

# Advancing Cancer Research with Next-Generation Protein Sequencing™ on Platinum® by Quantum-Si

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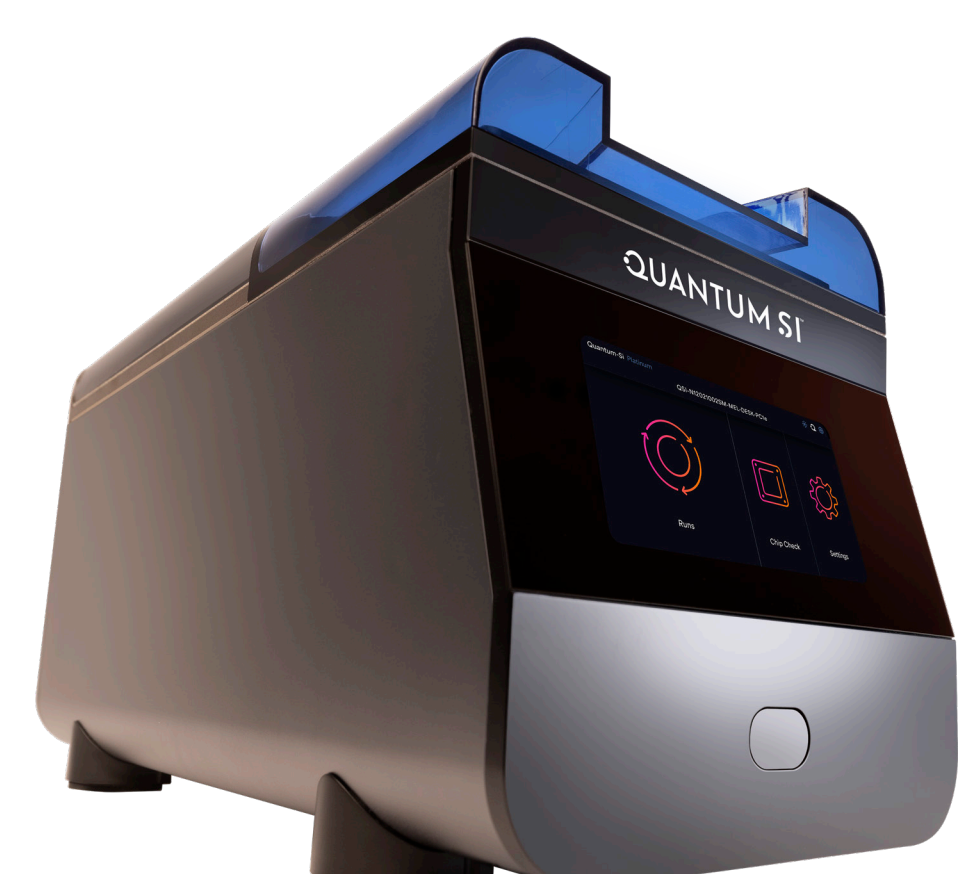
## INTRODUCTION

Sequencing proteins and correlating amino acid changes to biological function is critical to advancing cancer research. Next-Generation Protein Sequencing™ (NGPS) on Platinum® enables researchers to identify and characterize proteins with single-molecule resolution in a simple workflow and on a benchtop instrument.

To demonstrate the versatility of Platinum and the use of Kinetic Signatures, we sequenced various types of samples, including recombinant proteins, protein mixtures, immunoprecipitated proteins, and peptides with PTMs. First, we sequenced a series of interleukins (IL4, IL6, IL7, IL13, IL20, and IL34) individually or within protein mixtures. Interleukins are cytokines that play vital roles in cancer by modulating immune responses, promoting inflammation, and influencing tumor microenvironment, impacting tumor growth and the efficacy of treatments. Additionally, we demonstrated the platform's ability to sequence IL6 immunoprecipitated from human serum and correctly identified IL6 as the top protein against a reference panel of 7,921 proteins, highlighting its potential in analyzing complex biofluids.

Finally, we demonstrated the unique potential of Platinum to detect PTMs relevant to cancer using kinetic signatures by successfully identifying arginine citrullination in protein vimentin, an onco-protein that promotes cancer cell mobility and invasion into surround tissues.

