Aurora

POWERED BY MMS TECHNOLOGY

The One-Drop Protein Characterization Solution

Precise, Automated, and Ultra-Sensitive Biomolecule Characterization

REDSHIFTBio

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Introducing Aurora, powered by MMS Technology

Aurora is purpose-built to deliver ultra-sensitive and precise higher order structure measurements of your biomolecules from one drop of sample - with **CONFIDENCE.**

What is MMS Technology?

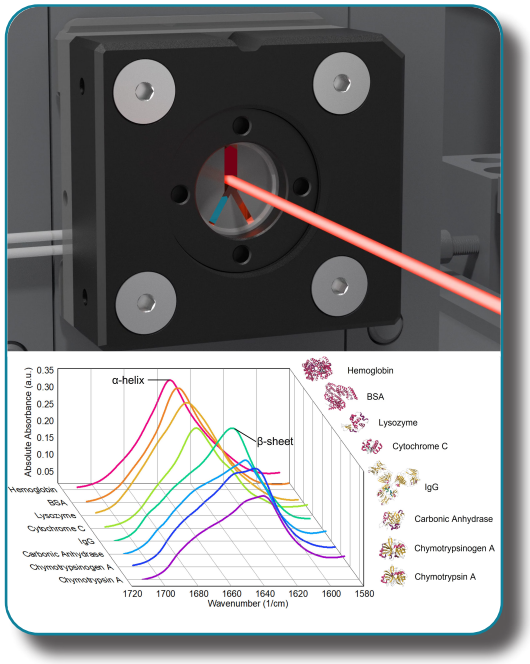
Microfluidic Modulation Spectroscopy (MMS) combines a Quantum Cascade Laser, a microfluidic flow cell, and a powerful software package to produce high resolution secondary structure information about your biomolecules of interest.

This novel and fully-automated technique generates ultra-sensitive and precise structural measurements of your biomolecules, including proteins, nucleic acids, AAVs, biotherapeutics, and binding events. MMS generates a high resolution, 1 wavenumber spacing, differential absorbance spectrum across the Amide I region.

MMS directly addresses the limitations of traditional spectroscopic methods by enabling direct, label-free analysis over a wide concentration range in complex buffer formulations, without the need to buffer exchange or dilute your precious samples.

Why MMS Technology?

- Accurate and reproducible measurements across a broad concentration range from 0.1mg/mL to >200mg/mL.
- Real-time buffer/background subtraction enables structural analysis under relevant conditions, without needing to buffer exchange.
- High resolution IR spectra of Amide I region.
- Walkaway automation with the convenience of a standard 96-well plate.



How MMS adds value to your research

By incorporating MMS into your suite of analytical tools, you will add the value of monitoring stability, structure, similarity, and intermolecular aggregation - all measured from a single automated run, with only **one drop** of sample and analyzed with a simple, state-of-the-art spectral analysis engine.

Key Features and Benefits of Aurora

Minimal quantities of precious samples are no longer a limitation

- 50µL of sample at 0.1mg/mL is all you need for highly reproducible data

The secondary structure characterization tool for all your applications

- Characterize the HOS of a wide range of biomolecules including proteins, peptides, antibodies, mRNA, ADCs, and AAVs by measuring structural changes due to buffer/pH/formulation, stress, point mutations, binding partners, and storage conditions.
- Save time and money by collecting spectral data, under experimentally/therapeutically relevant conditions; no need to buffer exchange or dilute prior to measuring.

Benchtop-friendly Design

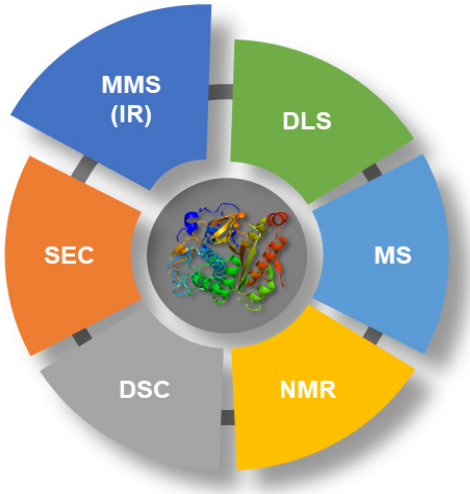
- Space-saving, all-in-one analytical unit with integrated touchscreen.
- Intuitive user interface provides at-a-glance-determination of run status.

Complete automation from sample analysis to data processing

- Reduce user error with minimal sample manipulations
- Monitor the critical relationship between structure and function in less time, with higher-quality data
- Simple automation minimizes training and removes the need for dedicated super users.
- No spectroscopy expertise required- *delta* software analyzes the data and provides meaningful conclusions.

The **BENEFITS** of measuring **HIGHER ORDER STRUCTURE**

- Track and maintain the critical relationship between structure and function.
- Identify conditions and processes that introduce undesired structural changes or aggregation.
- Test mechanistic hypotheses behind changes in activity and stability with structural information.
- Publish sooner and finish projects on-time with high repeatability and sensitivity minimizing inconclusive results and reliance upon orthogonal techniques.



Why add Aurora into your laboratory?

ACADEMIC RESEARCH:

Frustrated by FTIR and CD?

- Aurora gives high quality and reproducible results without the challenges and limitations of historical secondary structure tools.

Limited by how much material you can express or purify?

- Aurora only requires 50µL of sample for triplicate measurements at a concentration as low as 0.1 mg/mL.

Not a spectroscopy or protein structure expert?

- No problem, ***delta*** software analyzes the data and provides the answers you need.

Challenged by a need to train new students and post-docs or sending your samples to the core for analysis?

- Not anymore, just pipette your sample and matched buffer into a standard 96-well plate and the Aurora wizard walks you through getting your run started.

Looking to generate experimental data to support a computational program?

- Aurora is easy to use, requires minimal sample, and automation makes it a breeze to generate a lot of data very quickly.

PHARMACEUTICAL LABORATORY:

Want to add high quality structural assessment earlier in the drug development process?

- Aurora only needs 50µL of sample so you can add structure determination earlier in development, ensuring only the best candidates move forward.

Struggling to perform formulation screens because of buffer incompatibilities or low throughput platforms?

- Aurora is highly automated and widely buffer compatible, enabling broad buffer screens and ***delta*** software makes it easy to compare samples from a formulation screen to identify optimal formulations, stability profiles, and storage conditions, minimizing costly downstream failures.

Need to measure Critical Quality Attributes (CQAs) and verify lot-to-lot reproducibility?

- Aurora's reproducibility and ability to measure higher order structure in formulation buffer at formulation concentration enables you to collect the data you need for your regulatory filings for biologic drugs.

Working with biosimilars and need to compare HOS with originator molecules in formulation buffer?

- Aurora enables comparisons between biosimilar and originator molecules at formulation concentration and in formulation buffer, with exceptional reproducibility; yielding high confidence results.

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

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