BIOCH 6763 
NAPS - Second Examination 
Nucleic Acid-Protein Synthesis 
Nucleic acids Synthesis & Other Dynamic Processes 

Name_________________ 
Examiner: Mali 
28 March, 2006 

The total points on the exam are 100. Course points (15) will be determined proportionately. 

I. Relationships (15 points, 3 each) 

Complete the following thoughts with “>”, “<” or “=”.

A. The size of a nucleosome particle is ______ the size of an RNA polymerase II complex.

B. The half-life of a message without a 5’-cap structure but an intact polyA tail is ______ the half-life of a message with an intact 5’cap but no polyA tail.

C. The length of a 100 bp DNA bound by RecA protein is ______ the length of same 100 bp DNA not covered by RecA.

D. The number of nicks required to resolve a Holliday junction by translocation is ______ the number of nicks required to resolve the same Holliday junction by resolution.

E. The number of predicted genes based on human genome sequence analysis is ______ the number of observed proteins.

II. Matching (16 points) 

We discussed the synthesis of various RNA templates by three different RNA polymerases. Indicate the appropriate polymerase(s) associated with the aspects outlined. Your answers can be abbreviated as I, II or III to indicate RNA polymerase I, RNA polymerase II or RNA polymerase III, respectively. Some questions in this section have multiple correct answers.

This question will be graded as follows. The number of correct answers for all statements will be totaled and multiplied by three. That number will be regarded as your intermediate score unless that number is greater than 16, in which case your intermediate score will be 16. Then, one point will be deducted for each incorrect response.
1. Recognizes a diverse set of promoter sequences ____________________.

2. Processivity of this polymerase is NOT a vital factor for synthesis of the RNA product______________.

3. Deregulation of this polymerase is associated with predisposition to uncontrolled cell proliferation ____________________.

4. Synthesizes bulk of the RNA in a cell ________________________.

5. Post-translational modifications on this polymerase are important for all three stages of RNA synthesis – initiation, elongation and termination ____________.

III. Matching B (18 points; 3 points each)

The left column contains some techniques that were used to make some of the determinations discussed in this section. Match the technique with the determination. There is one best answer for each technique.

1. Exon trapping ______ A. Identify naked DNA.
2. Psoralen crosslinking ______ B. Protein complexes
3. Dnase I hypersensitivity ______ C. To identify coding sequences in a DNA fragment
4. Skew analysis ______ D. The half life of specific mRNAs.
5. Transcriptional pulse-chase ______ E. Identification of origins of replication
6. Immunoprecipitation____ F. Actively transcribed rDNA genes

IV. Common features (21 points, 3 each)

What are the common features of each of the following sets (be as specific as possible)?

a. T-antigen, DnaA, UL-9, Cdc6
b. Histone H2A, Histone H2B, Histone 3, Histone 4 but not Histone 1

c. RuvB, RecBCD, DnaB proteins of *E. coli*

d. RecA, SsB, Replication protein A (RPA)

e. Cap, silent rDNA, heterochromatin

f. PolyA polymerase, dephosphorylated PolII, AAUAA

g. snRNPs, GTAG, DEAD/DEAH box helicases

IV. Short essay (20 points, 10 points each)

a. RNA, being single-stranded, is a labile molecule when compared to double-stranded DNA. Yet the default state of mRNA in a eukaryotic cell is ‘stability’. What does this statement imply? What structural features render this stability to mRNA molecules?
b. Compartmentalization improves efficiency and specificity of biological processes. Do you agree or disagree with this statement? Substantiate your answer with a specific example based on the discussions on RNA stability.

V. Result Interpretation (10 points)

The yeast genome has 142 rDNA repeats in tandem. A mutant yeast strain was created by deleting 100 rDNA repeats. The mutant yeast strain has no visible phenotype and grows like wildtype (WT) cells in minimal media. On examining the rDNA transcription by Psoralen crosslinking, it was observed that less than 50% of rDNA sites were active in the WT cells, while all the 42 rDNA repeat units in the mutant were active. However, the number of polymerase molecules per gene was approximately two-fold more in the mutant (~100 polymerase molecules per gene) compared to the WT cells (~50 polymerase molecules per gene). Interpret these results with reference to regulation of rRNA synthesis in yeast.