Biophysical Chemistry I, Fall 2010

Homework Assignment #2, due Sept. 21

1. Download the 1ZNF entry from the PDB. If you examine the file in a text editor, you will see that there are 37 copies of the structure, identified by cards with the word "MODEL" in the first five characters (i.e. "MODEL 1" through "MODEL 37"). For this assignment, please work *only* with MODEL 1. Click on the "molecule of the month features", and read about this structure. Write a *short* summary (3-4 sentences) about the biological significance of zinc fingers.

2. Make a list of the backbone hydrogen bonds in the structure (MODEL 1 only). These will be C=O...H-N units where (for the purposes of this assignment) the distance between O and H is less than 2.3 Å. Make a table showing the donor residue (the one with the NH group), the acceptor residue (with the C=O group) and the N...O and H...O distances. Identify hydrogen bonds that correspond to an α-helix, a 3_{10} helix, or to a β structure.

3. Read the brief introduction to sequence similarity searches in Wikipedia: *http://en.wikipedia.org/wiki/FASTA*. Convert the 1ZNF sequence to FASTA format (see *http://en.wikipedia.org/wiki/FASTA_format*). (You should ignore the "blocking" groups ACE and NH2 at the beginning and the end of the struture.) Submit your FASTA format as the answer to this question.

4. Go to "advanced search" at the PDB web site, choose the query type "Sequence (blast/fasta)" and enter your FASTA format sequence for this zinc finger; leave other parameters at their defaults. Submit the search to find other structures in the PDB with similar amino acid sequences. Report the PDB code and title of the five top "hits".

5. The first hit should be to 1ZNF itself. Click on the "display full alignment" tab to verify that you have an exact match. For the second hit, show the sequence alignment, and discuss the extent to which the amino acid sequence of the second hit resembles and differs from that of 1ZNF itself.