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SPECIFIC PROTEIN MEASUREMENT AND QUANTITATION USING TUNABLE LASER SPECTROSCOPY

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SUMMARY

While UV-Vis spectroscopic analysis is commonly used to measure protein concentration, it struggles to accurately quantify protein titer exceeding 100 mg/mL without dilution. However, as monoclonal antibody (mAb) formulations are trending towards significantly higher concentrations (for instance, 200-300 mg/mL), the Nirrin NXT has emerged as a simpler solution. This system utilizes a tunable laser and relies on near-infrared (NIR) spectroscopy to generate a unique and quantifiable protein signature. It offers wide dynamic range, accuracy, and precision, all without the need for dilution.

EXPERIMENTAL PROCEDURE

A sample containing 100 mg/mL of a commercial mAb in a 20mM Histidine buffer (pH adjusted with HCl) was prepared and measured using an NXT

prototype following the protocol below. The sample was then analyzed using the NXT software and a validated NISTmAb spectrum from the embedded library. Next, the sample spectrum was re-analyzed using a Nirrin

patented mAb characterization protocol and a unique software-generated mAb spectrum for the drug substance.

- 1. Pipette 15 µL of deionized water on the sample pedestal and scan (background)
- 2. Clean with Kimwipe
- 3. Pipette 15 µL of sample and scan (in seconds)
- 4. Select analytes for quantitation, run analysis, and obtain quantitative results

RESULTS: THE EFFECT OF MAB SPECIFICITY ON EXCIPIENT MEASUREMENTS



Illuminating insights

CONCLUSIONS

The Nirrin NXT tunable laser platform and patented mAb characterization protocol can generate a unique NIR spectral signature for a drug product. Using a NISTmAb library spectrum, the system accurately predicted the concentration of a proprietary mAb product, but excipient concentrations did not match the sample formulation. The Nirrin patented mAb characterization calculated a unique spectral signature of the proprietary mAb, enabling an accurate concentration determination for both protein and excipient components. NXT is the first-in-class, at-line solution for quantitative protein and excipient measurements in downstream bioprocessing.

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