

Biochemistry and Molecular Biology 400
Final Examination
Fall 1997
December 19, 1997

Instructor: Hardison

This examination has 35 questions for a total of 200 points. **All** are multiple choice; most are worth 5 points, but 5 are worth 10 points each. Please answer the questions on the enclosed answer sheet. **BE SURE TO ENCODE YOUR STUDENT NUMBER AND TEST FORM ON THE ANSWER SHEET!**

THIS IS FORM A, and has answers.

Useful information and equations are at the end, and are followed by a blank page for additional space you may need to solve the problems. You may wish to tear these off and use them throughout the exam.

PLEASE TURN IN ONLY THE ANSWER SHEET; you may keep the exam. Answers will be posted promptly in the hall of the first floor of S. Frear. Good luck!

1. (5 pts) Which of the following proteins bind to specific sequences in DNA via a basic segment plus a leucine zipper motif (the bZip motif)?

- [1] *lac* repressor from *E. coli*
- [2] CAP protein (or catabolite activator protein) from *E. coli*
- [3] repressor, product of the *cI* gene
- [4] mammalian AP1

- a. 1, 2, 3 b. 2, 4 c. 1, 3 d. 3 e. 4

e is correct

2. (5 pts) What is the histone fold?

- a. A helix-loop-helix-loop-helix motif in histones, through which the heterodimers H3-H4 and H2A-H2B form.
- b. The interaction domain between acetylated N-terminal tails of histones.
- c. A helix-turn-helix motif involved in sequence-specific DNA recognition by histones.
- d. A helix-turn-helix motif involved in protein-protein interactions in the octamer of histones in the nucleosome core.

a is correct.

3. (5 pts) Which statement(s) about the interaction of histones and DNA in the nucleosome core (is) are true?

- [1] Histones bind to DNA exclusively through electrostatic interactions.
- [2] Each heterodimer (H3-H4 and H2A-H2B) in the nucleosome core makes a DNA binding site covering about 25 bp.
- [3] Most contacts between histones and DNA are to specific sequences identified in the major groove of the DNA.
- [4] The major domain for interaction with DNA is the basic N-terminal tail of each histone.

- a. 1, 4 b. 2, 4 c. 1, 3, 4 d. 1 e. 2

e is correct

4. (10 pts) Which statement(s) about acetylation of histone N-terminal tails are true?

- [1] Acetylation of the histone N-terminal tails is associated with active transcription.
- [2] Acetylation of the histone N-terminal tails is associated with chromatin assembly.
- [3] The protein Gcn5p is a histone acetyl transferase involved in regulation of many genes in yeast.
- [4] The protein PCAF is a histone acetyl transferase involved in regulation of many genes in mammalian cells.
- [5] Acetylation of histones is a stable modification, i.e. once the acetyl group is added, it is rare for it to be removed.

- a. 1, 3, 4 b. 1, 2 c. 1, 3, 5 d. 1, 2, 3, 4 e. 2, 5

d is correct, 6 pts for a, 4 pts for b.

5. (5 pts) Which of the following statements about regulation of the *lac* operon in *E. coli* are correct?

- [1] The operon is negatively regulated by a repressor when the inducer is bound to the repressor.
- [2] Transcription of the operon is stimulated by binding of the complex cAMP-CAP.
- [3] The *lac* repressor prevents binding of RNA polymerase.
- [4] The *lac* repressor bound to its operator decreases the rate of the closed to open transition of the RNA polymerase-promoter complex.

Correct choices are:

- a. 1, 2, 3, 4
 - b. 2, 4
 - c. 2, 3
 - d. 1, 3
 - e. 2, 3, 4
- b is correct**

For the next two questions, assume you are studying a mammalian gene (let's call it *FINI*) whose transcription is increased in CV1 kidney cells in the presence of the protein AP1. That increased transcription requires the presence of the AP1 binding site (TGAGTCA) at a site 200 bp 5' to the minimal promoter.

6. (5 pts) You obtain a derivative of the CV1 line of kidney cells that no longer produce the proteins P300/CBP. Transcription of the *FINI* gene is no longer increased in the presence of AP1. Based on the known activities of P300/CBP, what do you conclude?

