Name: ______________________________

MCB 100A/ChemC130 Midterm 1 2008

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. A-minor motif
B. R value
C. rmsd
D. net result of the exchange of interactions in folded and unfolded states
E. Ramachandran plot
F. van der Waals contact
G. rotamer
H. covalent bond
I. cross-strand purine stack
J. protein denaturation
K. AUG
L. C3' endo sugar pucker
M. tetraloop
N. X-ray crystallography
O. major groove
P. sensitive to base hydrolysis
Q. accessible surface area
R. ionic interaction

i) _ commonly occurs at the end of RNA stems
ii) _ reflects the overall quality of a NMR structure
iii) _ determined by van der Waals contacts in a tripeptide
iv) _ long-range noncovalent interaction
v) _ closest favorable interaction
vi) _ commonly occurs where three RNA strands come together
vii) _ RNA
viii) _ each base pair displays a unique pattern of H-bond donors and acceptors
ix) _ used to define atoms on the "inside" and "outside" proteins
x) _ combination of low-energy side-chain dihedral angles

2a. Draw the structure of 3'-deoxyadenosine 5'-triphosphate **(6 pts.)**

2b. This molecule is the triphosphate form of a drug, cordycepin, which is an inhibitor of poly-A synthesis at the 3' end of mRNA. At high concentrations it affects all RNA synthesis. What is the basis of inhibition? **(3 pts.)**

Name: ________________________________

2c. Why does this molecule (cordycepin triphosphate) fail to inhibit DNA synthesis? **(3 pts.)**

3a. For <u>transcription</u> and <u>translation</u>, list 1. the information–containing template, 2. the “monomer” substrate and 3. the “polymerase” that catalyzes polymer synthesis. **(12 pts.)**

	Transcription	**Translation**
Template		
Monomers		
Polymerase		

3b. What is the common metabolite whose hydrolysis is coupled to all the reactions involving nucleotides in DNA replication, transcription and translation? **(4 pts.)**

4. Match the amino acids to their common reactions. Use each letter only once. **(8 pts.)**

Asp-Pro ___	A. Deamidation
Gln ___	B. Oxidation
Asn-Gly ___	C. Isomerization
Cys ___	D. Cleavage

5. Which physical force or effect provides the dominant driving force for each of these structural patterns **(12 pts.)**:

a. The tendency of RNA stems to line up with the helix axes aligned.

b. The A-minor motif and ribose zipper.

c. The occurrence of 20 or more consecutive nonpolar amino acids in transmembrane helices.

d. The tendency of charged groups in proteins to be surrounded by groups of opposite charge.

e. The requirement for positively charged ions to stabilize nucleic acid structures.

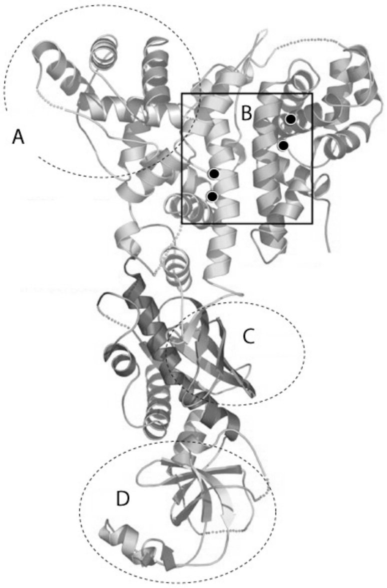
f. Intercalation of bases in the structure of tRNA.

Name: ______________________________

6. Which of the following amino acid sequences is most likely to form an amphipathic α-helix? Briefly explain two different reasons for your choice **(12 pts.)**.

a. NPEALKDAFKQVAHRMKQLARG **a.**
b. KPKKIQVDASFSVRLDVDIRRQ
c. PRWILVAVLFFCTMILVIAVRG

7. The ribbon diagram of the ~750-amino-acid, RNA-cutting enzyme "dicer" from *Giardia* is shown on the right.



7a. The dicer sequence has two separate segments that show 29/103 and 36/139 sequence identities to a bacterial enzyme called ribonuclease (RNase) III. What two additional pieces of information from sequence analysis would you use to evaluate whether or not these segments of dicer contain the RNase active sites? **(8 pts.)**

7b. This dicer cuts double-stranded RNA into pieces that are 25 base pairs long. The distance from region A to region D is ~100 Å. If the active site of dicer is in region B, which additional region of the protein do you think is required to measure the precise length of RNA for cleavage and why did you pick this region? **(6 pts.)**

7c. List two other enzymes (in addition to dicer) that form large or elongated structures that also recognize or act on distant parts of a RNA molecule. **(6 pts.)**