Apollo

POWERED BY MMS TECHNOLOGY

Your Solution to Protein Characterization has Landed

REDSHIFTBio®
See change®

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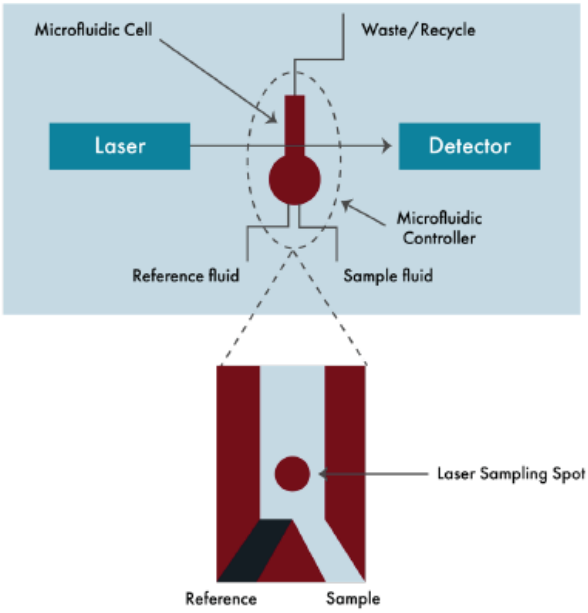
What is MMS Technology?

- Novel, fully automated technique providing ultra-sensitive, ultra-precise structural measurements of proteins and biomolecules
- Accurate and reproducible measurements with broad concentration range from 0.1 mg/ml to >200 mg/ml allows measurements in native conditions
- 20x faster and 30x more sensitive to changes in structure than CD or FTIR*
- Real-time buffer subtraction minimizes background noise and interference from excipients



Why add MMS into your development workflow?

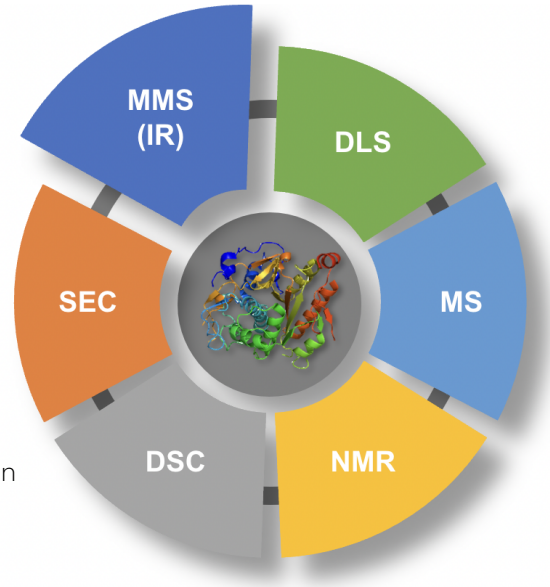
DISCOVERY: Incorporate structural monitoring to add more robust selection criteria for candidate screening.

FORMULATION: Automatically analyze and compare samples across a formulation study to predictively identify optimal buffer formulations, stability profiles, and storage conditions before locking in conditions eliminating costly downstream failures.

MANUFACTURING: Track stability and structure as Critical Quality Attributes (CQAs) across the entire manufacturing process to guarantee safety, efficacy, and functionality.

The BENEFITS of measuring HIGHER ORDER STRUCTURE

- Track and maintain the critical relationship between structure and function from Discovery to Formulation to Manufacturing securing a faster route to market
- Identify conditions and process steps that introduce undesired structural changes or aggregation due to intermolecular interactions
- Add meaning to changes in activity due to detected changes in folding at the secondary structural level
- Improve quality through all stages of the development process by monitoring stability and similarity

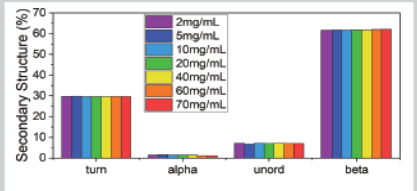


How MMS adds value to your development toolkit

By incorporating MMS into your analytical suite of tools, you will add the value of monitoring stability, structure, similarity, and intermolecular aggregation all measured from a single automated run powered by ultra-high precision fluidics and detection, and processed using a state-of-the-art intuitive analytical engine.

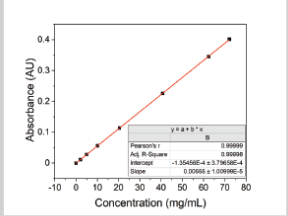
*Journal of Pharmaceutical Sciences, JAN 2020

Higher Order Structure



HOS and Quantitation results from a concentration series of NIST mAb RM 8671 showing the linearity and consistent structural populations for samples ranging from 2 - 70 mg/mL

Quantitation

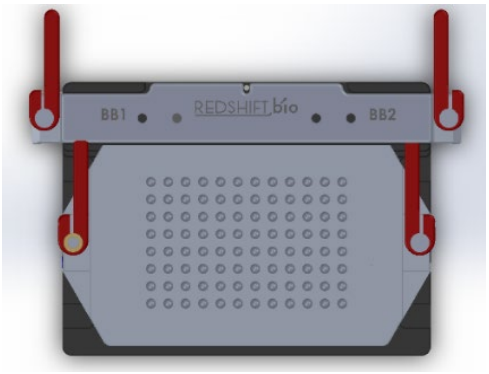


Introducing **Apollo,** Powered by **MMS** Technology

Apollo, RedShiftBio's second generation flagship system, features novel MMS technology and is your solution to structural characterization. **Apollo** is purpose-built to deliver ultra-sensitive, ultra-precise structural measurements of biomolecules informing you about the integrity of your biomolecules - with **CONFIDENCE**.

