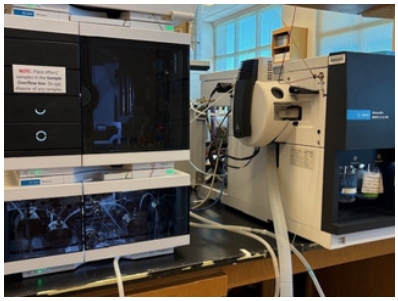
ISSUE #02

EGMIC Monthly Newsletter

EMORY UNIVERSITY
Emory Glycomics and Molecular Interactions Core
Emory Integrated Core Facilities

TECHNOLOGY HIGHLIGHT:

USING AGILENT 6545XT ADVANCEDBIO LC/MS Q-TOF TO CHARACTERIZE BOTH MAJOR AND MINOR INTACT PROTEIN VARIATIONS WITH <10 PPM ACCURACY



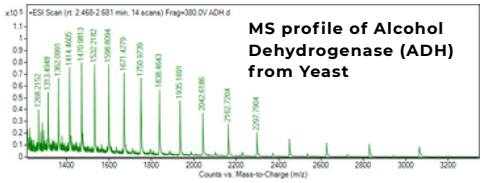
✦ July 2025

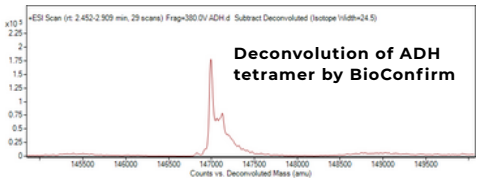
Mass Spectrometry for Intact Protein Analysis

Our core facility offers LC/MS analysis of protein samples using the Agilent 1290 Infinity II LC system coupled with the 6545XT AdvancedBio LC/Q-TOF, equipped with an Agilent Jet Stream Source. The 6545XT's extended mass range enables highly sensitive detection and in-depth characterization of native proteins, intact proteins, and noncovalent protein complexes. Its exceptional mass accuracy and resolution in the high-mass range make it an ideal tool for advanced protein analysis.

All raw mass spectrometry (m/z) data are processed using Agilent MassHunter Qualitative Analysis software. The molecular weight of proteins and their complexes is determined through a deconvolution process, using either Agilent BioConfirm or the iFAMS program.

For more information or to schedule an analysis, please contact our team.





	Native Protein	Intact Protein
Application	• Protein in Naïve stage • noncovalent protein complex	• Protein • protein sub units
LC setting	• Size Exclusion Chromatography (SEC) column, • Aqueous buffer at neutral pH such as 100 mM ammonium acetate, pH 7	• PLRP-S column (C18 column) • Binary buffer system with organic solvent with acid. For example: A: Water with 0.1% Formic Acid, B: Acetonitrile with 0.1% Formic Acid
Sample preparation	• Needs to preserve the protein sample at neutral pH and volatile aqueous solution such as ammonium acetate or ammonium format. Sample desalting and buffer exchange are needed before MS analysis. • Inject 1 - 5 µL of protein at 1 to 10 µg/µL.	• No special preparation is needed. Organic solvent and acid buffer enhance sample desolvation and ionization. • 0.5 µL of protein at 1 – 10 µg/µL, or 0.5 µg protein
MS results	Fewer charges and low abundance	High abundance

Software update

New BioConfirm Software Version 12.0 Now Available

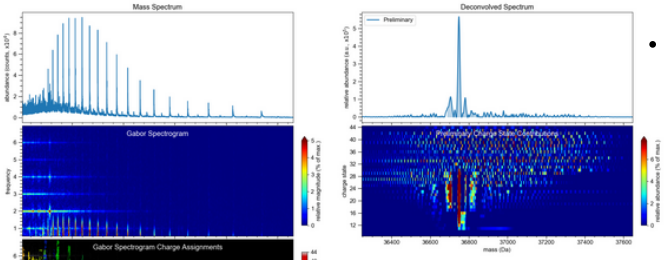
We're pleased to announce that Agilent BioConfirm analysis software version 12.0 has been installed on the data analysis workstation in our core facility. This latest version offers enhanced customization options for user preferences and workflows. A quick reference guide for using the new version is posted next to the workstation, and a full user manual is available on the desk for your convenience.

Please note: Older versions (v10.0 and v11.0) of BioConfirm remain available on the computer connected to the LC/Q-TOF instrument for compatibility and continuity. If you have any questions or need assistance, feel free to reach out to our team.

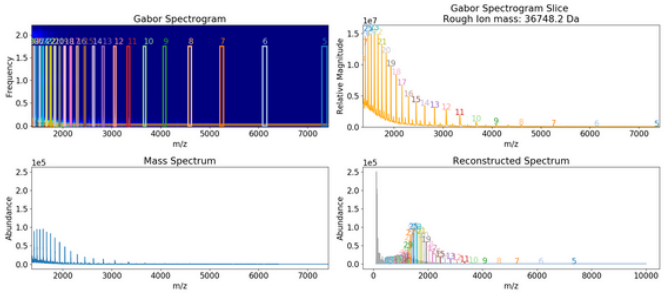
New Deconvolution Software: iFAMS v6.3 (Quant)

We're excited to introduce iFAMS v6.3 (Quant), a powerful mass spectrometry data analysis tool developed by the Prell Lab at the University of Oregon. This software is designed to determine the mass of proteins and other large molecules and is particularly effective for analyzing protein mixtures. Our core facility will be integrating iFAMS v6.3 (Quant) into our MS data analysis workflow as a valuable alternative deconvolution option. Stay tuned for guidance on how to use the software or reach out to our team with any questions.

https://github.com/prellgroup/iFAMS/releases



- **Deconvolution of ADH monomer using iFAMS 1-Click process.**



- **Deconvolution of ADH monomer using iFAMS mannul selection process.**

2025 AMS Conference - July 20-23 at Georgia Tech

The Advancing Mass Spectrometry (AMS) for Biophysics and Structural Biology Conference will be held July 20–23, 2025, at Georgia Tech. This biennial event brings together experts in mass spectrometry and its applications in structural biology and biophysics. We're proud to share that our Scientific Director, Dr. Blaine Roberts, has been invited to speak at this prestigious conference.

https://advancingms.org

2025 SFG Conference - November 9-12 at San Diego

The 2025 Annual Meeting of the Society for Glycobiology will take place November 9–12 at the Sheraton San Diego Hotel & Marina. This year's theme, "World Glyco Expo," highlights global advancements in glycobiology research and applications. Abstract submissions are due by Friday, July 11, 2025, at 11:59 PM (ET). For more information and updates, visit the conference website or contact the organizing committee.

https://www.glycobiology.org/annual-meeting