AQS³™ pro

See change™ in
protein characterization

REDSHIFTbio™

The AQS³pro: A new spectroscopy platform for protein characterization

See change

- In how you make measurements, analyze data and present information
- In your ability to detect and monitor structural change
- In your efficiency

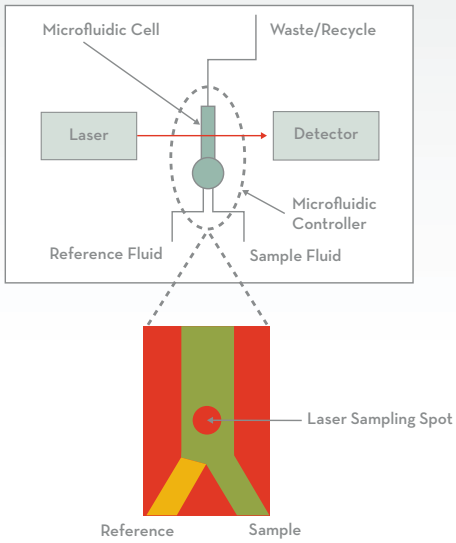


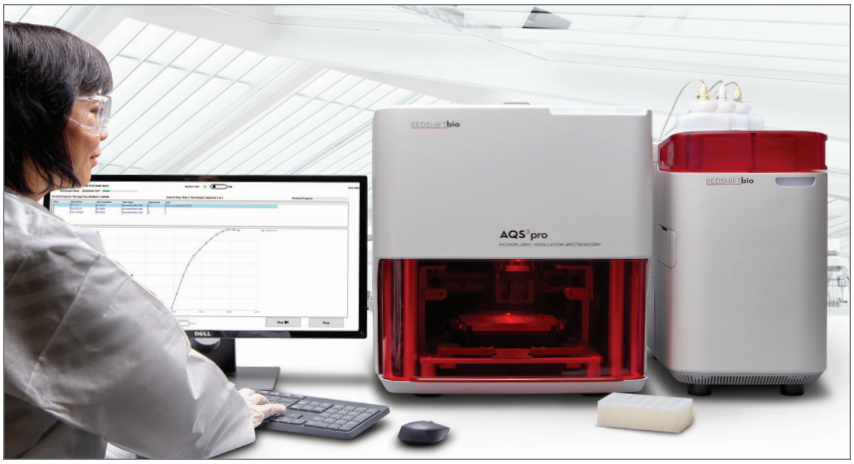
Diagram of the platform shows the tunable laser which probes the protein solution through a microfluidic cell. The microfluidic cell rapidly alternates between sample and reference (buffer) streams to continuously and automatically perform background subtraction which dramatically improves measurement precision, accuracy, and signal-to-noise.

The advantages of Microfluidic Modulation Spectroscopy (MMS)

MMS is a novel and efficient technique for label-free protein analysis that directly addresses the limitations of current technologies. MMS provides drift-free, background subtracted, high sensitivity measurements of the secondary structure of proteins across four decades of concentration—from 0.1 to > 200 mg/mL.

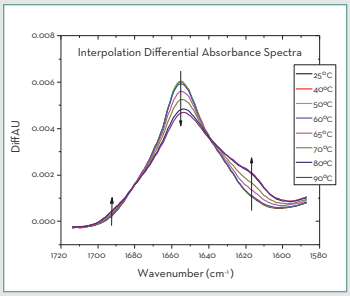
- Automated multi-sample analysis for walk away operation
- Increased sensitivity to see change reproducibly and in fine detail
- The widest concentration range to characterize biotherapeutics
- Analytical software that easily transitions data into insight

The AQS³™pro will change how you measure protein and peptide structure. Powered by MMS, it ramps up the sensitivity, dynamic range, accuracy and utility of IR spectroscopy. Designed for five key measurements—aggregation, quantitation, stability, similarity, structure—the AQS³pro directly supports protein research and progress through the biopharmaceutical development pipeline.