- a. AP1 acts directly on RNA polymerase to recruit it to the *FINI* promoter.
- b. AP1 binds to its recognition sequence 5' to the gene and transcribes the *FINI* gene.
- c. AP1 requires P300/CBP to bind to its recognition sequence in the DNA.
- d. P300/CBP are general transcription factors required at all promoters transcribed by RNA polymerase II.
- e. AP1 activates the *FINI* gene via a P300/CBP-dependent mechanism, such as histone acetylation.

e is correct.

7. (5 pts) In further experiments, you show that the activation domain of AP1 can bind specifically and with high affinity *in vitro* to the TAFII40 subunit of the general transcription factor TFIID. You then obtain a derivative of the CV1 kidney cell line that lacks TAFII40 and discover that transcription of the *FINI* gene is still increased in the presence of AP1. What do you conclude?

- a. AP1 acts directly on TFIID via its subunit TAFII40 to recruit RNA polymerase to *FINI* promoter.
- b. AP1 in association with TAFII40 will bind to the sequence TGAGTCA in the DNA to increase transcription of the *FINI* gene.
- c. AP1 does not require TAFII40 to activate transcription of the *FINI* gene.
- d. TAFII40 is required at promoters transcribed by RNA polymerase I and III, but not those transcribed by RNA polymerase II.
- e. TAFII40 mimics the activity of P300/CBP.

c is correct.

8. (10 pts) Which statements about the subunit of RNA polymerase from *E. coli* are correct?

- [1] It is needed for assembly of the RNA polymerase.

- [2] Its carboxy terminal domain (CTD) will bind to an UP sequence located 5' to the -35 and -10 boxes of the promoters of genes encoding rRNA and tRNA.
- [3] Its carboxy terminal domain (CTD) will interact with CAP when bound to a class I promoter to enhance binding of the RNA polymerase to the promoter.
- [4] Its amino terminal domain (NTD) will interact with CAP when bound to a class II promoter with a resultant increase in the rate of the isomerization from closed to open complex.

- a. 1, 2, 3, 4
- b. 1, 2, 3
- c. 2, 3
- d. 1, 2
- e. 1

a is correct; 5 pts for b; 4 pts for c and d; 3 pts for e

For the next four questions, consider the following hypothetical data on regulation of an operon in a bacterium. The genes encoding enzymes required for metabolism of galactose, such as galactokinase and galactose phosphate epimerase, are inducible. Thus the enzymes are produced in abundance in the presence of this sugar, but in the absence of galactose, they are produced at very low levels. Four genes or loci, *galA*, *galB*, *galC*, and *galD*, affecting the activity or regulation of these enzymes were studied in a series of haploid and diploid strains. In the following table, wild-type alleles of the genes or loci are indicated by a + under the letter of the *gal* gene or locus and mutant alleles are indicated by a - under the letter. The activities of the two enzymes, galactokinase and galactose phosphate epimerase, were assayed after growth in the absence or presence of galactose. The units of enzyme activity are 100 = induced activity of the wild-type enzyme (in the presence of galactose), 1 = uninduced activity of the wild-type enzyme (in the absence of galactose), and 0 = no measurable activity. In the diploid analysis, one copy of each operon is present in each cell.

Strain number	<i>gal</i>	Galactokinase .		Galactose phosphate epimerase .	
		- galactose	+ galactose	-galactose	+ galactose
Haploid	A B C D				
1	+ + + +	1	100	1	100
2	- + + +	0	0	1	100
3	+ - + +	1	1	1	1
4	+ + - +	1	1	1	1
5	+ + + -	1	100	0	0
Diploid	A B C D/A B C D				
6	- + + +/+ + + -	1	100	1	100
7	+ - + +/- + + +	1	1	2	101
8	+ + - +/- + + +	1	100	2	200
9	- - + +/+ + - -	1	100	1	1

9. (5 pts) Which option best describes the phenotype with respect to the two enzymes for strains 3 and 4?

- | | |
|-----------------------------|--------------------------------------|
| <u>Galactokinase</u> | <u>Galactose phosphate epimerase</u> |
| a. activated | activated |
| b. no activity | inducible |
| c. noninducible | noninducible |
| d. constitutive, high level | constitutive, high level |
| e. inducible | no activity |

c is correct

10. (5 pts) Which genes encode the enzymes? Choose the option with the correct gene under each enzyme.

