

TRANSCRIPT

Interview with an EMSL researcher:

Robby Robinson

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Hi, I'm Robby Robinson and I'm a scientist here at EMSL. One of the things I've been working on are better ways to analyze intact proteins using mass spectrometry.

I'm going to be presenting some of this work at ASMS. The work that I will present there is demonstrating how we develop ways to integrate both top-down and bottom-up proteomics.

The reason we integrate top-down and bottom-up proteomics is to take advantage of the strengths of both of these methods. For example, the strength of top-down proteomics is that you see so much of the complexity of the biological systems. You see all the different proteins and the post-translation modifications that are naturally part of these biological systems. We use bottom-up proteomics to make identifications of what these proteins are that we see in the top-down proteomics.

We use several different analytical platforms that we have available here at EMSL. The key feature of doing top-down proteomics is to use our high-field, ion cyclotron resonance mass spectrometers. These instruments have the resolution and the mass-measurement accuracy that is required to analyze samples of this kind of complexity.

The other technology that we've been able to take advantage of is our HPLC platforms. We are able to resolve and separate out the components in these complex mixtures.

So these studies, using the top-down and bottom-up integrated proteomics method is going to improve our fundamental understandings of biological systems. And also understand how different post-translation modifications play a role in the different regulatory pathways in these biological systems.

This not only improves our fundamental understanding, but also helps us find new ways to apply this understanding to help find cures for diseases, to help improve biological remediation methods, and also to work on improving some of these biological sources as potential energy applications.