

Homework for Protein Bioinformatics 260.841 class on 12 and 14 April, 2005:

1. Draw a schematic of a tandem mass spectrum (i.e. the fragmentation spectrum) when the following peptide is fragmented: SGNYWK. Assume that the doubly charged version of this peptide is fragmented and draw only the Y series of ions and label the peaks.

2. How are the entries within the RefSeq database categorized? Which ones among these categories are the most reliable entries?

3. Name 5 limitations of 2D gels? What are the some of the disadvantages of using 2D gels for quantitation?

4. List some pros and cons of *in vitro* methods for relative quantitation.

5. List some of the reasons why it is difficult to visualize phosphorylated peptides in a typical LC-MS/MS experiment.