- | | |
|----------------------|--------------------------------------|
| <u>Galactokinase</u> | <u>Galactose phosphate epimerase</u> |
| a. <i>galA</i> | <i>galB</i> |
| b. <i>galC</i> | <i>galD</i> |
| c. <i>galA</i> | <i>galC</i> |
| d. <i>galB</i> | <i>galC</i> |
| e. <i>galA</i> | <i>galD</i> |

e is correct

11. (5 pts) Which gene or locus shows *cis* dominance, i.e. the particular allele that is in *cis* to the reporter gene is dominant?

- a. *galA*
- b. *galB*
- c. *galC*
- d. *galD*
- e. none of the genes

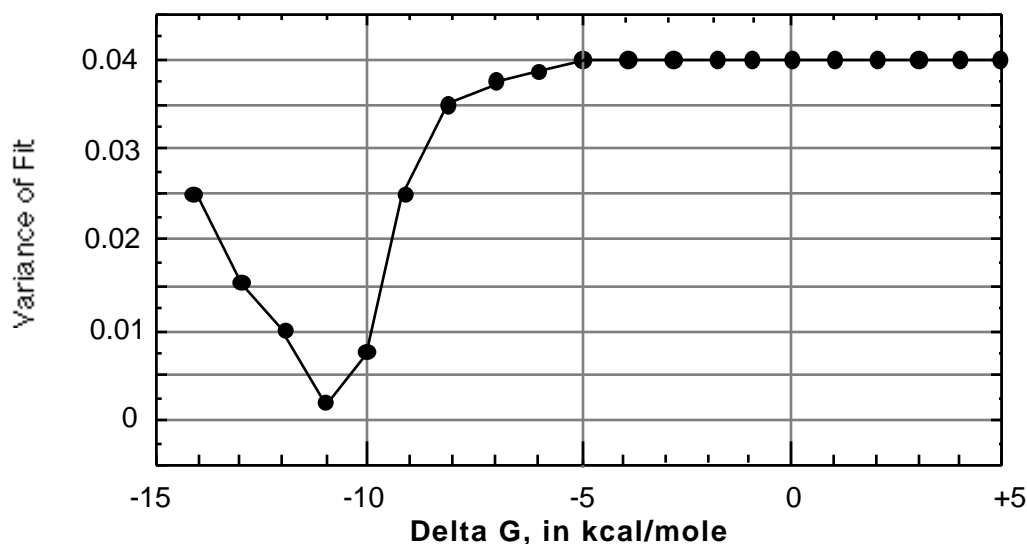
b is correct

12. (5 pts) Which statements about the regulation of the *gal* operon in this bacterium are supported by the data presented?

- a. The gene *galC* encodes an activator that binds to the DNA sequence at *galB* in the presence of galactose but not in the absence of galactose.
- b. The gene *galB* encodes an activator that binds to the DNA sequence at *galD* in the presence of galactose but not in the absence of galactose.
- c. The gene *galD* encodes a repressor that binds to the operator sequence *galA* in the absence of galactose but dissociates in the presence of galactose.
- d. The gene *galC* encodes a repressor that binds to the operator sequence *galB* in the absence of galactose but dissociates in the presence of galactose.

a is correct, 2 points for d

For the next two questions, let's imagine that you mixed increasing amounts of the DNA binding protein called AP1 with a constant amount of a labeled duplex oligonucleotide containing the binding site (TGAGTCA). After measuring the fraction of DNA bound by AP1 (i.e. the fractional occupancy) as a function of [AP1], the data were analyzed by nonlinear, least squares regression analysis at a wide range of possible values for ΔG . The error associated with the fit of each of those values to experimental data is shown below; the higher the variance of fit, the larger the error.



13. (5 pts) What is the most accurate value of ΔG for binding of AP1 to this duplex oligonucleotide?

- a. -14 kcal/mole
- b. -11 kcal/mole
- c. -8 kcal/mole
- d. -5 kcal/mole
- e. +5 kcal/mole

b. is correct, the minimum in error is the maximum in accuracy.