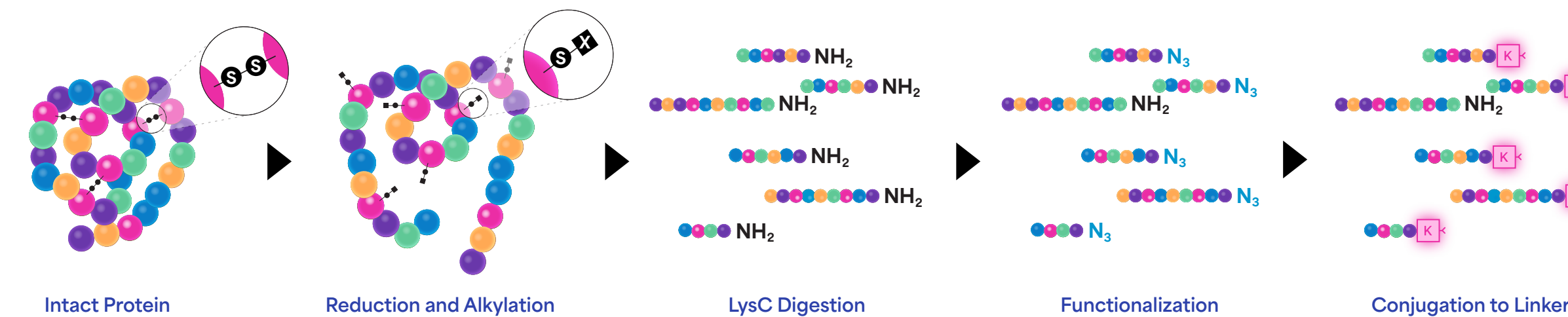
Next-Generation Protein Sequencing data enables new discoveries in cancer research. Kinetic signatures make these discoveries possible by unveiling key information about changes in amino acid sequence and PTMs that can be correlated to cancer genes and phenotypes.



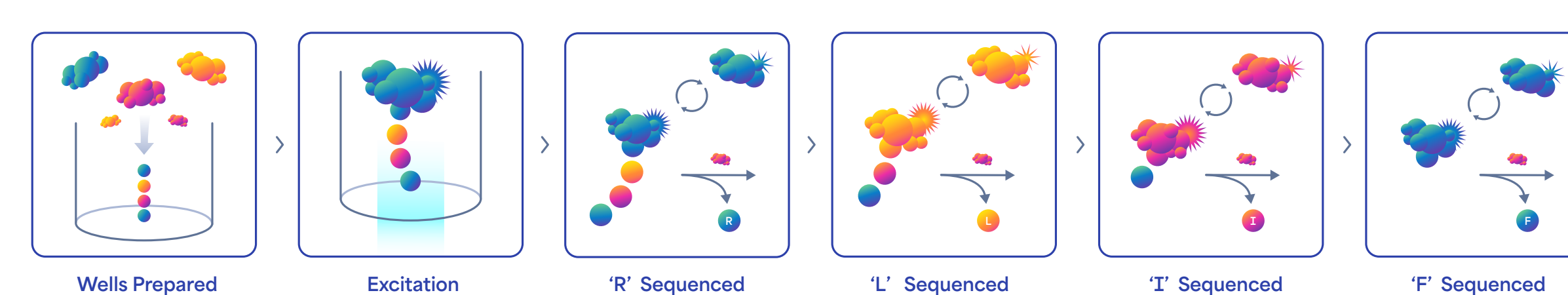
## METHODS

- Proteins are reduced, alkylated, and digested with LysC.
- Peptides are functionalized, conjugated, and immobilized on the surface of Quantum-Si's semiconductor chip.
- Fluorescently labeled N-terminal amino acid (NAA) recognizers and aminopeptidases are added to the semiconductor chip.
- Fluorescence lifetime, intensity, and kinetic properties of NAA binding events generate a unique kinetic signature.
- Kinetic signatures are converted into amino acid calls to identify peptides and proteins.

