QUANTUM SI™

DATA SHEET

Platinum® Pro Instrument and Sequencing Kit V3 Data Sheet

INTRODUCTION

Platinum Pro, the worlds first Next-Generation Protein Sequencer™, generates real-time single-molecule protein sequencing data, utilizing artificial intelligence and kinetic signatures to revolutionize our understanding of proteins in a user-friendly benchtop platform. Platinum Pro's sequencing approach creates a kinetic signature unique to the amino acid sequence based on direct interactions with N-terminal amino acid recognizers. Platinum Pro enables protein identification and variant detection without complex workflows or advanced expertise, making proteomics accessible for every lab.

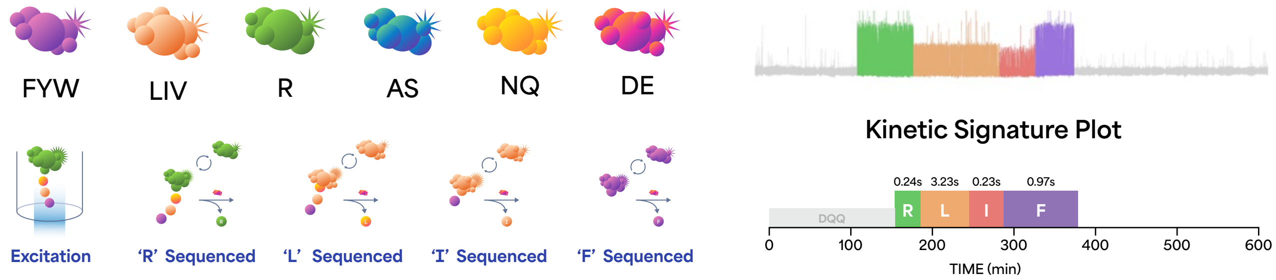


Figure 1. Kinetic signatures uniquely identify proteins and proteoforms. (A) Recognizers bind amino acids in a peptide sequence, then aminopeptidases cleave at each amino acid. The binding kinetics of each recognition event are captured over time. (B) The timing and order of recognition events generates a kinetic signature for each peptide across thousands of wells; this signature is then aligned to a reference sequence to identify the peptide.

ENHANCED PROTEIN INSIGHTS WITH SEQUENCING KIT V3

The Sequencing Kit V3 (Catalog # 910-00038-00) is the third generation of sequencing reagents and chips designed for the Platinum Pro instrument. With this upgraded chemistry, the power of our single-molecule sequencing is amplified by the addition of aspartic acid (D) recognition and improved performance of the LIV, NQ, and R recognizers. This augmented recognition, coupled with optimizations in reagent formulation and chip surface chemistry, enhances the performance of the Sequencing Kit V3 by delivering increases in amino acids detected, read depth, and protein identification. Through continuous and rapid enhancements to our technology, Quantum-Si ensures that users investing in Platinum Pro are always equipped with the most advanced tools to unlock new protein sequencing applications.

IMPROVEMENTS IN DETECTION YIELD MORE PEPTIDES IDENTIFIED

INCREASED PEPTIDES DETECTED

Enhancements in the amino acid calling and alignment algorithms in Sequencing Kit V3 have resulted in higher quality data calls, allowing richer data capture on the sequencer. As an example, programmed death ligand 1 (PDL1) was sequenced with Platinum, with a focus on the number of peptides detected with a false discovery rate (FDR) of <10%. With Sequencing Kit V2, 4 peptides with FDR <10% were detected. In contrast, with Sequencing Kit V3, for a similar number of ~6,000 total alignments, 6 peptides with FDR <10% were observed. (Figure 3).

Figure 2. Sequencing coverage of PDL1 (FDR <10) using Sequencing Kit V2 vs V3 on the Platinum instrument.

INCREASED READ LENGTH

When performing Next-Generation Protein Sequencing™ (NGPS) with Platinum Pro, read length refers to the average number of recognition segments observed for a given peptide. The higher the read length, the more coverage and information can be obtained for that peptide. To demonstrate an increase in read length using Sequencing Kit V3 compared to V2, we sequenced our control peptide mix. Component and formulation changes have resulted in an approximately two-fold increase in the read length per peptide when using Sequencing Kit V3.

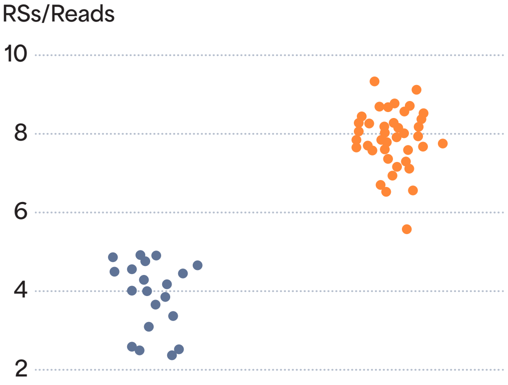


Figure 3. Plot of recognition segments (RS) per read demonstrates the read depth gains for a control peptide mix from Version 2 to Version 3 chemistry.