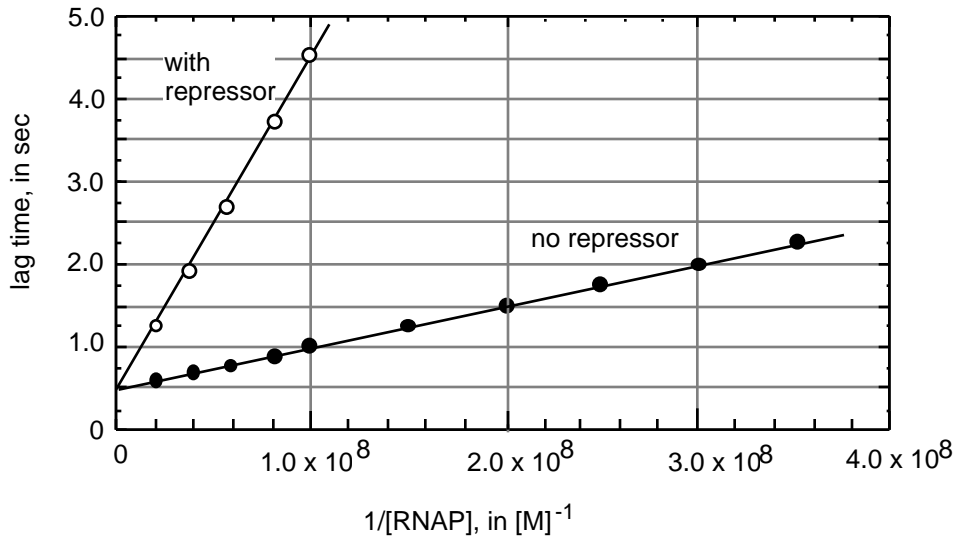
14. (5 pts) What is the most accurate measure of the equilibrium constant, K_s , for binding of AP1 to this duplex oligonucleotide?

- a. $2.09 \times 10^{-4} \text{ M}^{-1}$
- b. $4.79 \times 10^3 \text{ M}^{-1}$
- c. $7.73 \times 10^5 \text{ M}^{-1}$
- d. $1.25 \times 10^8 \text{ M}^{-1}$

e. $2.02 \times 10^{10} \text{ M}^{-1}$

d. is correct ($1.25 \times 10^8 \text{ M}^{-1}$; $G = -RT \ln K_s$)

For the next two problems, consider a hypothetical eubacterial operon in which the operator overlaps the -10 region of the promoter. Using an abortive initiation assay, measurement of the lag time before production of abortive transcripts as a function of the inverse of the RNA polymerase concentration ($1/[\text{RNAP}]$) gave the results shown below. The filled circles are the results of the assay in the absence of repressor, and the open circles are the results in the presence of repressor bound to the operator.



15. (5 pts) What is the value of the forward rate constant (k_f) for closed to open complex formation under the two different conditions?

- | k_f , no repressor | k_f with repressor |
|------------------------------|---------------------------|
| a. 2.0 per sec | 0.2 per sec |
| b. 0.5 per sec | 5.0 per sec |
| c. 2.0 per sec | 2.0 per sec |
| d. 0.5 per sec | 0.5 per sec |
| e. 4.0×10^8 per sec | 1.0×10^8 per sec |

c is correct, 2 per sec under both conditions; the y-intercept is 0.50 sec, which is $1/k_f$

16. (10 pts) What is the value of the equilibrium constant (K_B) for binding of the RNA polymerase to the promoter under the 2 conditions?

- | K_B , no repressor | K_B with repressor |
|--------------------------------------|-------------------------------------|
| a. $2.0 \times 10^7 \text{ M}^{-1}$ | $2.0 \times 10^9 \text{ M}^{-1}$ |
| b. $2.25 \times 10^8 \text{ M}^{-1}$ | $2.5 \times 10^{10} \text{ M}^{-1}$ |
| c. $1.25 \times 10^7 \text{ M}^{-1}$ | $2.0 \times 10^8 \text{ M}^{-1}$ |
| d. $1.0 \times 10^8 \text{ M}^{-1}$ | $1.25 \times 10^7 \text{ M}^{-1}$ |

e. $1.0 \times 10^{-9} \text{ M}^{-1}$ $2.5 \times 10^{-10} \text{ M}^{-1}$

d is correct, $1.0 \times 10^8 \text{ M}^{-1}$ without repressor, $1.25 \times 10^7 \text{ M}^{-1}$ with repressor. The forward rate constant does not change, but binding constant is decreased, consistent with a promoter occlusion model for the repressor. The graph shows an increase in slope with no change in the y-intercept in the presence of the repressor, so this means that the binding constant decreased. Note that d is the only option with reasonable binding constants that showed this decrease. The binding constants were calculated from the slopes of $0.5 \times 10^{-8} \text{ sec M}$ in the absence of repressor, $4.0 \times 10^{-8} \text{ sec M}$ in the presence of repressor, and $k_f = 2 \text{ sec}^{-1}$ (previous problem).

