

# Improving Separation and Characterization of Proteoforms and Protein Complexes Using CEMS and ECD Fragmentation

Webinar - Tuesday, March 24, 2020 1:00 PM Eastern

Dr. Liangliang Sun and Xiaojing Shen

Michigan State University - Department of Chemistry

## Webinar

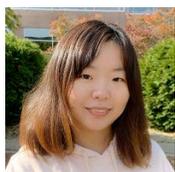
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Dr. Liangliang Sun is an Assistant Professor in the Department of Chemistry at Michigan State University. He joined MSU in August 2016. Before that, he worked with Prof. Norman Dovichi at University of Notre Dame as a postdoctoral fellow (2011-2012) and a Research Assistant Professor (2013-2016).

He received his Ph.D. degree in Analytical Chemistry in 2011 from Dalian Institute of Chemical Physics, Chinese Academy of Sciences, advised by Profs. Yukui Zhang and Lihua Zhang. He got his bachelor degree in Bioengineering in 2005 from Dalian University of Technology, China.



Xiaojing Shen received her B.S. degree in chemistry from Nanjing University, China, in 2015. Currently, she is a Ph.D. candidate under the supervision of Professor Liangliang Sun in the Department of Chemistry at Michigan State University.

Her research project focuses on investigating online capillary zone electrophoresis (CZE)-tandem mass spectrometry (MS/MS) for denaturing and native top-down proteomics through improving separation and fragmentation of proteoforms and protein complexes.

Register here:

## CEMS/MSU

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Join Dr. Liangliang Sun and Xiaojing Shen from the Department of Chemistry at Michigan State University as they share their research on the characterization of proteins in proteoforms for pursuing a better understanding of protein function.

## Abstract

Studying the function of proteins in cells is vital for understanding the underlying molecular mechanisms of disease and development. Post-translational modifications (PTMs) can influence protein conformations and function. Understanding protein function requires a deeper characterization of proteoforms and their associated protein complexes.

Top-down proteomics (TDP) aims to delineate proteoforms and protein complexes on a global scale and in discovery mode. It has achieved substantial progress in the last decade. However, many challenges remain, including but not limited to high-capacity separation and extensive fragmentation of proteoforms and protein complexes.

In this talk, we will introduce capillary electrophoresis-mass spectrometry as a useful tool for highly efficient and high-capacity separation of proteoforms and protein complexes as well as the combination of electron capture dissociation and collision-induced dissociation as a powerful technique for nearly 100% backbone cleavage of proteins smaller than 30 kDa. We employed an Agilent G1700 Capillary Electrophoresis with CMP EMASS-II CE-MS ion source interface, 6545XT AdvanceBio LC/Q-TOF mass spectrometer and e-MSion ECD cell in these studies.

## Presentation Outline

- Introduction
- CZE-MS with ECD for Denaturing Top-down Proteomics– Find and Characterize the Proteoforms
- CZE-MS for Native Top-down Proteomics of Protein Complexes
- Conclusion

