



# Proteomics and Informatics

**Bioinf 551/ Chem 551/ BiolChem 551/  
Path 551/ BioMedEng 551**

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**GSI:** TBA

**Lecture:** Tuesdays, Thursdays 1:00 – 2:30 PM, 2062 Palmer Commons

This is a lecture course on proteomics and its biomedical applications. Proteomics – the study of the totality of the protein complement of an individual organism – is a very timely topic, both in basic science and in biomedical research and applications. This course will begin with a thorough study of proteomics technology based on mass spectrometry (MS) technology, but will also touch upon alternative approaches. Informatics based methods of study are extremely important in this area, and will be discussed in detail.

**Prerequisites:** This is an interdisciplinary course, so students are expected to come from different backgrounds.

Topics covered in this course include:

1. Introduction to proteomics: protein chemistry and mass spectrometry
2. MS-based protein identification
3. Analysis of post-translational modifications (including phosphoproteomics)
4. Quantitative proteomics
5. Protein interaction networks and protein complexes
6. Data mining and analysis of large scale proteomic datasets
7. Clinical applications
8. Non-MS based (e.g. protein arrays) proteomic methods
9. Metabolomics
10. Proteomics and systems biology (pathway analysis, integration with transcriptome data, etc)