Your name: _____

Homework for Protein Bioinformatics 260.655 class on 1 April 2008:

Due at the start of class Tuesday, April 8, 2008

1. What is primary goal of 'Structural Genomics'?

2. Crystallography and NMR.

2a. Which experimental technique is responsible for the majority of the structures deposited in the Protein Data Bank?

2b. When x-rays interact with a protein, they can be scattered by the [protons, electrons, neutrons] of the protein atoms. [circle one choice].

2c. Scattered x-rays form a diffraction spot (also called a reflection) when they have the same [intensity, spin, phase]. [circle one choice].

2d. The location of a diffraction spot on the detector contains information about:

2e. The intensity of a diffraction spot on the detector contains information about:

2f. There are two properties associated with each diffraction spot that are necessary for determining a structure using x-ray crystallography. What are these two properties and which one is not recorded by x-ray detectors?

2g. NMR structure determination involves perturbing the unpaired spins of atomic nuclei with a [magnetic field, electric field, force field]. [circle one choice].

2h. What is the only element commonly found in proteins that contains an unpaired spin in its nucleus?

2i. What are two other isotopes that are typically used as labels to introduce unpaired spins into protein samples for NMR?

2j. Which experimental technique can tackle molecules greater than 40,000 Daltons in mass?

2k. Which experimental technique allows you to study molecules in solution?

2l. Which experimental technique typically generates a greater number of observables (data points) than the number of refinement parameters used to fit the structural model?

2m. Why is the ratio of observables to refinement parameters important?