Exam Due: Thursday, November 16 in class - no exceptions

This examination is open book, but is to be worked on ***independently***. Once you have begun working on the exam, you may not discuss any aspect of the exam with *anyone* other than C. Martin. This includes any discussions with anyone after you are done with the exam, but before November 16.

You are on your honor.

Note: The following questions are looking for short, concise, but complete answers. Overly long responses typically indicate a lack of thorough understanding, and will be scored accordingly. Be concise. Lay out all of your thoughts before you write your final answer. Choose only those relevant.

1) Go to the Protein 1 site on the Exam Web page.

a) (15 points) Draw a topology diagram for this protein. What class of protein is it?

b) (10 points) What interaction(s) drive folding for this protein?

c) *Extra credit*: (5 extra points) what is unusual about this protein (at least two things)?

2) Go to the Complex 2 site on the Exam Web page.

a) (10 points) Explain the stabilizing interaction(s) that Tyr 34 on chain C makes with amino acids in chain A (protein-protein interaction).

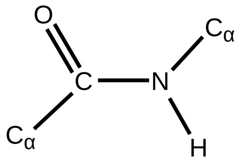
b) (10 points) Arg 74 on chain C makes sequence specific contact with the RNA. Explain the important aspects of this contact.

c) (5 points) Arg 74 on Chain C is also weakly "buttressed," to stabilize the above interaction. Explain the buttressing.

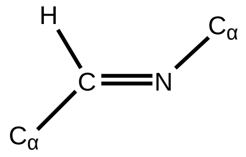
d) (5 points) Is the interaction between chain B and the RNA similar to the classic helix-turn-helix interaction that we learned about in class? Explain.

e) (5 points) Draw a "topology diagram" (2D representation) of the RNA. How many co-axially stacked helices are there? Explain

3) Assume that the protein backbone were composed of imine linkages , instead of the normal peptide linkage.



Peptide



Imine

For proteins in general, how would this change effect:

For the folding reaction: $\text{Unfolded} \rightleftharpoons \text{Folded}$

a) (10 points) hydrophobic standard free energy of folding ($\Delta G_{\text{hydrophobic}}$)

b) (10 points) H-bonding standard free energy of folding ($\Delta G_{\text{H-bonding}}$)

c) (10 points) electrostatic standard free energy of folding ($\Delta G_{\text{electrostatic}}$)

d) (5 points) configurational entropy of the folded protein (S_{config})

e) (5 points) configurational entropy of the random coil (S_{config})