



University of Virginia Researchers Publish New Study on Tropomyosin Proteoforms Showcasing Quantum-Si's Next-Gen Protein Sequencer™ Platinum®

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Published Preprint Demonstrates Platinum's Capability to Discriminate Peptide Variants with Single Amino Acid Resolution

BRANFORD, Conn.--(BUSINESS WIRE)--Nov. 7, 2024-- [Quantum-Si Incorporated](#) (Nasdaq: QSI) ("Quantum-Si," "QSI" or the "Company"), The Protein Sequencing Company™, today announced a newly released preprint publication on BioRxiv, from Dr. Gloria Sheynkman at the University of Virginia School of Medicine. In the publication, Sheynkman and team demonstrate the application of Quantum-Si's Platinum™ single-molecule benchtop sequencer to distinguish proteoform-informative peptides within the human tropomyosin (TPM) gene family. This study highlights Platinum's ability to achieve single amino acid resolution, revealing variations that differentiate crucial tissue-specific and modified protein forms.

Titled "*Protein Sequencing with Single Amino Acid Resolution Discerns Peptides that Discriminate Tropomyosin Proteoforms*," the preprint describes how the Platinum sequencer differentiates TPM1 and TPM2 paralogous peptides that vary by only a single amino acid. It also explores the instrument's ability to resolve phosphotyrosine modifications and TPM2 splice variants, underscoring the potential for NGPS to advance multi-omics research by providing insight into proteoform presence, structure, and function. (<https://www.quantum-si.com/preprint-110724/>)

"Our data highlight Platinum's ability to accurately distinguish all major types of proteoform variation within the TPM gene family," said Dr. Sheynkman. "This provides a more precise window into complex protein families, and this capability to precisely sequence and distinguish peptide variations paves the way for numerous applications in disease research and biomarker discovery."

The study further explores Platinum's capability to differentiate highly similar peptides that may define isoforms with distinct functions. Platinum's single amino acid resolution enables it to detect sequences with molecular weights that challenge traditional mass spectrometry (MS) techniques, making it a complementary tool for MS and an asset for proteomics researchers focused on nuanced peptide differences.

"This collaboration with Dr. Sheynkman and her team at the University of Virginia highlights Platinum's role in pushing the boundaries of proteomics," said Jeff Hawkins, CEO of Quantum-Si. "Seeing our instrument empower researchers to unravel proteomic complexity at the single-molecule level is exciting. This work not only establishes our technology's unique capabilities but also exemplifies the impactful discoveries it can make possible for researchers."

For more information on Quantum-Si's technology and research applications, please visit [The Protein Sequencing Company™ Quantum-Si](#)

About Quantum-Si Incorporated

Quantum-Si, The Protein Sequencing Company™, is focused on revolutionizing the growing field of proteomics. The Company's Platinum® instrument enables Next-Generation Protein Sequencing™ that advances proteomic research, drug discovery, and diagnostics beyond what has been possible with existing proteomic tools. Learn more at [quantum-si.com](https://www.quantum-si.com) or follow us on [LinkedIn](#) or [X](#).

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