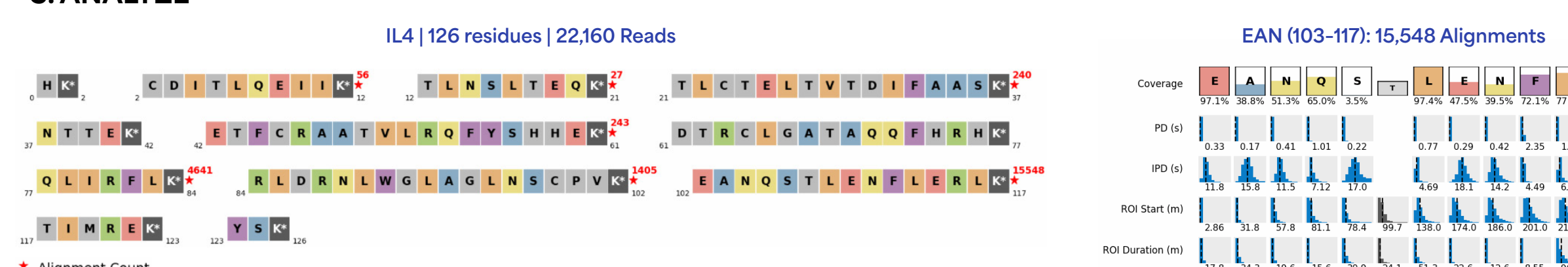
### 1. PREPARE



### 2. SEQUENCE



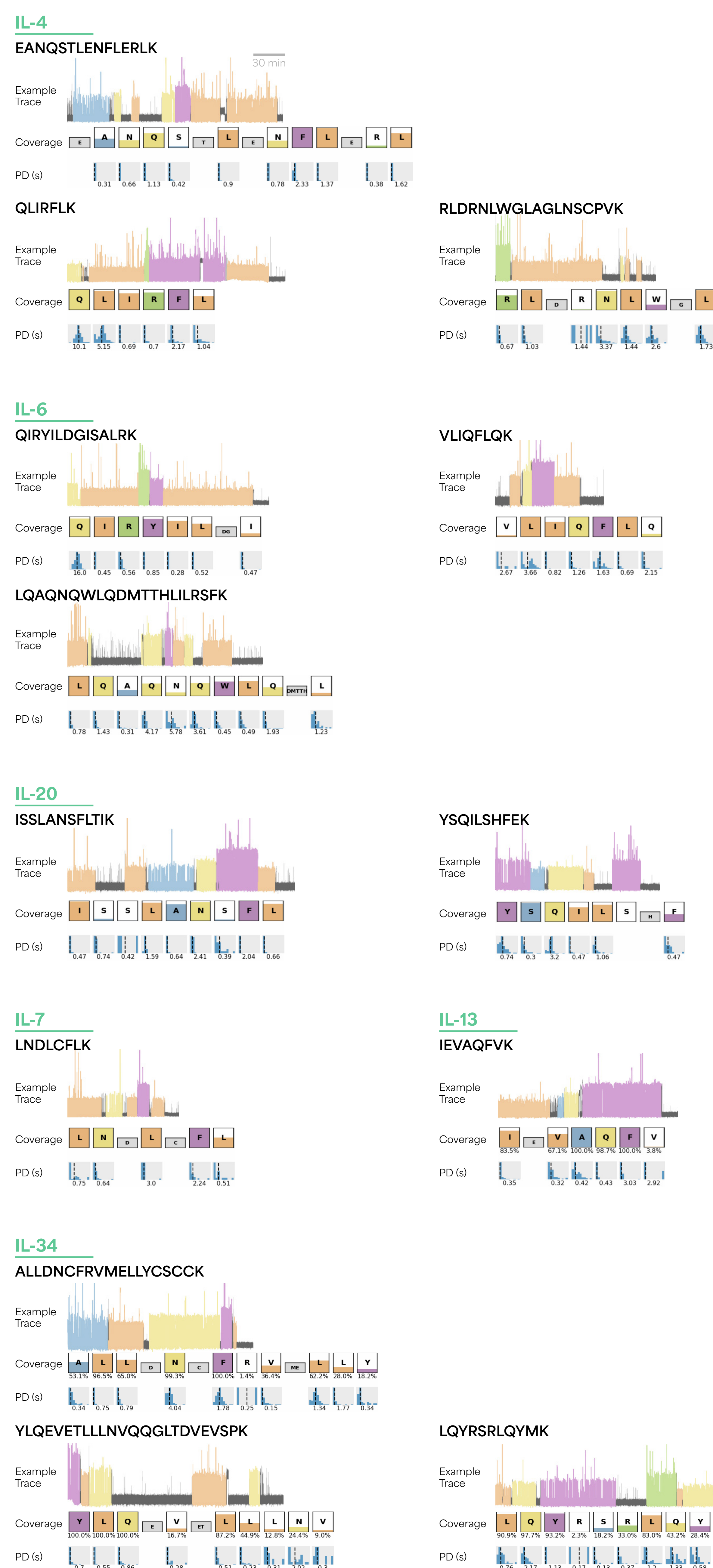
### 3. ANALYZE



## RESULTS

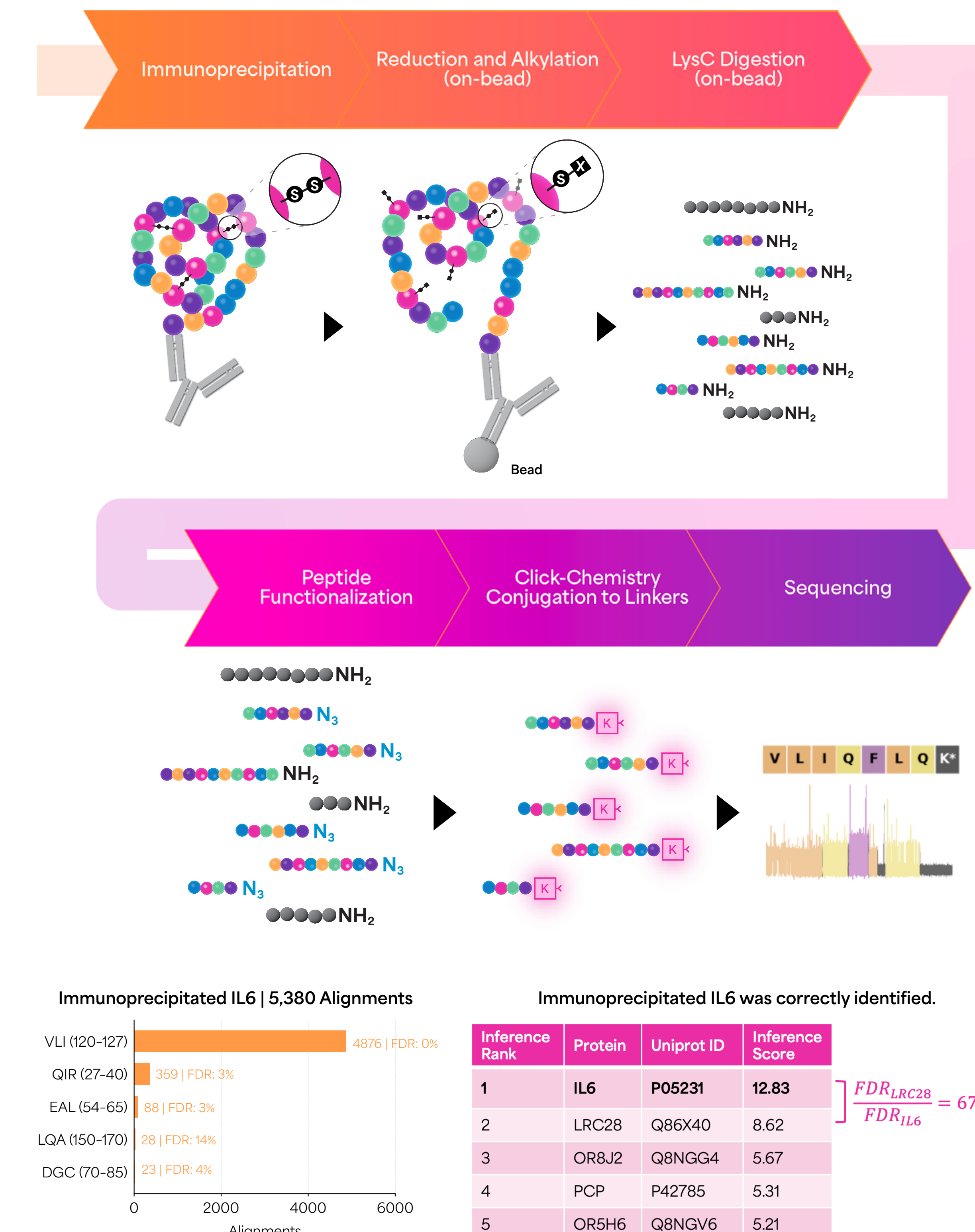
### Accurate Identification of Interleukins

A series of interleukins was successfully sequenced with Platinum either individually or within protein mixtures.



