BC367, Fall 2019 Problem set #4 Due: Friday, September 27th

(Don't forget that each question should be answered on a separate sheet of paper. Also, please *type* your narrative answers.)

1. Which of the following peptide sequences is most likely to form an alpha helix when part of a larger, globular protein? Explain.

    a. CRAGNRKIVLETY

    b. SEDNFGAPKSILW

    c. QKASVEMAVRNSG

2. In performing an MS/MS experiment on an unknown protein, your peptide fingerprint analysis software died before you can get the sequence of your last peptide fragment. Luckily, you have the CID spectrum. Using the following m/z values from this spectrum to identify the peptide sequence (assume perfect CID cleavage, *i.e*. each peak is a clean 'b' or 'y' fragment).

    116.03426
    134.04483
    187.07138
    247.12889
    286.13979
    346.19731
    399.22386
    417.23442
    514.2508
    532.26136

3. If you were using MS/MS to determine the identity of a short peptide and the mass of one of the residues corresponded to leucine, which of course could just as likely be isoleucine. How could you differentiate Leu and Ile experimentally?

4. You are trying to measure the concentration of a purified protein of known sequence that has 5 aromatic residues (all Trp) using ultraviolet absorbance spectroscopy, but you don't know the actual extinction coefficient. Why might the actual extinction coefficient be different than that of tryptophan itself? Propose an experiment to measure and calculate the actual extinction coefficient.