Key Features and Benefits of Apollo

- Analyze up to 47 samples in triplicate for structure, similarity, and stability on a completely automated, walk-away platform
- Characterize the HOS for a wide range of biomolecules including proteins, peptides, antibodies, mRNA, ADCs, and AAVs to identify and predict structural changes that may occur under development, formulation, and storage conditions
- Compare HOS and similarity profiles for biosimilars, innovators, parent, and variant compounds for confidence in structural similarity and activity to inform screening activities upstream and formulation development downstream



96-Well Carrier featuring Buffer Station

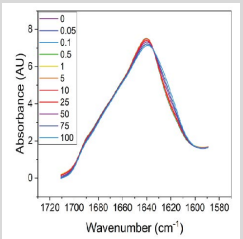
- Save time and money by collecting spectral data in individual wavenumber increments across the Amide I band to monitor and detect undesired changes at any point during drug development and manufacturing
- Balance sensitivity with precision for high and low viscosity samples via flexible 96- and 24-well plate formats
- Free-up valuable time by scheduling routine maintenance such as system washing, laser calibration, and error handling to run unattended

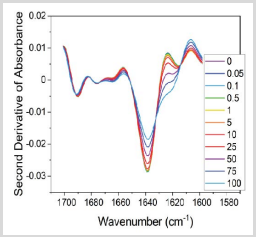
delta - the key to ***optimal*** SPECTRAL ANALYSIS

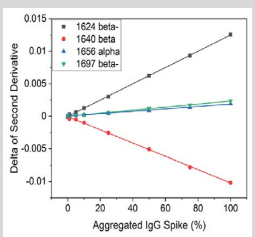
The analytical engine behind the MMS hardware is **delta**, the processing software with an easy-to-use interface designed to generate high-quality, comparative spectral results to inform you about the stability and structure of your biomolecules.

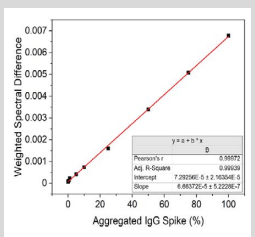
- Automatic generation of differential, background subtracted spectra with no subjective intervention
- Intuitive user interface for analysis of IR spectra including second derivative analysis, similarity by area of overlap, weighted spectral difference (WSD), principal component analysis (PCA), and higher order structure (HOS)
- Easily compare HOS and the similarity profiles for all samples, tracking the parameters that are most relevant to your study

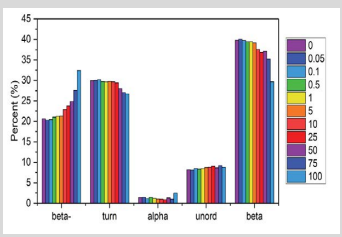
Absolute Absorbance, 2nd Derivative, Changes in Structural Motifs, WSD, and HOS results for Aggregated IgG











System Specifications

System Summary

Measurement Method	Microfluidic Modulation Spectroscopy
Measurement Type Supported	Mid-Infrared Absorption
Protein Measurements	Secondary Structure, Similarity, Stability, Intermolecular Aggregation, Quantitation

Automation and Hardware

Well Plate Formats	96-Well and 24-Well Plate Formats
Additional Buffer Station	Available for 96-Well Plate; 25 mL capacity for 2 Additional Buffers
Protocol Generator	Protocol Editor and Quick Start to Schedule Runs and Maintenance
Performance Verification	System Suitability Test
Maintenance	Integrated Wash Station, System Cleaning, and Laser Calibration
Plate Cooling	Optional 10°C Hold Temperature (96-Well Only)

Optical Source and Detector

Optical Source	Quantum Cascade Laser
Spectral Range	1590 - 1710 cm^{-1}
Detector	TE cooled MCT (liquid nitrogen free)
Microfluidic Cell	Replaceable

Software

Control and Analytics	delta software with 21 CFR Part 11 Support (optional upgrade)
Operating System Data	Windows 10 and 11 Compatible
Export Data Format	Comma-Separated Values (.csv)

Sample

Concentration Range	0.1 to 200 mg/mL
Repeatability	>98% for 2 mg/mL Lysozyme in Water (Area of Overlap)
Replicates per Well	3 (96-Well); >3 (24-Well)
Nominal Volume per Replicate	50 uL per Replicate
Typical Analysis Time for 3 Replicates	18 minutes
Plate Capacity	47 unique samples in same buffer per 96-well plate

Dimensions and Weights

Analyzer Unit	22 H x 18.25 W x 18.5 D, 80 lbs
Electronics Unit	25 H x 10.5 W x 18 D, 40 lbs

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