

# AuroraTX<sup>↑</sup>

POWERED BY MMS

## Thermal Ramping Characterization Solution

*Cleaner, Faster, More Critical Biophysical Insights into RNA, Proteins, and More*



**REDSHIFTBio<sup>↑</sup>**

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# Introducing **Aurora TX**, powered by MMS Technology

**Aurora TX** is designed to deliver ultra-sensitive, fully-automated, and precise structural measurements of a wide range of biomolecules from one drop of sample - with **COMPLETE ACCURACY**.

## 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.

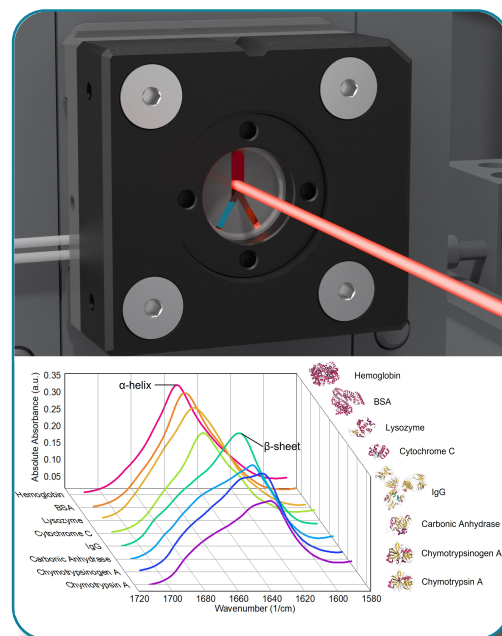
This novel and fully-automated technique generates ultra-sensitive and precise structural measurements of your biomolecules, including RNA, proteins, biotherapeutics, peptides, AAVs, binding, and more. MMS generates a high resolution differential absorbance spectrum across the data-rich mid-IR fingerprint region. Now, with **thermal ramping** capability, you can assess stability even more closely to unlock even greater insights.

MMS directly addresses the limitations of traditional spectroscopic methods by enabling easy-to-perform, label-free analysis over a wide concentration range in complex buffer formulations, without the need for buffer exchange, dilution of precious samples, or spectroscopy expertise.



## Why MMS Technology?

- ▶ Accurate and reproducible measurements across a broad concentration range from 0.1 mg/mL to >200mg/mL.
- ▶ Real-time buffer/background subtraction enables structural analysis under relevant conditions, without needing to buffer exchange.
- ▶ No spectroscopy expertise or complicated sample preparation required.
- ▶ 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, intermolecular aggregation, and concentration - 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 TX

### Gain more insights into your precious samples

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

### The secondary structure characterization tool for all your applications

- Characterize the structure of a wide range of biomolecules including RNA, LNPs, proteins, peptides, antibodies, ADCs, and AAVs by measuring change in stability due to buffer/pH/formulation, stress, point mutations, binding, and storage time/conditions.
- Save time and money by collecting spectral data, under experimentally/therapeutically relevant conditions; no need to buffer exchange or dilute prior to measuring.
- Thermal ramping applies stress in a repeatable and automated fashion to induce structural change and guide decision-making and candidate ranking, saving valuable R&D time.

### Benchtop-friendly Design

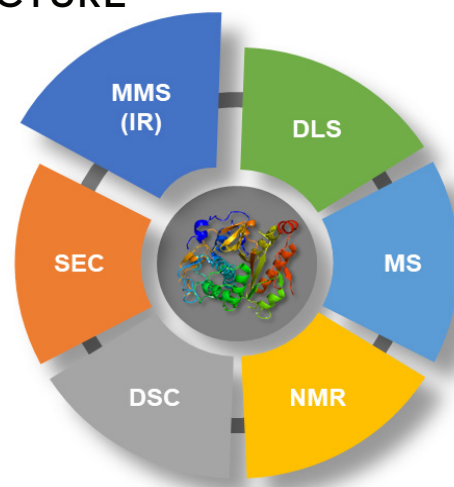
- Space-saving, all-in-one analytical unit with integrated touchscreen.
- Intuitive user interface provides at-a-glance-determination of run status.
- Streamlined optional buffer station enhances throughput by integrating up to 8 buffers directly into the system during analysis.

### 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.
- Full automation minimizes training and removes the need for dedicated super users.
- No spectroscopy expertise required to interpret results- *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.





## RNA and LNP analysis with MMS

Aurora TX, powered by Microfluidic Modulation Spectroscopy, presents a pioneering strategy for RNA structure analysis. Aurora TX makes analyzing RNA structure a breeze, utilizing nearly drift-free, background-compensated scans of the Amide I band (1700-1600  $\text{cm}^{-1}$ ), typically used on proteins, but also ideal for nucleic acid characterization. Unlike conventional methods, Aurora TX provides unparalleled sensitivity and precision, effortlessly overcoming challenges of traditional spectroscopic techniques, such as manual workflows, buffer interference and background subtraction. This enables easy detection and comparison of RNA changes that are vital for therapeutic development. Our technology also boasts the capability to deliver multiple measurements in a single analysis, unveiling a wealth of insights including structural changes, stability, concentration variations, and RNA-to-LNP ratio, all with walk-away automation. Furthermore, robust *delta* software offers you an uncomplicated approach to RNA structural data collection and interpretation of results.

## Why add Aurora TX into your laboratory?

### PHARMACEUTICAL LABORATORY:

- Aurora TX allows you to add high quality structural assessment earlier in the development process, regardless of whether your project is related to drug, nucleic acid, or vaccine development. Only 50 $\mu\text{L}$  of sample enables structure determination at an early stage, ensuring only your best candidates move forward.
- Aurora TX eliminates the struggle to perform formulation screens because it is fully automated and widely buffer compatible, enabling broad buffer screens and higher throughput. *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.
- Aurora TX's reproducibility and ability to assess Critical Quality Attributes (CQAs) and verify lot-to-lot consistency. You can measure higher order structure in formulation buffer at formulation concentration, so you can collect the data you need for your regulatory filings for biologic drugs.
- Aurora TX enables HOS and stability comparisons between biosimilar and originator molecules at formulation concentration and in formulation buffer, with exceptional reproducibility and the ability to thermal ramp; yielding high-confidence results.

### ACADEMIC RESEARCH:

- Aurora TX gives high quality, reproducible results, and thermal ramping capability without the challenges and limitations of historical secondary structure tools like CD and FTIR.
- Only 50 $\mu\text{L}$  of sample for triplicate measurements at a concentration as low as 0.1 mg/mL.
- No spectroscopy expertise needed, *delta* software analyzes the data and provides the answers you need. Aurora TX is easy to use, and automation makes it a breeze to generate a lot of data quickly for any application, including generation of experimental data to support a computational program.
- Minimal training required, just pipette your sample and matched buffer into a standard 96-well plate and the Aurora TX wizard walks you through getting your run started. Additionally the optional buffer station can enhance the ease of use and sample throughput.

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

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