Beyond the Genome: How Quantum-Si's Platinum™ Identifies Protein Sequence Often Overlooked by Genomics Data

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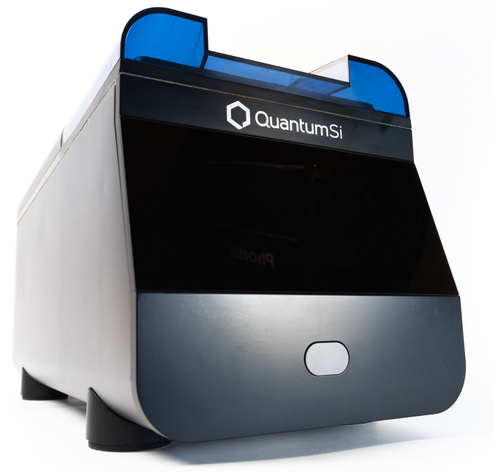
INTRODUCTION

Next-generation protein sequencing is a transformational tool for protein science to unlock new insights into the function of proteins in health and disease. Quantum-Si's Platinum™ technology brings the insights of protein sequencing to every lab with a space-friendly benchtop instrument, a simple end-to-end workflow, and single-molecule resolution that enables detection of protein variants and modifications.

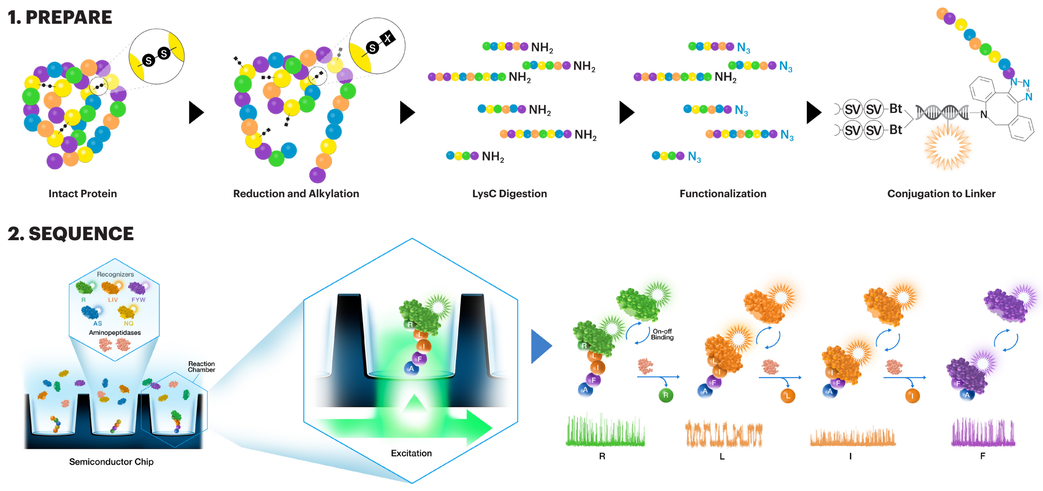
Herein, we employed Platinum to sequence and identify all components of a mixture of proteins, as well as protein bands extracted from electrophoresis gels.

Results demonstrate that Platinum can be used to effectively identify protein variants with single-molecule resolution using a simple workflow.

