

CLINICAL AND APPLIED PROTEOMICS (MS)

The Master of Science in Clinical and Applied Proteomics is designed for science graduates and those already working in the field of scientific research who wish to pursue or advance their career through specialized study in the exciting field of Proteomics and Mass Spectrometry. This program is a combination of innovative, didactic online study of theory, combined with two in-person hands on laboratory rotations in order to provide students with the freedom to study from anywhere while still gaining access to operational training with some of the most specialized, modern equipment available.

Curriculum

The Master of Science in Clinical and Applied Proteomics requires 30 credit hours. The time limit to complete all the work towards the degree is one year.

Code	Title	Hours
CAMS 401	Theory and Physics of Mass Spectrometry	4
CAMS 402	Chemistry of Protein Separation	4
CAMS 403	Introduction to Mass Spectrometry Instrumentation	2
CAMS 411	Computation and Bioinformatics for Proteomics	3
CAMS 412	Clinical Considerations and Biomarker Development	3
CAMS 413	Advanced Mass Spectrometry Approaches	2
CAMS 491	Mass Spectrometry Lab Rotation A	5
CAMS 492	Mass Spectrometry Lab Rotation B	5
CAMS 493	Capstone Design - Applications in Mass Spectrometry A	2
CAMS 494	Capstone Design - Applications in Mass Spectrometry B	2
Total Hours		30

The didactic classes will take place online. The laboratory rotation will take place in person at the Loyola University of Chicago's Health Sciences Campus in Maywood, IL.

Graduate & Professional Standards and Regulations

Students in graduate and professional programs can find their Academic Policies in Graduate and Professional Academic Standards and Regulations (<https://catalog.luc.edu/academic-standards-regulations/graduate-professional/>) under their school. Any additional University Policies supercede school policies.

Learning Outcomes

Upon completion of this program, students will be able to:

1. Understand how compounds can be isolated for analysis based on their chemical properties.
2. Describe the physics of each step of mass spectrometry.
3. Read and interpret mass spectra.
4. Identify the best mass spectrometry approach for a given situation.

5. Perform all steps, from sample preparation to data analysis, of the mass spectrometry analysis workflow.
6. Be able to explain the bioinformatic analysis of mass spectra and how to choose the most appropriate approach for a given situation.
7. Develop a project based on a clinical or applied mass spectrometry question.