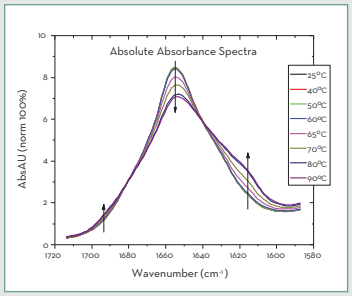
RedShiftBio's MMS system features a powerful analytics package which quickly and easily processes data.

Data Flow Analysis of BSA at 1.0 mg/mL



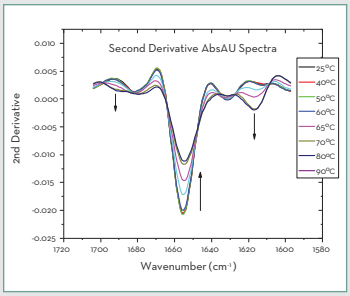
Differential Absorbance Spectra >

Continuous, rapid modulation between the sample solution and buffer reference streams produces a differential absorbance signal.



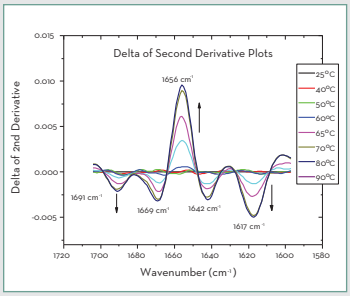
Absolute Absorbance Spectra >

Buffer subtraction and concentration normalization enable direct protein-protein structural comparisons.



Second Derivative Spectra >

Second derivative spectra accentuate the specific structural differences between protein samples.



Delta of Second Derivative >

Delta of second derivative plots highlight structural differences and change in protein samples.

The AQS³pro: Redefines your protein characterization workflow

Sensitivity

The inherent advantages of MMS, combined with the optical design of the instrument and automated protocols give the AQS³pro sensitivity well beyond that of other spectroscopic systems. When sensitivity is increased, you can be more confident that the differences you measure are real. Whether you are looking for the onset of aggregation, small similarity differences, or process-induced structural changes, the AQS³pro boosts the sensitivity of IR spectroscopy, significantly enhancing its value for biologic characterization.

Dynamic range

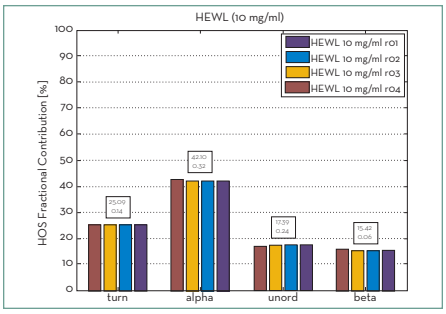
As a drug candidate progresses through the biopharmaceutical pipeline, sample characteristics change, especially in concentration. The AQS³pro measures over a much wider concentration range than most other protein characterization techniques, without sample dilution or concentration. So instead of changing techniques as your sample concentration changes, eliminate the need for multiple instruments and create more coherent and consistent datasets.

Automation

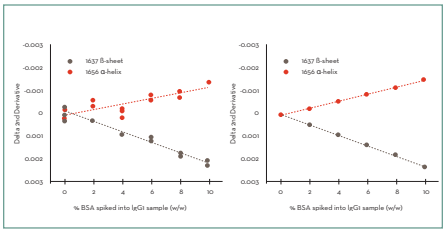
The AQS³pro is highly automated for walkaway operation, to maximize your productivity. With a multi-sample autosampler and intuitive software that streamlines your analytical workflow—from running samples to data processing—it delivers reproducible results you can trust, with significantly reduced labor requirement.