V Y Q F R D S R F N E Y L A Q K*

R F N E L Q F D I S R Y L A N K*

Q R Y N E L F A Q D I W R Y S K*

S Y L N E F V A Q L W R F N E K*

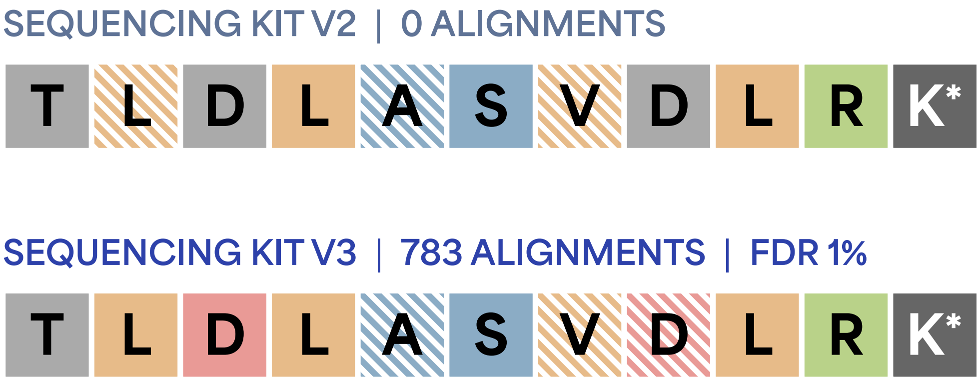
W L S D A I W R Y S E L F Q A K*

E I A R D Y L Q W S R I F E V A R L K*

Figure 4: The single control peptide previously used with V2 kits has been replaced with a new control peptide mix of 6 peptides to provide detection diversity and characterize read length detection increases enabled by the Sequencing Kit V3.

IMPROVEMENTS IN AMINO ACID DETECTION

The addition of D recognition, as well as improvements in other recognizers, has enabled the Platinum instrument to detect more peptides than ever before. As an example, we sequenced cerebral dopamine neurotrophic factor (CDNF) with Platinum, with a focus on the TLD (104-115) peptide, which was not detected with Sequencing Kit V2 (Figure 1). With Sequencing Kit V3, the introduction of D recognition, coupled with the improvements in the LIV recognizer, enabled strong detection of this peptide with 783 alignments and a false discovery rate (FDR) of 1% (Figure 1).



SEQUENCING KIT V2 | 0 ALIGNMENTS

T L D L A S V D L R K*

SEQUENCING KIT V3 | 783 ALIGNMENTS | FDR 1%

T L D L A S V D L R K*

Figure 5. Sequencing Kit V3 allows detection of the TLD (104-115) peptide in CDNF.

CONFIDENT PROTEIN ID THROUGH INFERENCE

Overall, enhancements in detection ability, read depth, and sequencing quality have resulted in a greater number of peptides detected in our representative sample set above. This improvement also enhances the confidence of accurate protein identification through the Platinum Analysis Software Protein Inference workflow.

The Protein Inference workflow compares the observed kinetic signatures from sequencing data to a database of predicted kinetic signatures from thousands of proteins in the human proteome. A protein Score is then calculated based on putative kinetic signature matches, and an estimate is provided of the likelihood that the sample contains a given protein.

V2 Sequencing Kit

Rank	Inferred Protein	Score	Likelihood
1	LMNB1	0.148507	13.8%
2	NRIP3	0.137489	12.84%
3	MERB1	0.051603	5.02%

V3 Sequencing Kit

Rank	Inferred Protein	Score	Likelihood
1	LMNB1	15.461991	99.99%
2	RAI2	0.844246	57.01%
3	THAP5	0.107635	10.2%

V2 Sequencing Kit

Rank	Inferred Protein	Score
1	NGAL	4.305186
2	LMNB1	2.537423
3	PARVB	0.882006
4	IL18R	0.38113
5	NRIP3	0.298326

V3 Sequencing Kit

Rank	Inferred Protein	Score
1	NGAL	9.339086
2	IL18R	1.730583
3	LMNB1	1.452077
4	IL6	1.249302

Figure 6. Sequencing Kit V3 improves the confidence of LMNB1 identification in a single protein sample and enhances the capability to confidently detect the NGAL, IL18, LMNB1, and IL6 as the most likely candidates in an equimolar mixture of the four proteins.

As seen in the tables above, the V3 Sequencing Kit demonstrates a leap forward in protein inference confidence compared to the V2 Sequencing Kit. For example, the LMNB1 protein inference not only increased in Score from 0.14 to 15.46 and Likelihood from 13.8% to 99.99%, but also showed a much larger separation of the top inferred protein from the second most likely protein. Furthermore, in an equimolar mixture of NGAL, IL18, LMNB1, and IL6, the inference workflow accurately detected all four proteins confidently using the V3 Sequencing Kit and accompanying software package.

These advancements are particularly valuable for researchers who need precise and reliable protein identification in high-resolution proteomic analysis. The noticeable increase in Scores, whether in single-protein or mixture scenarios, highlights the kit's superior performance across different research contexts.

Note: Scores may vary slightly between runs. Be sure to reference your specific results for the most accurate data.

WHERE CAN PROTEIN SEQUENCING TAKE YOUR RESEARCH?

Protein identification and inference powered by kinetic signatures is amplified by the addition of aspartic acid (D) recognition, enhancements to our kinetic database, and our A.I.-powered software model. The ability to sequence proteins accurately using kinetic signatures unlocks new possibilities in proteomics, as demonstrated in our application notes for barcoding, biomarker detection, and whole human serum protein identification.

PLATINUM SPECIFICATIONS

Instrument dimensions*	19.45 × 8.46 x 9.91 in 49.39 × 21.50 x 25.18 cm
Bench space	26.00 × 17.00 x 16.00 in 66.04 × 43.18 x 40.64 cm
Weight	27 lb (12 kg)
Power Cable (included)	IEC 60320 C13 connector (IEC 60320 C14 inlet)
Fuses	250VAC 10A Fuse (2)
On-Board Storage	456 GB
Temperature	15–25°C 59–77°F
Humidity	35–55%

ORDERING INFORMATION

Product	Catalog Number
Platinum Instrument	910-10904-00
Sequencing Kit V3	910-00038-00