

# What protein is that?

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Imaging mass spectrometry (IMS) makes it possible to see the spatial distribution of molecules in a thin tissue section based on their molecular masses. It is a powerful tool for biomarker discovery, but identifying proteins detected by IMS remains a difficult task.

Jeffrey Spraggins, Ph.D., and colleagues in the Mass Spectrometry Research Center, now report an improved technology for protein identification in IMS.

The investigators automated liquid extraction surface analysis, which involves dispensing small volumes of solvent onto the tissue surface to extract proteins and other compounds, following by traditional protein-identification (proteomic) techniques.

In the March 15 *Rapid Communications in Mass Spectrometry*, they report robotic surface micro-extractions from thin tissue sections using a glass capillary setup, coupled directly to liquid chromatography/[mass spectrometry](#) for [proteomic analysis](#). They found improved reproducibility and droplet resolution with the robotic extraction.

Coupling the extraction directly to the analysis is more suitable for high-throughput spatial proteomic experiments and will aid in the challenge of identifying proteins observed by IMS.

**More information:** Daniel J. Ryan et al. Protein identification in imaging mass spectrometry through spatially targeted liquid micro-extractions, *Rapid Communications in Mass Spectrometry* (2017). [DOI:](#)

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