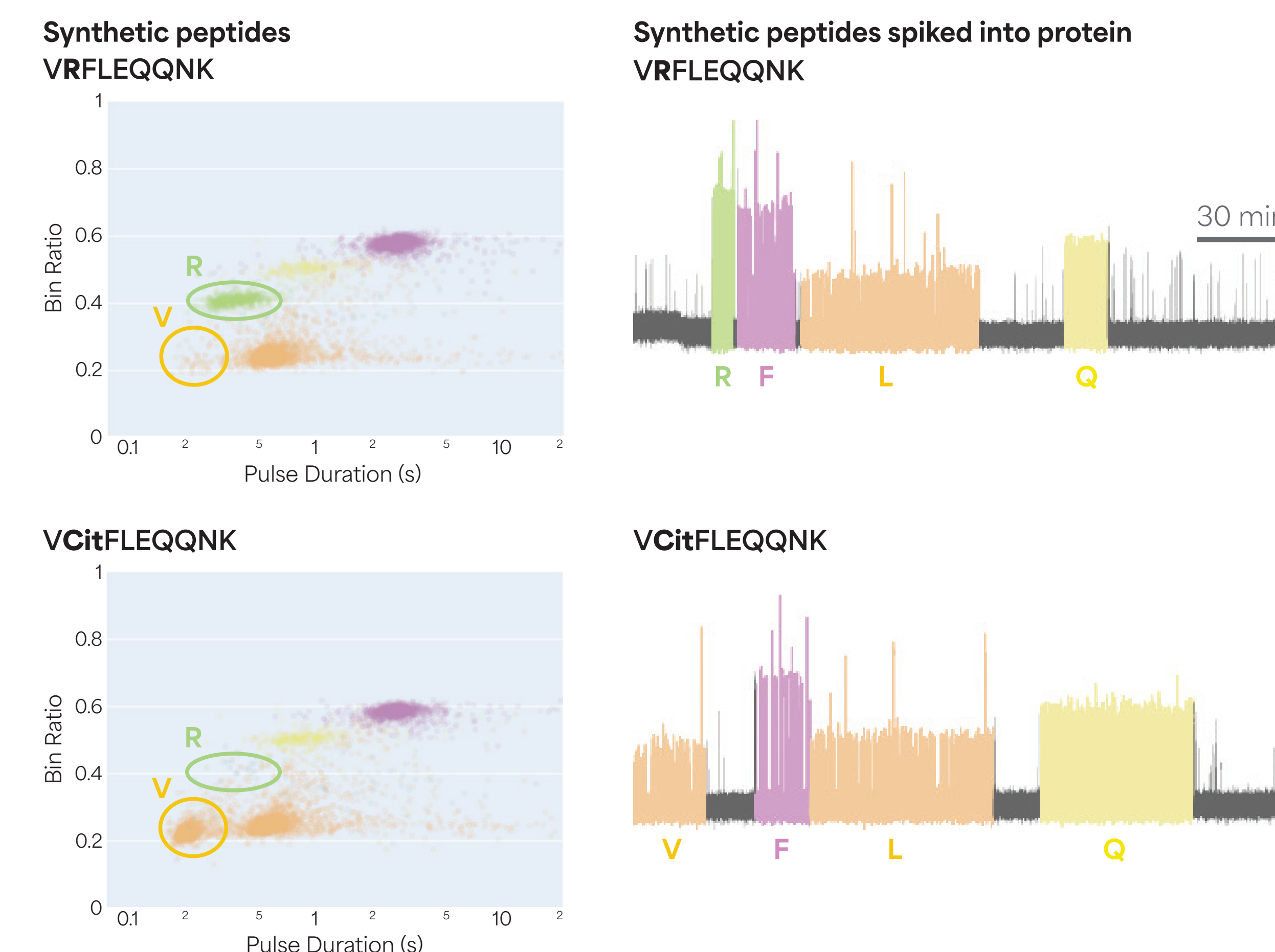
### Accurate Identification of IL6 Immunoprecipitated from Human Serum

IL6 immunoprecipitated from human serum was correctly identified as the top protein against an 7,921-protein reference panel.



### Detection of Arginine Citrullination from Peptides Derived from Vimentin

Citrullination led to the recognition of the first V residue, while the recognition of the second R residue was eliminated.



## REFERENCE

Brian D. Reed et al, Science 2022, 378 (6166) 186-192.  
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