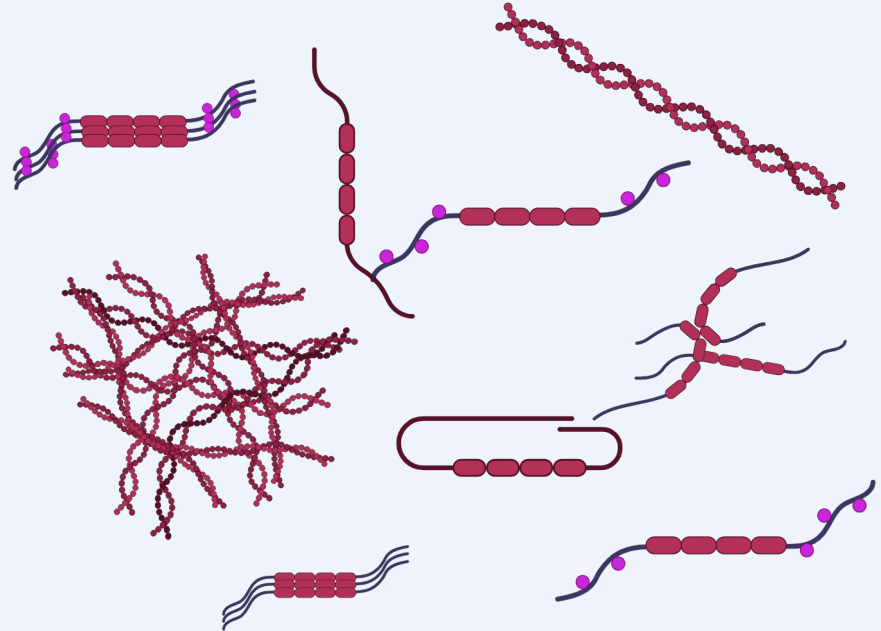


Nanopore

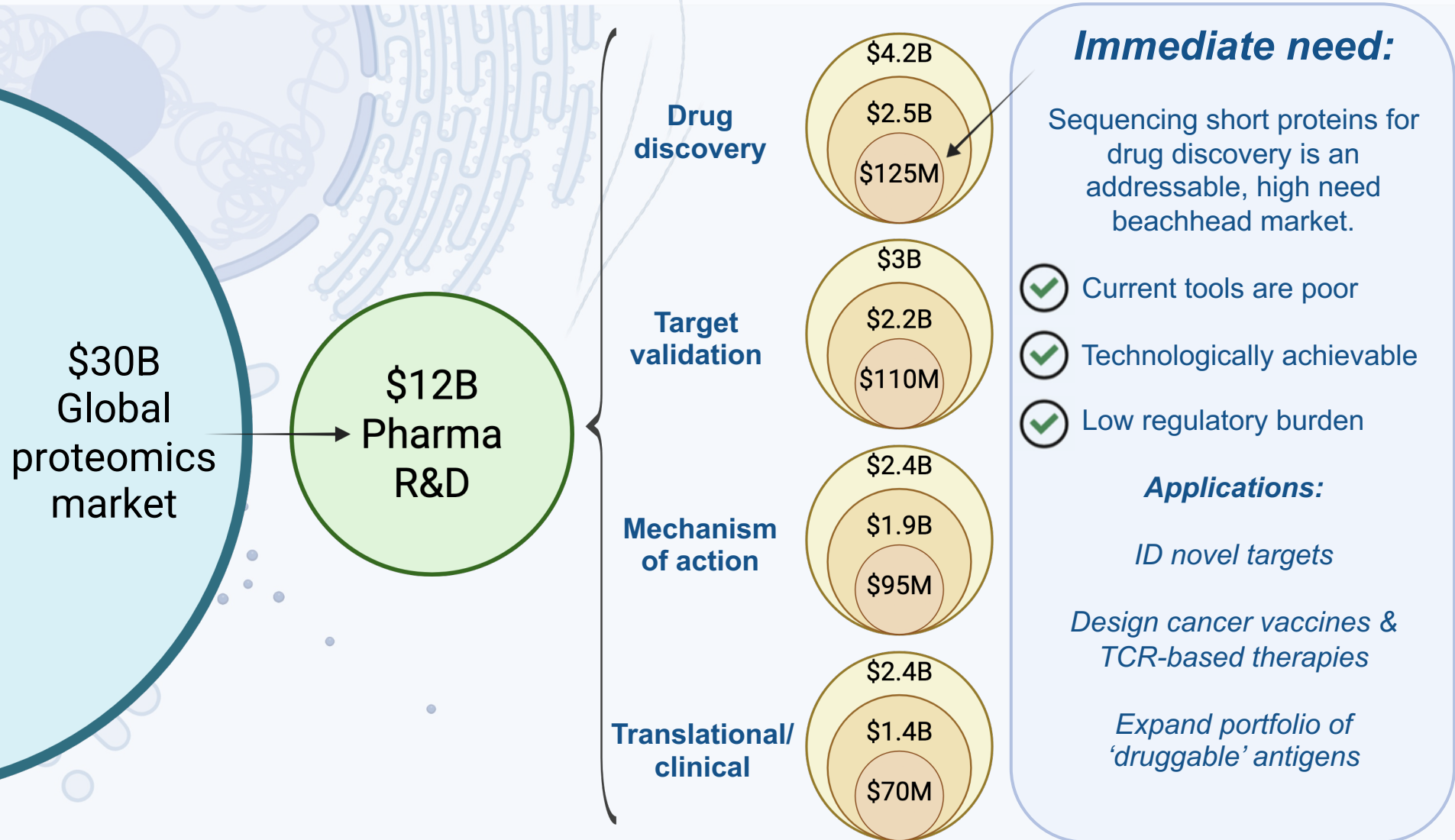


Mass spec











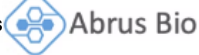
















Primary Bioscience sees the full picture



The need for superior proteomics spans pharma R&D



We're building a high-throughput protein sequencer – leave your DNA reference at home

	Read ALL letters and modifications	Unbiased data (no DNA readout!)	Ultra-high throughput
			
			
  			
 			
    			

Our technology reads proteins directly - no binders or tags.

Markets in medicine and beyond are desperate for better protein tools

Areas of growth

Early adopters

Drug discovery
(neoantigen seq.)



Drug target
discovery



Biologics
manufacturing



Diagnostics



Personalized
therapeutics



Long term potential

Biodefense



Agriculture



Environmental
proteomics



Forensics



Unforeseen
applications



Go to market strategy: follow the genomics playbook

The Illumina model: drive adoption with a service, grow revenue with instruments & consumables.

Stage 1

Beta-testing

Service based protein sequencing for industry and academic researchers

Low barrier-to-entry option will drive adoption

Early revenue stream

Stage 2

Sequencing as a service

Early access *de novo* protein sequencing service to KOLs

Early partnerships to demonstrate capability

Results-based revenue

Stage 3

