Problem 1: Use the site: http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_seccons.html to predict the secondary structure of one of your favorite proteins.

Problem 2: Use the web server AGADIR to study the helical content of KETAAKFERQHM.
   a). Calculate the helicity per residue at pH 7, 278 K, and an ionic strength of 0.1 M.
   b). Study how the helical content of the peptide change with respect to pH. Use a temperature of 278 K and an ionic strength of 0.1 M.
   c). Repeat a) by mutating the second E into A. Does E enhance or diminish helical formation?
   d). Repeat a) by mutating the twelfth H into A. Does H enhance or diminish helical formation?
   e). Repeat a) by acetylating the N terminus of the peptide. Does acetylation increase or decrease helical content?
   f). Repeat e) by blocking the N terminus of the peptide by a succinate.

Problem 3: Use Swiss PDB viewer to build a homology model of one of your favorite proteins. (Note that you may not be able to build a model of your protein using this method. Why? If not, pick another protein.)