For the next three questions, consider a repressor protein, called R, that binds to the operator, called O, of a eubacterial operon with the following binding constants. The subscript s refers to binding to the specific DNA sequence at the operator, the subscript ns refers to non-sequence specific binding. In the presence of an inducer, the binding constant to the specific site is reduced by a factor of 100, as indicated by the equation for $K_{s,ind}$, whereas the value for $K_{ns,r}$ does not change in the presence of inducer.

This bacterial genome has about $4.6 \times 10^6 \text{ bp}$, and with only one genome per cell and a cell volume of $1 \times 10^{-15} \text{ L}$, this gives a concentration of nonspecific binding sites of $7.6 \times 10^{-3} \text{ M}$, and a concentration of specific binding sites of $1.7 \times 10^{-9} \text{ M}$ (this is $[D_{s \text{ total}}]$ which is also $[O_{\text{total}}]$). There are 450 molecules of the repressor per cell, giving a total repressor concentration of $7.5 \times 10^{-7} \text{ M}$.

The following equations apply:



$$K_{s,r} = \frac{[RO]}{[R][O]} = 10^{10} \text{ M}^{-1} \quad (\text{eqn 2})$$

$$K_{ns,r} = \frac{[RD_{ns}]}{[R][D_{ns}]} = 10^5 \text{ M}^{-1} \quad (\text{eqn 3})$$

$$K_{s,ind} = \frac{[RO]}{[R][O]} = 10^8 \text{ M}^{-1} \quad (\text{eqn 4})$$

17. (5 pts) What fraction of the operator sites are bound by repressor in the **absence** of inducer?

a. 1×10^{-10}

b. 0.001

c. 0.91

d. 0.50

e. $1 \times 10^{+10}$

c is correct, 0.91

18. (5 pts) What fraction of the operator sites are bound by repressor in the **presence** of inducer?

a. 1×10^{-8}

b. 0.090

c. 0.0091

d. 0.005

e. 1×10^8

b is correct, 0.090

19. (5 pts) Assuming that the operon is expressed when an operator is no longer bound by the repressor, the 100 fold decrease in K_s in the presence of the inducer leads to how much induction of the operon? The ratio of expression in the presence of inducer to that in the absence of inducer is:

a. 100

b. 10

c. 1

d. 0.1

e. 0.01

b is correct, the operon is expressed at a 10-fold higher level ($0.91/0.09 = 10.1$; this is the ratio of free operators in the presence of inducer, which is $1.00 - 0.09 = 0.91$, to free operators in the absence of inducer, which is $1.00 - 0.91 = 0.09$)

20. (10 pts) The kinetics of reassociation of the genomic DNA of a plant resolved into three components with the following characteristics.

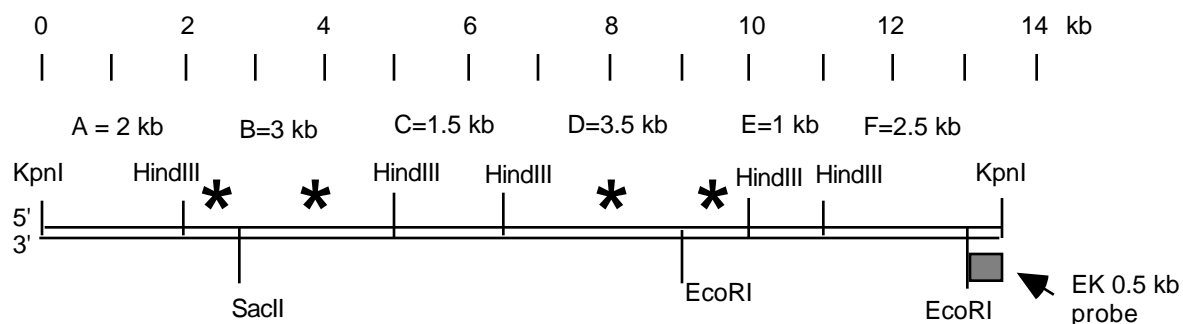
Component	fraction of genome	measured $C_{0t_{1/2}}$
I	0.2	10^{-3}
II	0.4	1
III	0.4	10^3

