Identifying Cancer-Specific Proteins Using Next-Gen Protein Sequencing™ (NGPS™)

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Challenge: Investigating the mechanisms of non-response to cancer therapies using expensive tools such as mass spectrometry, which have long turnaround times and often struggle to detect subtle protein variations

Innovation: A platform that identifies novel cancer-specific targets and potential antibody drug candidates by comparing cancer proteins with those in healthy tissue

NGPS Integration: Used alongside mass spectrometry, offering orthogonal data for target validation, which is confirmed using CRISPR knockout experiments

Advantages: Accessible with single-molecule resolution, NGPS detects subtle protein variations and provides a detailed view of cancer-specific proteins, accelerating discovery timelines in oncology research

Q: Can you tell us about Sanavia and the importance of protein sequencing?

A: Sanavia Oncology is an oncology company focused on developing antibody therapeutics targeting novel cancer markers. Our platform enables discovery of cancer-specific targets and antibodies against these targets. My role covers all aspects of protein science, from generating and characterizing protein targets to solving their structures and understanding their roles in cancer.

Our interest in NGPS using the Quantum-Si's Platinum® instrument stems from our need to better characterize novel cancer targets. Although we're still in the early stages of adopting the technology, we see it as a crucial tool in our target identification workflow.

Q: What challenges led you to explore protein sequencing with the Platinum instrument?

A: A major challenge in oncology is understanding why some cancer patients do not respond to current therapies. Our platform helps us explore novel cancer-specific targets in those patients and identify potential antibody drug candidates. However, to fully understand our targets and their mechanisms of action, we need to examine how cancer proteins differ from normal ones.

While mass spectrometry is a powerful tool for proteomics, it has limitations. We see Platinum technology as an approach that could enhance our ability to characterize these cancer-specific proteins, ultimately making our research more efficient.

Q: How is Platinum being integrated into your workflow?

A: In our target identification workflow, our samples are typically analyzed by mass spec, but as an early-stage biotech with limited capital and physical space, we don't have internal MS capabilities and so we are currently outsourcing to a core MS facility with long turnaround times.

Having the Platinum instrument allows us to run parallel analyses for cross-validation. By using mass spec and protein sequencing as orthogonal approaches, we gain greater confidence in our data. Once we identify a promising target, we validate it using techniques like CRISPR knockout experiments. Overall, this workflow helps us understand how cancer-specific proteins contribute to disease progression.

Q: What has your experience with the Platinum instrument been like so far?

A: From our initial evaluation to its purchase, installation, and training, the experience has been very positive. The support team, including our field applications scientist, has been extremely helpful.

Q: What is your long-term vision for the Platinum instrument in your research?

A: Our goal is to rapidly and accurately characterize cancer targets to develop better therapies. The ability of the Platinum instrument to provide single-molecule sequencing offers a detailed view of protein variation within samples, helping us understand why certain targets are crucial for cancer progression.

The combination of speed and detailed molecular insights is invaluable in oncology, where each cancer type, and sometimes each patient, presents unique protein expression patterns. As we refine our approach, I see Platinum playing a key role in accelerating discoveries and making our research more impactful. And I'm excited to see where Quantum-Si takes this technology. There are clear opportunities for increased automation, higher throughput, and even richer data analysis. Protein sequencing is a unique and valuable tool in our research, and I look forward to future advancements that will further enhance its capabilities.