Biochemistry 465 Biological Information Processing Exam II (100 points total)

Your Name: Prof. Jason Kahn. Univ. Maryland November 20, 2008

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 examination 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. (16 pts) DNA Sequencing

(a; 10 pts) Briefly describe how a whole microbial (i.e. relatively small, ~ 2 Mb) genome is determined, given that individual sequence reads are much shorter (~ 1 kb).

(b; 6 pts) Briefly define "bioinformatics" and describe one application.

2. (10 pts) Protein-DNA interaction

(a; 5 pts) Explain what sequence-specific direct readout is, and why it generally occurs in the DNA major groove rather than the minor groove.

(b; 5 pts) Give an example of protein-DNA recognition by deformability (a.k.a. induced fit) : name the protein and describe in what way deformability plays a role in specific recognition.

3. (25 pts) DNA replication

(a; 9 pts) DNA polymerase fidelity relies on two independent checking steps. The first checking step is the fingers closing around the bound triphosphate, which is much slower for the incorrect triphosphate. The second checking step is very slow extension of a mismatch. Explain why the nearly nonspecific $3' \rightarrow 5'$ exonuclease is essential to the actual ability to use the second checking step. Name but do not draw the type of mechanism we described for all transesterifications. State why it is important that the exonuclease reaction be irreversible.

(b; 6 pts) Why is a polymerase error rate of $1/10^5$ adequate for a virus but not for *E. coli*? Why can an error rate of $1/10^5$ or more be tolerated in transcription and translation?

(c; 10 pts) Sketch the trombone model for DNA replication when the lagging strand polymerase is half way through making an Okazaki fragment, labeling all the proteins involved.

4. (26 pts) DNA Repair

(a; 14 pts) Briefly describe the types of DNA lesions repaired by BER, NER, and MMR. Which one has the most general scope of action, and how is it believed to recognize its target?

(b; 12 pts) Sketch the pathway of NER repair, including all enzymes needed.

5. (23 pts) Transcription

(a; 9 pts) How do prokaryotic and eukaryotic RNA polymerases manage to escape the promoter and progress into processive elongation (two answers)? Why must any RNA polymerase be processive?

(b; 8 pts) Sketch and label the E. coli ternary elongation complex (TEC) in a paused conformation.

(c; 6 pts) What is transcription-coupled DNA repair and why does it make biological sense?

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