**CSB 450H1F – PROTEOMICS IN SYSTEMS BIOLOGY**

24L

**Lecturer:**

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**Prerequisite:** BIO230H1/255H1, BCH210H1

This course will emphasize students’ discussion and interaction in the classroom and provide a foundation for students to effectively evaluate primary literature. Typically each session consists of a lecture followed by discussion of an article in proteomics. The goal of the course is, therefore, to assist students in developing skills in critical analysis of scientific literature and to become well versed in this emerging field of proteomics.

In the post Genome era we are inundated with an exhaustive amount of genetic data. More than 100 genomes have been sequenced to date, however, less than 20% of this data provides useful functional information on cellular processes. Incidentally, we are still unable to annotate the complete repertoire of the human genome. Our estimate of the number of coding regions is highly dynamic - this number varies by more than 50%. We now believe that the human genome consists of approximately 20K coding regions. It is astonishing that such a small number of genes produces more than 100K proteins – if we still believe the “one gene one protein dogma.” We will look at current approaches that promise to unravel the mystery of the proteome. These approaches include 2D-gel electrophoresis, protein-protein interactions, structural biology, and mass spectrometry. We will look at proteome dynamics, regulations, and products under different cellular conditions.

**Required Text:** No required textbook. Articles will be assigned from the primary literature and will serve as a basis for discussion.

**Evaluation:** assignment (20%), discussion, questions, critical evaluations of primary literature, (45%), final exam (35%).