MCB 110
First Midterm
SIX PAGES

NAME:

SID Number:

Question	Maximum Points	Your Points
I	27	
II	32	
III	35	
IV	33	
V	24	
	151	

This exam must be written in PEN if you want the option of a regrade.
DO NOT USE WHITE OUT. If you need a fresh page, ask for it during the exam.

Question I (27 points)

DNA binding proteins can favor a particular conformation of bound DNA in the protein-DNA complex. This structural stabilization of a particular DNA conformation is a crucial function of several DNA binding factors discussed in class. **For EACH of A-C below, answer EACH question 1-3.** Single-line length answers are sufficient, but provide enough detail to identify how the protein is distinct from other proteins discussed in class in its specificity of DNA structural stabilization.

1. What is the DNA structure stabilized by binding of the protein? Answer for only the initial DNA binding event. Include ALL biologically relevant features of the bound DNA.

2. Why is this DNA structural change an important biochemical activity of the protein? The answer should indicate why the structure formed by protein binding is important for the immediately subsequent reaction in the pathway.

3. DNA binding involves multiple protein subunits together, with subunits either preassembled into a multimer or assembled on the DNA by cooperative binding. Why is it necessary for the protein biological function that the structural change involves more than a single protein subunit's length of DNA binding site?

A. RecA

1.

2.

3.

B. DnaA

1.

2.

3.

C. RuvA

1.

2.

3.

Question II (32 points)

A. (16 pts) Polymerases that share a feature can differ in other features. For the pair of enzymes listed in 1-2 below, indicate FOR EACH ENZYME the primer and template specificity as RNA AND/OR DNA - one feature will be shared, one will be different for each pair of enzymes.

1. Pol III and Pol delta
(a) Primer

(b) Template

2. Telomerase and terminal deoxynucleotidyl transferase (TdT)
(a) Primer

(b) Template

B. (16 pts) Numerous examples of DNA-associated proteins that slide on dsDNA were described in class. **For EACH of the proteins A-D below, answer EACH question 1-2.**

1. What are the biological requirements for loading on dsDNA? Explain with regard to any necessary DNA structure AND/OR any other protein required as a loading chaperone.

2. Is the protein an ATPase?

A. Ku
1.

2.

B. Sliding clamp (*E. coli* beta or eukaryotic PCNA)
1.

2.

C. MutS/MutL complex
1.

2.

D. DnaB
1.

2.

Question III (35 points)

Nucleases (more broadly defined as enzymes that nick or cut DNA) must have DNA sequence AND/OR structure specificity to limit their biochemical activity to suit their cellular function. **For EACH enzyme listed in a-g below, answer EACH question 1-3.**

1. (2 pts) What feature(s) of a DNA/RNA substrate are necessary for the action of this nuclease?
2. (1 pt) Is there a covalent protein-DNA intermediate in the reaction?
3. (2 pts) What number of strands (Watsons and/or Cricks) get cleaved in the biologically occurring reaction? Answer 1, 2 or 4. If the biological reaction has concerted action of more than one subunit of the nuclease (*e.g.* a protein dimer), answer for the biologically functional protein multimer.

(a) Type I topoisomerase

1.
2.
3.

(b) Base excision repair glycosylase

1.
2.
3.

(c) Pol I RNA primer degradation activity

1.
2.
3.

(d) Exonuclease processing activity required to allow RecA/Rad51 binding

1.
2.
3.

(e) Ruv C

1.
2.
3.

(f) Mut H

1.
2.
3.

(g) Site-specific recombinase enzyme (like phage lambda integrase, for example)

1.
2.
3.

Question IV (33 points)

For each of 1-3 below, give answers for A-C:

A. (3 pts) What is a type of DNA damage that will be fixed by the listed type of DNA repair? Pick only one example of damage, but be as specific as necessary in description of the DNA substrate.
B. (6 pts) State two proteins **SPECIFIC for ONLY this repair pathway** and in one sentence describe the function/activity of each protein. If you don't remember the name of the protein, give its specificity of binding or activity in sufficient detail to identify it uniquely.
C. (2 pts) How many DNA strands have to have the phosphodiester backbone ligated as a consequence of *this* pathway of DNA repair? The answer here is one or two (*i.e.*, one or both strands of the Watson-Crick duplex).

1. Nucleotide excision repair

A.

B.

i.

ii.

C.

2. SOS response (OK to answer protein state specific to SOS even if the protein is not specific)

A.

B.

i.

ii.

C.

3. Non-homologous end-joining (the NHEJ discussed as DNA repair, not VDJ recombination)

A.

B.

i.

ii.

C.

Question V (24 points)

Two inverted repeat sequences could be subject to four different mechanisms of DNA rearrangement covered in class. For each of the recombination pathways below, indicate the fate of the DNA between the inverted repeats AND the fate of the flanking DNA in the biological process. Brief single-word answers will be sufficient if they are precisely descriptive.

1. One step of V(D)J recombination

Between inverted repeats:

Flanking sequences:

2. Site-specific recombination

Between inverted repeats:

Flanking sequences:

3. Transposon excision from the donor site (assume there is no target site integration)

Between inverted repeats:

Flanking sequences:

4. Inappropriate homologous recombination

Between inverted repeats:

Flanking sequences: