Name: _____

MCB 100A/ChemC130 Midterm 1 2010

Please write your name on the first page.

1. Find the letter below that best matches the following statements. Use a letter only once. **(20 pts.)**

A. GNRA tetraloop
B. amplifies X-ray scattering
C. reveal fluctuations or motions in DNA
D. two or more strands with one face exposed to solvent
E. usually 5 or more buried strands
F. R-factor
G. traps a nonphysiological structure
H. phylogenetic tree
I. multiple sequence alignment
J. BLAST
K. brings together different stems into a continuous helix
L. van der Waals interaction
M. jelly roll
N. ionic interaction
O. often recognized by hydrogen bonds from side chains in a helix
P. hydrogen bond
Q. NOEs
R. measure of quality of an NMR structure

i) _ weakest attractive force
ii) _ structures of DNA-protein complexes
iii) _ a computational tool for identifying potential functional sites
iv) _ parallel beta sheets
v) _ rmsd
vi) _ coaxial stacking
vii) _ strength depends on angle as well as distance
viii) _ crystal
ix) _ makes pairwise comparisons of protein and nucleic acid sequences
x) _ stabilizes the attached stem

2a. To expand the genetic code to efficiently incorporate new amino acids into proteins, Jason Chin and coworkers reported this week the creation of a new genetic code that is read in quadruplets instead of triplets (Neumann et al., *Nature*, Feb 14, 2010). List three fundamental modules of the translational machinery they would have to change to create cells that read a quadruplet code. **(9 pts.)**

2b. What is the maximum number of codons available in a quadruplet code? **(5 pts.)**

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2c. Why is it important or significant to expand the genetic code? Aren't the 20 biological amino acids enough to encode all the chemical diversity needed for protein structures? **(4 pts.)**

2d. Draw the chemical structures of two different (biological) hydrophobic side chains. Please include hydrogens. **(6pts.)**

3a. What are two ways that nucleic acids coordinate metal ions? **(6 pts.)**

3b. Contrast the roles of these two kinds of coordination in stabilizing specific nucleic acid structures. **(6 pts.)**

4a. Draw a Ramachandran diagram for a typical amino acid that is not glycine or proline. Label the axes and mark the regions of this diagram that correspond to α-helix and β-sheet. **(6 pts.)**

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4b. Do the residues in loops necessarily (always) populate different regions of the Ramachandran diagram compared to the residues in secondary structures? Why or why not? **(4 pts.)**

4c. Define a side-chain rotamer. **(6 pts.)**

5a. In contrast to soluble proteins, membrane proteins can have a single, isolated, stable helix. What accounts for the stability of an isolated helix in the membrane but not in solution? **(6 pts.)**

5b. The hydrophobic tails of the mycolic acid outer layer of the *M. tuberculosis* cell wall are about 80 Å thick. How many residues would it take for an α-helix to span this unusual hydrophobic layer? **(4 pts.)**

5c. What subset of β-sheet structures can span a membrane? Are these parallel, mixed or anti-parallel sheets? **(6 pts.)**

6a. Why is the E-value produced by BLAST a more sensitive metric of sequence relatedness than % sequence identity? **(6 pts.)**

6b. List two patterns or principles of protein structure embodied in the environment classes used for 3D-1D profiles **(6 pts.)**