Sell instruments

Sell instrumentation to pharma, CROs, and university core centers

Large, high-value customers want in-house instrumentation

Continued revenue from proprietary biosensor & consumable reagent sales

Our team is led by sequencing & protein characterization experts

Stacy Anderson, PhD
Founder/CEO



- Protein discovery & market need
- Protein engineer
- Dev HT protein screening process at Stratos Genomics / Roche (acq.)

Lindsey Williams, PhD
Co-founder/CSO



- 2 exits
- Sequencing platform acq. by PacBio
- Most accurate DNA sequencing tech on the market
- Commercialized >10 products



We are supported by top-quality collaborators & partners

Collaborators



Hamed Tabatabaei Ghomi, PhD
Prof. Computational Modeling, Kings College London
CEO of ComplexiCom
Algorithm development



David Rider, PhD
Prof. of Chemistry, Western Washington University
Joint National Science Foundation STTR grant awarded for biosensor development



Dan Fu, PhD
Prof. of Chemistry, University of Washington
Prototype development of Raman imaging system: resolution + throughput



Sanjeev Koppal, PhD
Prof. of Electrical and Computer Engineering (Computer Vision), University of Florida
Development of ultra-high throughput spectral collection

Advisors



Shane Bowen, PhD
Experienced proteomics entrepreneur
Palamedix CEO (acquired by SomaLogic), CTO Standard BioTools, Ex-Illumina