AQS³delta analytical software

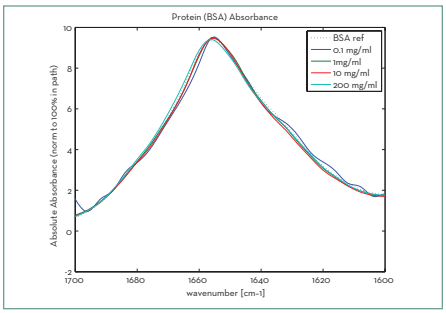
The AQS³pro is perfectly paired with AQS³delta software which provides a suite of analytical tools that capitalizes on your high quality data. These deliver consistent, fully traceable results in seconds. Concerned about stability? Then track changes between spectra, at individual locations or across structural motifs. Or analyze similarity with the Area of Overlap tool. Take a look at the data flow analysis below to see how the AQS³delta software processes and presents data to maximize its value.



MMS has excellent repeatability. (Hen Egg White Lysozyme @10mg/mL over 30 days



In a 'spike' experiment, MMS (right) is demonstrably more sensitive for the detection of Bovine Serum Albumin (BSA—predominantly α-helix structure) in Immunoglobulin (IgG1—predominantly β-sheet structure) than conventional FTIR (left)



MMS has a very wide dynamic range (BSA measurements at concentrations in the range 0.1 to > 200 mg/mL).

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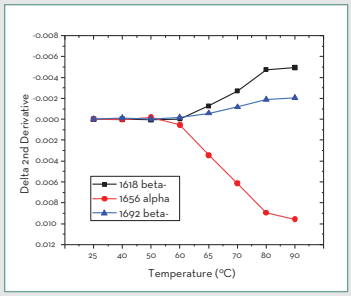
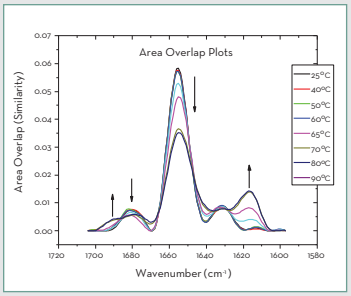


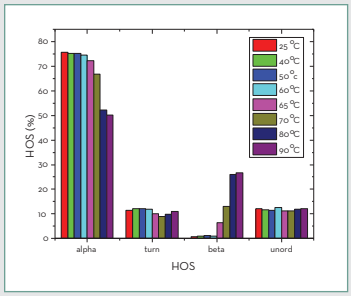
Stability >

Protein stability can be assessed by tracking changes in secondary structure motifs.



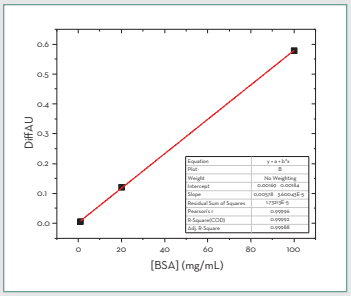
Similarity >

Protein similarity can be compared using area of overlap plots.



Higher Order Structure >

Higher order structure analysis quantifies the fractional content of different secondary structure motifs.



Quantitation

Proteins can be quantified over a linear concentration range that extends from 0.01 to > 200 mg/mL.

See change™

AQS³™ pro

System Summary	
Measurement Method	Microfluidic Modulation Spectroscopy
Measurement Type	Mid-infrared absorption spectroscopy
Supported Protein Measurements	Secondary structure, similarity, chemical and quenched thermal stability, aggregation, quantitation
Fraction Collection	Supports most common collectors
Automation	
Well Plate	24 wells (12 sample pairs)
Calibration and Cleaning	Integral wash, cleaning and calibration
Optical Source and Detector	
Optical Source	Continuous wave quantum cascade laser
Spectral Range	1590–1710 cm^{-1}
Detector	TE cooled MCT (liquid nitrogen free)
Microfluidic Cell	User replaceable
Software	
Operating System	Windows
File Format	CSV
Analytics	AQS³delta
Physical Characteristics–Nominal	
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
Sample	
Concentration for Structure	0.1 – > 200 mg/mL
Concentration for Quantitation	0.01 – > 200 mg/mL
Typical Repeatabilitiy	> 98% at 1 mg/mL (area of overlap)
Structure (HOS) Repeatability	1% at 1.0 mg/mL (1σ)

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Class 1 Laser Device Complies with 21 CFR Chapter 1, Subchapter J, Part 1040.10

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