## **QUANTUM SI**

## Quantum-Si Announces Presentation on the Use of Next-Generation Protein Sequencing<sup>™</sup> to Detect Disease-Relevant Proteoforms at the Festival of Genomics and Biodata

June 10, 2024

BRANFORD, Conn.--(BUSINESS WIRE)--Jun. 10, 2024-- <u>Quantum-Si Incorporated</u> (Nasdaq: QSI) ("Quantum-Si," "QSI" or the "Company"), The Protein Sequencing Company<sup>™</sup>, today announced a presentation byGloria Sheynkman, Ph.D., Assistant Professor in the Department of Molecular Physiology and Biological Physics at the University of Virginia at the Festival of Genomics and Biodata conference being held in Boston on June 12-13, 2024.

The presentation, titled "Next Generation Proteomics to Detect Disease-Relevant Proteoforms" will be on Wednesday, June 12<sup>th</sup> at 2:50 p.m. on the Omics Stage and will describe the application of Quantum-Si's Next-Generation Protein Sequencing ("NGPS") to identify protein variants that have a role in complex disease.

Dr. Sheynkman and her team at the University of Virginia are using advanced analytical and computational approaches to identify and understand how proteomic variation underlies human disease and to capture alternative splicing variants. They are developing approaches to discover novel disease proteoforms, assay proteoform-specific functions, and elucidate the molecular mechanisms by which proteoforms rewire cellular networks to drive disease states.

NGPS is a complementary, powerful technology that reveals proteoforms that are difficult to distinguish with antibodies and sometimes mass spectrometry. The Quantum-Si platform uses dye-labeled amino acid recognizers to distinguish subtle amino acid variations in isoform-specific peptides, generating new proteoform insights related to human health and disease.

In this presentation, Dr. Sheynkman will describe creation of a database for long-read-guided interpretation of protein isoforms and construction of a map of protein isoforms for splicing events associated with bone mineral density in the human fetal osteoblast (hFOB) cell line. Using this approach the lab derived a list of actin-binding tropomyosin (TPM1/2)-informative peptides and TPM2 isoform-informative peptides from their long-read transcript database, then utilized the Quantum-Si Platinum® instrument to differentiate synthetic peptides that correspond to TPM1/2 paralogs and spliceoforms. Overall, single molecule sequencing with orthogonal methods facilitates proteogenomics and the transition from the discovery to proteoform scoring phase.

## About Quantum-Si Incorporated

Quantum-Si, The Protein Sequencing Company<sup>TM</sup>, is focused on revolutionizing the growing field of proteomics. The Company's suite of technologies is powered by a first-of-its-kind semiconductor chip designed to enable next-generation single-molecule protein sequencing and digitize proteomic research in order to advance drug discovery and diagnostics beyond what has been possible with DNA sequencing. Learn more at <u>quantum-si.com</u> or follow us on <u>LinkedIn</u> or <u>X</u>.

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Investor Contact Jeff Keyes, Chief Financial Officer ir@guantum-si.com

Media Contact Katherine Atkinson, SVP, Commercial Marketing media@quantum-si.com

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