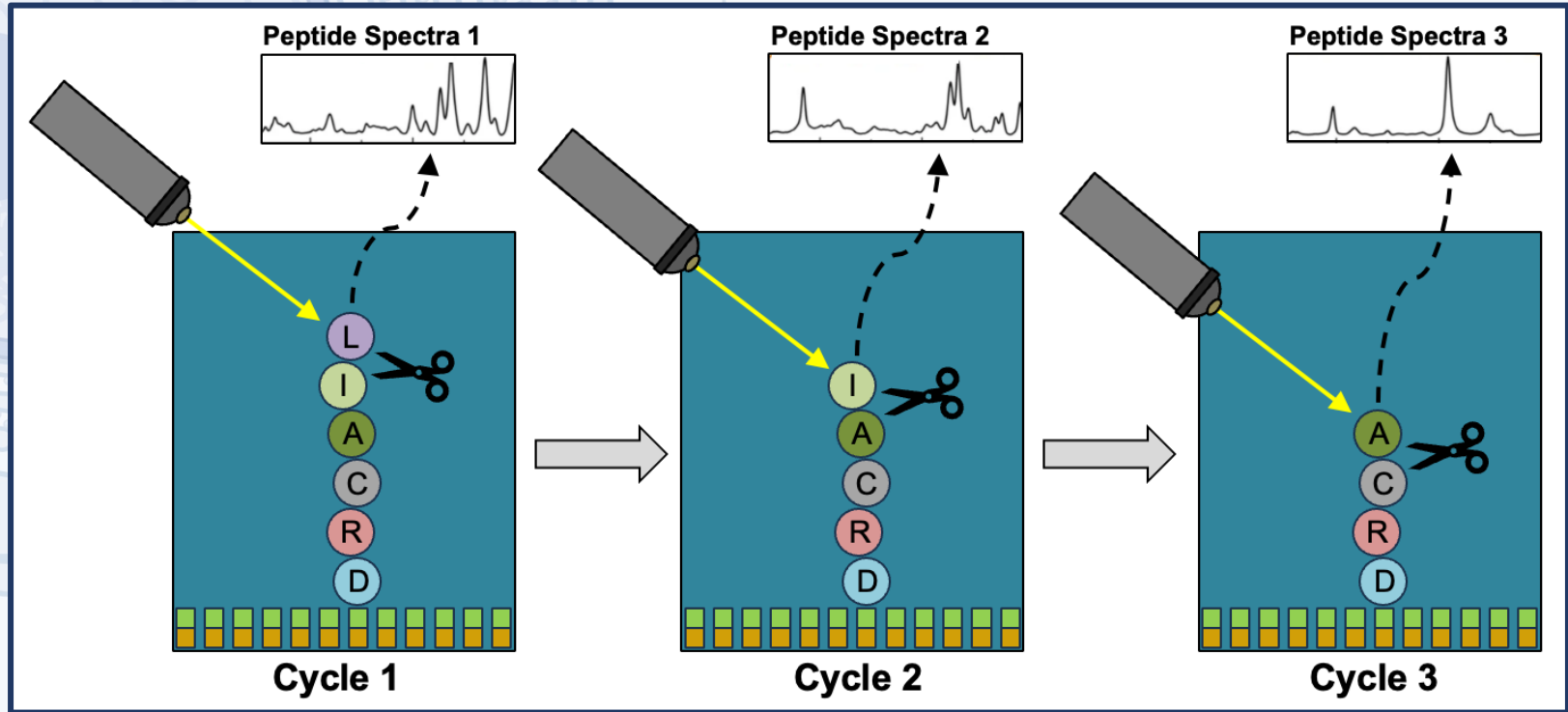


Zachary Schultz, PhD
Prof. of Chemistry & Biochemistry, Ohio State University
20+ years of analytical chemistry and chemical detection
SERS, nanomaterials and active plasmonics expert

Entrepreneurship and funding support



Our single molecule protein sequencing scheme



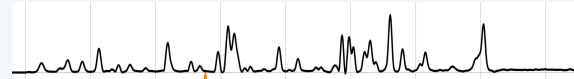
- Raman spectroscopy is used to determine the amino acid composition of proteins
- Iterative cycles of amino acid cleavage and spectra comparison is used to determine the sequence

Our technology has progressed from concept to sequencing in only 90 days

We can read ALL canonical amino acids and every mod we've tested



Phospho-Y



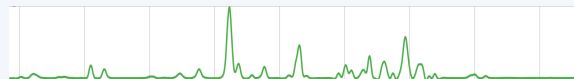
Phospho-T



Phospho-S



Hydroxy-P



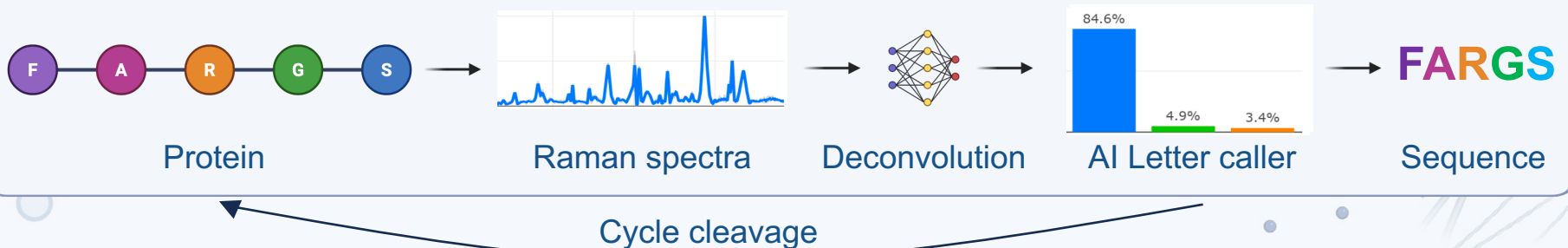
Acetyl-S



Acetyl-K



- ✓ Each amino acid has a distinct spectra that we can ID
- ✓ Protein composition can be derived from deconvoluting amino acid fingerprints from protein spectra



Preseed 70% closed, \$500K allocation remaining

\$2.1M raised to date

- ✓ Tech milestones accomplished
- ✓ Team in place
- ✓ Foundational IP protected

Closing \$500k

- ◆ Final tech demo to show differentiation and breadth



1517



INDIE BIO





PRIMARY
BIOSCIENCE

Join us in unlocking the
most valuable data in biotech

stacy@primarybioscience.com