The measured $C_{0t_{1/2}}$ values are for the mixture of all three components in genomic DNA. Under identical conditions, a phage genome with a complexity of 10^5 renatures with a $C_{0t_{1/2}}$ of 1. Assume that the slow renaturing component III is single-copy. What is the **repetition frequency** of components I and II?

	Component I	Component II
a.	10^6	10^3
b.	4×10^4	400
c.	20	4×10^4
d.	10^{-3}	1

a. is correct.

Use the following information for the next 5 problems. A map of a 13.5 kb *Kpn*I fragment of genomic DNA containing the *FINI* gene is shown below. The fragments from a *Kpn*I + *Hind*III digest that hybridize to *FINI* mRNA are marked with the large asterisks



21. (5 pts) When the *Eco*RI site at position 9 kb on the map is end-labeled on the bottom strand, hybridization to *FINI* mRNA protects the labeled DNA from digestion by S1 nuclease, whereas hybridization to *FINI* mRNA does not protect DNA end-labeled at the *Eco*RI site on the top strand. What is the direction of transcription of the *FINI* gene?

- 5' to 3' left to right; the bottom strand is the template for RNA polymerase.
- 5' to 3' left to right; the top strand is the template for RNA polymerase.
- 5' to 3' right to left; the bottom strand is the template for RNA polymerase.
- 5' to 3' right to left; the top strand is the template for RNA polymerase.

a is correct.

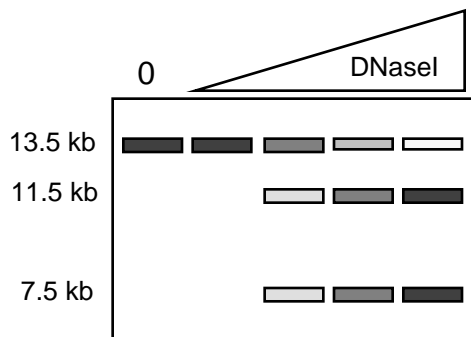
22. (5 pts) The cDNA clone for *FINI* mRNA was digested with a restriction endonuclease to generate a 5' half and a 3' half of the clone, which were used separately as hybridization probes against a Southern blot of a *Kpn*I + *Hind*III digest of the genomic DNA clone. The 3 kb *Hind*III fragment hybridized only to the 5' half of the *FINI* cDNA, whereas the 3.5 kb *Hind*III fragment

hybridized only to the 3' half of the *FINI* cDNA. What do you conclude about the gene or genes present in the 13.5 *KpnI* fragment?

- a. Two different genes, both related to *FINI* are present.
- b. A single *FINI* gene with no exons is present.
- c. A single *FINI* gene with four exons is present.
- d. A single *FINI* gene with at least two exons is present.
- e. Two different genes related to *FINI* are divergently transcribed from this region.

d. is correct.

23. (5 pts) The *FINI* gene is expressed in kidney cells. Nuclei from kidney cells were isolated and digested with increasing amounts of DNase I. The nuclear DNA was purified, digested with *KpnI*, separated on an agarose gel, transferred to a nylon membrane and hybridized with a radioactive 0.5 kb *EcoRI* to *KpnI* fragment (labeled EK0.5 kb in the map above). In the results shown below, the density of fill in the boxes is proportional to the intensity of the bands on the autoradiogram.



What do you conclude from these data? Please answer relative to the map (above) of the 13.5 kb *KpnI* fragment.

- a. Proteins are bound to the 7.5 kb and 11.5 kb DNA fragments.
- b. Proteins bound to the 7.5 kb and 11.5 kb DNA fragments compete for binding to the 13.5 kb DNA fragment.
- c. DNase I hypersensitive sites are present at positions 2 kb and 6 kb on the map.
- d. DNase I hypersensitive sites are present at positions 7.5 kb and 11.5 kb on the map.
- e. The *FINI* DNA sequence is resistant to cleavage by DNase I.

c is correct; 2 pts for d.

