Biochemistry 465 **Your Name:** _____

Biological Information Processing **Prof. Jason Kahn**

Exam I (100 points total) **March 2, 2006**

You have 80 minutes for this exam.

Exams written in pencil or erasable ink will not be re-graded under any circumstances.

Explanations should be concise and clear. I have given you more space than you should need.

You do not need a calculator for this exam, and no other study aids or materials are permitted.

Generous partial credit will be given, *i.e.*, if you don't know, guess.

Honor Pledge: At the end of the exam time, please write out the following sentence and sign it, or talk to me about it:

"I pledge on my honor that I have not given or received any unauthorized assistance on this examination."

1. DNA Structure and Base Pairing (30 pts):

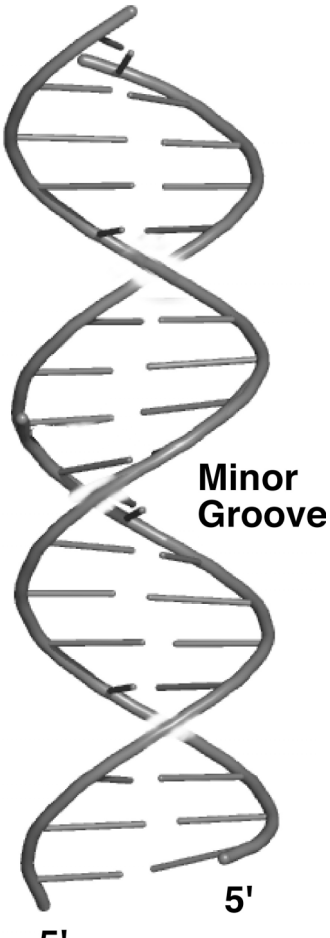
(a; 9 pts) Draw a possible non-Watson-Crick guanosine-adenosine base pair. You need not draw out the sugars.

Score for the page_____

(b; 9 pts) Sketch examples of each of the following moieties in the context of nucleic acid biochemistry and rank them in order of increasing negative free energy of hydrolysis: phosphoanhydride, phosphodiester, phosphomonoester.

(c; 4 pts) Why can't proteins recognize double-stranded RNA in a sequence-specific manner?

(d; 8 pts) Identify and fix the three errors in the picture of B-DNA at the right.



Score for the page_____

2. Secondary and tertiary structure (22 pts):

(a; 8 pts) What are the two most important structural elements stabilizing tertiary structure in RNA? How could you destroy tertiary structure in an RNA without disrupting secondary structure?

(b; 14 pts) Hydrogen bonding is one of the fundamental forces that stabilizes double-helical structure. What is the other fundamental force? One might suppose (incorrectly) that even though hydrogen bonds are strong interactions (as non-covalent bonds go) that they actually would not stabilize the hybridization of single strands to make a duplex. What is the argument for this non-effect, i.e. why did people think H-bonds weren't important? What is then the argument for the fact that they actually do stabilize duplex? What is the one-word reason for the reason that duplex structure melts out as temperature increases.

Score for the page_____

3. DNA tertiary structure (30 pts):

(a; 9 pts) At the right, draw in the remainder of the broken strand and fill in blanks in the dashed strand as necessary to end up with a drawing where the linking number Lk between the two strands is **+4**. Why are the nodes indicated with "0" irrelevant to the linking number?

(b; 4 pts) For the purposes of doing topology, why do we define the two antiparallel strands of B-DNA as running in the same direction?

(c; 4 pts) In the following list of terms, circle the ones which are always integers:

Helical repeat, linking number, writhe, number of base pairs, twist.

(d; 8 pts) Briefly describe some of the evidence that the helical repeat of DNA in solution is about 10.5, rather than the 10.0 seen in crystal structures.

Score for the page_____

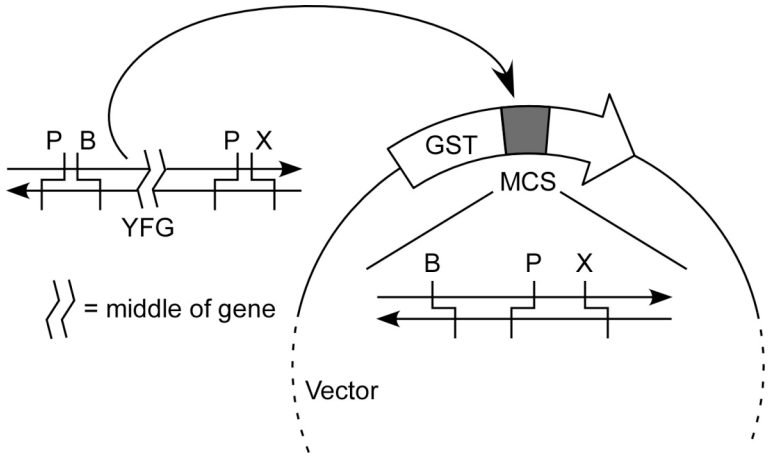
(e; 5 pts) Draw a toroidal superhelix with Wr = -4.

4. Methods (18 pts):

(a; 8 pts) Briefly describe the idea of the DNA microarray. Why is it important to compare two samples when doing these experiments?

Score for the page_____

(b; 10 pts) You would like to clone a gene into a vector in order to express a fusion protein. The multiple cloning site (MCS) sequence of the vector is sketched, and the YFG insert has the ends shown. Coworker 1 in the lab suggests using Pst I (P) cleavage followed by CIAP and T4 DNA ligase to clone the fragment, Coworker 2 suggests using Bam HI (B) and Xba I (X) instead of Pst I.



Sketch the probable products of trying to clone the gene using each coworker's advice. Which is preferable, and why? Note: this is a simple and straightforward cloning question. Don't worry about reading frames, fusion sequences, compatible digestion buffers, or the NSA.

Page	Score
1	
2	
3	
4	
5	
6	
Total	

Score for the page_____