

**PHCO 750****Short title:** Proteomics**Long title:** Proteomics Methods and Applications**Effective term:** Fall 2019 (five weeks, two 90-min class meetings each week M/W)**Course units/hours:** 1 credit hour**Grading basis:** (GRAD – H, P, L, F)**Course Component (lecture or lab):** Lecture & lab**Course Instructors:**

Laura Herring, PhD; Dept of Pharmacology (Course Director)

Lee Graves, PhD; Dept of Pharmacology (Guest Lecturer)

Dennis Golfarb, PhD; Dept of Pharmacology (Guest Lecturer)

**Course Description:**

The goal of this course is to familiarize students with the fundamental concepts of proteomics and its applications to real-world biomedical research. Lectures will focus on the fundamentals of mass spectrometry and three broad proteomics applications: expression proteomics, post-translational modification identification/quantitation, and affinity proteomics. Practical aspects of these applications, such as rigorous experimental design, sample preparation and data interpretation will be emphasized throughout the lectures. Students will also get hands-on experience preparing samples for LC-MS/MS analysis, as well as in-depth experience analyzing global quantitative proteomics data. Students will present on a specific topic assigned by the instructor.

There are no formal prerequisites for the course, but it is intended for 2<sup>nd</sup> year students and above who currently use or plan to use proteomics in their research.

**Course objectives** (learning outcomes):

Gain practical knowledge of mass spectrometry-based proteomics techniques in order to successfully design a rigorous proteomics experiment.

Gain experience preparing samples for proteomics analysis and analyzing proteomics data.

**Course Assignments**

Students will be given primary literature to read and a proteomics dataset to analyze.

**Assessments**

Grading will be based on attendance, participation in the class discussions, and student presentations.

**Course Format**

Students will attend ten 1.5 hr lectures and labs.

## **Course Schedule**

### **Session 1: Introduction to Proteomics**

- Historical perspective
- Mass spectrometry methods
- Proteomics applications

### **Session 2: Experimental design**

- Proteomics workflow overview
- Rigor and Reproducibility
- Validation

### **Session 3: Expression proteomics**

- Global quantitative proteomics analysis
- Spatial localization
- Clinical proteomics

### **Session 4: Post-translational modification (PTM) identification and quantification**

- Types of PTMs
- Single protein PTM analysis
- Global phospho and ubiquitin analysis

### **Session 5: Affinity proteomics**

- Protein-protein interactions
- Protein-nucleic acid interactions
- Protein-small molecule interactions
- Kinome profiling

### **Session 6: Lab**

- Lab - sample preparation

### **Session 7: Lab & lecture**

- Lab – MS analysis
- Lecture - Database searching, statistical and bioinformatics analysis

### **Session 8: Data analysis**

### **Session 9: Student presentations**

### **Session 10: Student presentations**