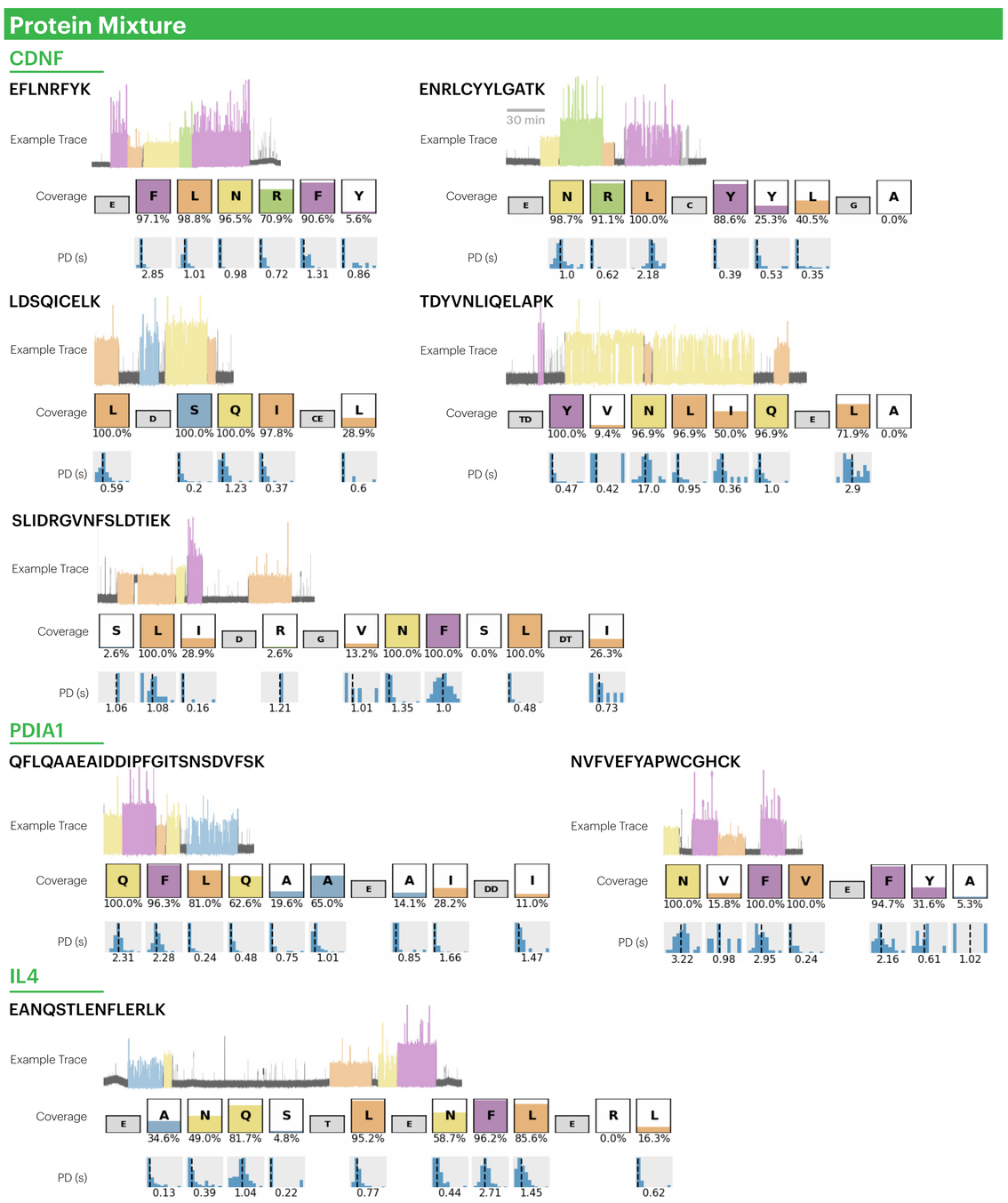


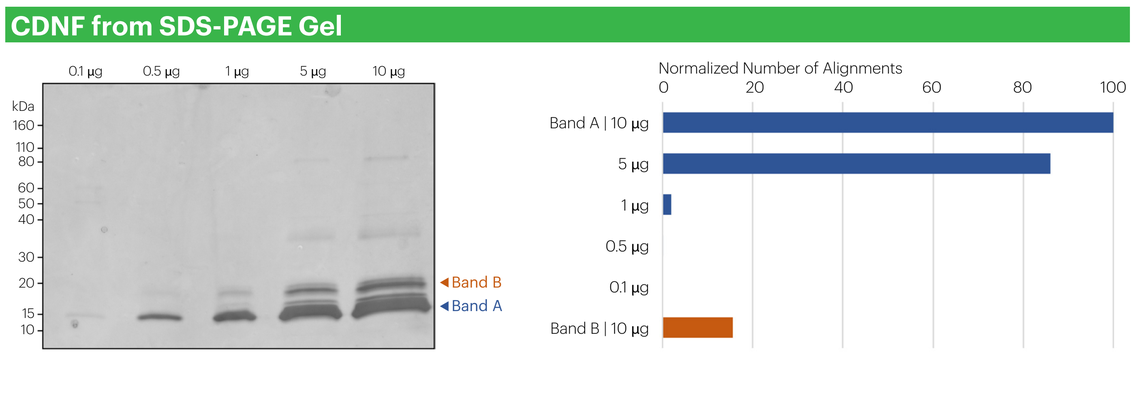
METHODS

- Proteins are reduced, alkylated, and digested with LysC.
- Peptides are functionalized, conjugated, and immobilized on the surface of a proprietary semiconductor chip.
- Fluorescently labeled N-terminal amino acid (NAA) recognizers and aminopeptidases are added to the semiconductor chip.
- Fluorescent lifetime and duration of each NAA binding event generates a unique kinetic signature.
- Kinetic signatures are converted into amino acid calls to identify peptides and proteins.



RESULTS AND DISCUSSION



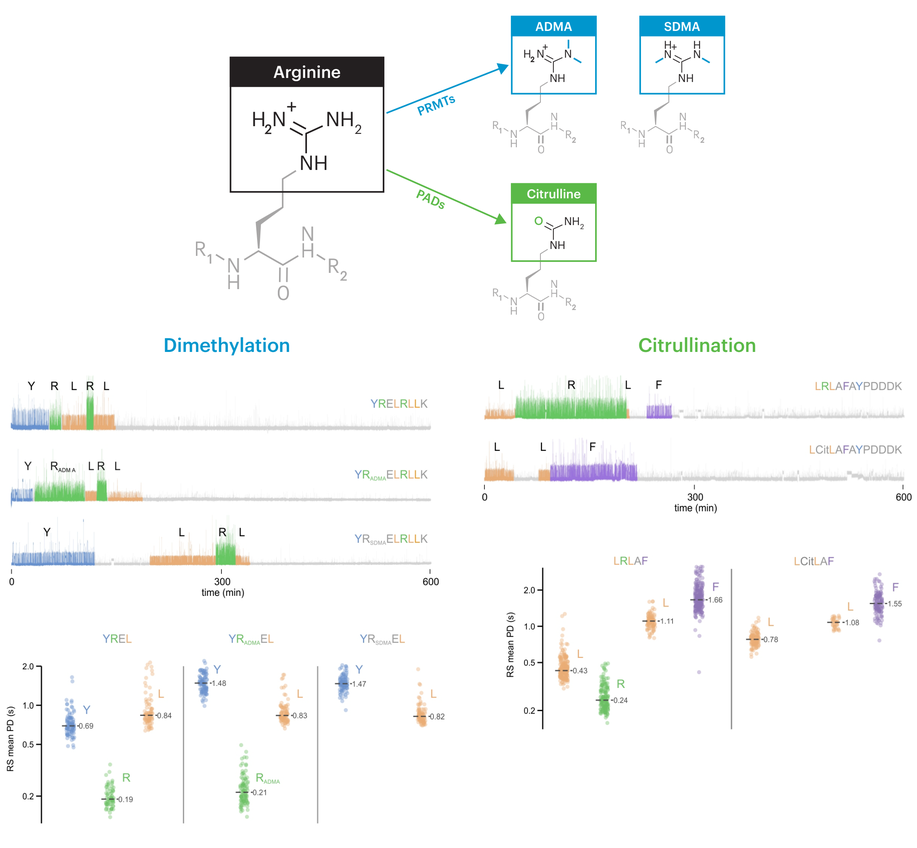


CONCLUSION AND OUTLOOK

Quantum-Si's Platinum next-generation protein sequencing workflow provides insights into all individual components of a protein mixture containing CDNF, PDIA1, IL4, and GMFB at single-molecule resolution.

CDNF extracted from SDS-PAGE gel was successfully sequenced with Platinum, offering an alternative method to antibody-based western blotting.

FUTURE DIRECTIONS extend towards uncovering post-translational modifications—a critical layer of information absent in genomic data. Preliminary results demonstrate our ability to detect dimethylation (asymmetric and symmetric) and citrullination of arginine.



REFERENCE

Brian D. Reed et al, Science 2022, 378 (6166)

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