24. (5 pts) Deletion of the 1.5 kb *HindIII* fragment labeled C in the map above causes a substantial decrease in the level of expression of the *FINI* gene in kidney cells. Addition of this DNA fragment at the 5' or 3' end of the mutated *FINI* gene (i.e. with the deletion of the 1.5 kb *HindIII* fragment) will restore high level expression, regardless of its orientation relative to the promoter. What do you conclude about the 1.5 kb *HindIII* fragment?

- a. It contains the promoter for a *FINI* gene.
- b. It contains an enhancer that is located 5' to the gene in the wild-type gene.
- c. It contains a silencer that is located 3' to the gene in the wild-type gene.
- d. It contains an enhancer that is located in an intron of the wild-type gene.
- e. It contains a silencer that is located between the two genes related to *FINI*.

d is correct; 3 pts for b.

In the choices below, the amino acid encoded by the altered codon is underlined.

Wild-type:

- a. AlaGlyGlyGlyGluArgArgArgCys
- b. SerTrpTrpTrpStop
- c. LysLeuValValValSerAlaGlyGlyVal
- d. AspThrAlaGlyGlyHisHisHisGlnLeu
- e. ThrProProAlaLeuThrThrThrSerLeu

Mutant:

- a. AlaGlyGlyGlyGluArgArgArgCys
- b. SerTrpTrpTrpStop
- c. LysLeuValValValSerAlaValGlyVal
- d. AspThrAspGlyGlyHisHisHisGlnLeu
- e. ThrProThrAlaLeuThrThrThrSerLeu

c is correct; 4 pts for d and e. This sequence and mutation are actually from the (proto)oncogene *HRAS*, and the designated mutation is tumorigenic.

27. (5 pts) Which of the following statements about protein synthesis in *E. coli* is true?

- a. The peptidyl transferase step requires hydrolysis of high energy phosphate bonds in GTP.
- b. Binding of f-Met-tRNA to the mRNA on the small ribosomal subunit utilizes ATP and an elongation factor.
- c. Translocation of the peptidyl-tRNA from the A site to the P site of the ribosome is catalyzed exclusively by an RNA component of the ribosome.
- d. Base pairing between a short segment of the 16S rRNA (in the small subunit) and its complement in the 5' untranslated region of the mRNA is used to recognize the initiator AUG.

d. is correct

28. (5 pts) How is high processivity achieved by *E. coli* RNA polymerase for the elongation phase of transcription?

- a. The subunit dissociates and the core polymerase forms a ring around the DNA template.
- b. The NusA protein forms a ring around the DNA template and then binds to the polymerase.
- c. The NusA protein provides additional helicase activity to the core polymerase.
- d. The protein Rho (or) enhances the helicase activity of the core polymerase.

a. is correct

29. (5 pts) Which of the following statements about introns and splicing of the precursors to mRNA are correct?

- [1] The initiating nucleophile for splicing of nuclear pre-mRNA is the 2' hydroxyl of an internal adenine nucleotide.
- [2] Introns begin with GU and end with AG.
- [3] Particular snRNPs bind at the branch point and the 5' splice site.
- [4] Assembly of a spliceosome require the cleavage of high-energy bonds from ATP.

- a. 2, 3b. 1, 4 c. 2, 3, 4 d. 1, 2, 3 e. 1, 2, 3, 4

e. is correct, 3 pts for c and d, 2 pts for a and b.

30. (5 pts) Which of the following proteins catalyze the polymerization of nucleotides? Do not choose an option with any incorrect responses.

- a. DnaA and PriA
- b. DnaG and telomerase

- c. DnaG and RecA
- d. UvrD and DnaB

b. is correct.

31. (5 pts) How does DNA polymerase III achieve high processivity? Choose the correct statement.

- a. The core () is inherently highly processive.
- b. The complex is a "clamp" that holds the polymerase core onto the template.
- c. The complex loads the β "sliding clamp" onto the primer-template junction, and after ATP hydrolysis the β clamp will exchange from the complex to the core.
- d. The β "sliding clamp" is irreversibly linked to the polymerase core.

c. is correct.

32. (5 pts) Which of the following *E. coli* DNA repair enzymes could be used to repair a thymine dimer in duplex DNA? Choose the option with the most correct responses; do not choose an option with any incorrect responses.

- [1] MutHLS
- [2] photolyase
- [3] Thymine-N-glycosylase plus AP endonuclease
- [4] UvrABC plus UvrD

- a. 1
- b. 2
- c. 4
- d. 1, 2, 4
- e. 2, 4

e. is correct; 3 pts for b or c.

33. (5 pts) Consider a circular, B form DNA molecule with a superhelical density of -0.05. (The superhelical density is W/T). Suppose that during initiation of replication, 50 base pairs unwind (untwist) without breaking the phosphodiester backbone. What will be the effect on the linking number (L) and the supercoiling (W)?

- a. The effect cannot be determined without knowing the length of the DNA molecule.
- b. $L = 0$ and $W = +5$
- c. $L = 0$ and $W = -5$
- d. $L = -5$ and $W = +5$

b. is correct. $\Delta T = -5$ (50 bp/10 bp per twist are removed), $\Delta L = 0$ since no covalent bonds in the DNA are broken and reformed, so $\Delta W = -\Delta T = +5$.

34. (5 pts) Which of the following is the best definition of *complementation* ?

- a. The synthesis of RNA from a DNA template.
- b. The acquisition of new genetic markers by bacteria (generating a new phenotype) by incorporation of added DNA.
- c. The synthesis of a polypeptide directed by mRNA.
- d. The production of a normal (or wild-type) phenotype from combinations (crosses) of two mutants.

d. is correct.

35. (5 pts) Which of the following enzymes catalyzes homologous pairing and invasion of single stranded DNA into a duplex during recombination?

- a. RecBCD
- b. RecA
- c. The 5' to 3' exonuclease activity of DNA polymerase I
- d. RuvC

b is correct.

The Genetic Code

1st	Position in Codon								3rd
	U		C		A		G		
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys	C
	UUA	Leu	UCA	Ser	UAA	Term	UGA	Term	A
	UUG	Leu	UCG	Ser	UAG	Term	UGG	Trp	G
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	U
	CUC	Leu	CCC	Pro	CAC	His	CGC	Arg	C
	CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg	A
	CUG	Leu	CCG	Pro	CAG	Gln	CGG	Arg	G
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	U
	AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser	C
	AUA	Ile	ACA	Thr	AAA	Lys	AGA	Arg	A
	AUG*	Met	ACG	Thr	AAG	Lys	AGG	Arg	G
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	U
	GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly	C
	GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly	A
	GUG*	Val	GCG	Ala	GAG	Glu	GGG	Gly	G

* Sometimes used as initiator codons.

Equations for complexity (N) and repetition frequency (R):

$$N_n = C_0 t_{1/2}^{\text{pure}, n} \times \frac{N^{\text{std}}}{C_0 t_{1/2}^{\text{std}}}$$

$$R_n = \frac{f_n G}{N_n} = \frac{C_0 t_{1/2}^{\text{mix single copy}}}{C_0 t_{1/2}^{\text{mix } n}}$$

Equation for specificity of binding of a protein (P) to DNA (K_s is the equilibrium binding constant to specific DNA sites, or D_s, K_{ns} is the equilibrium binding constant to nonspecific DNA sites, or D_{ns}):

$$\text{specificity} = \frac{K_s}{K_{ns}} = \frac{[PD_s]}{[D_s]} \times \frac{[D_{ns}]}{[PD_{ns}]} = \frac{[PD_s]}{[D_s]} \times \frac{[D_{ns}]}{[P \text{ total}] - [D_s \text{ total}]}$$

Relationship between G and K_{eq} , where K_{eq} is an equilibrium constant:

$$G = -RT \ln K_{eq}$$

$$R = 1.98 \times 10^{-3} \text{ kcal deg}^{-1} \text{ mol}^{-1}$$

$$T = 298^\circ \text{ K}$$

In an abortive transcription assay, the lag time between the mixing of reagents and the optimal rate of abortive transcript production is related to the concentration of RNA polymerase (or [RNAP]) by the following equation (K_B is the equilibrium constant for binding of RNAP to the promoter, and k_f is the forward rate constant for the closed to open transition):

$$\text{lag time} = \frac{1}{K_B k_f} \times \frac{1}{[RNAP]} + \frac{1}{k_f}$$

