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7.014 Problem Set 3

Please print out this problem set and record your answers on the printed copy.

Problem sets will not be accepted late.

Question 1

Hypothetical organism X has the following DNA sequence. Part of the promoter is indicated by the boxed sequence. Transcription starts at and includes the bold A/T base pair.

```
5′ [XXXX] TATTTGAT A G CTCTATGCAT GCATGGGTCC TGAAGTTCAG ATCTTTGAGT CATAGGAGTC 3′
3′ [XXXX] ATAAACTA T C GAGATACGTA CGTACCCAGG ACTTCAAGTC TAGAAACTCA GTATCCTCAG 5′
```

a) Give the RNA sequence of the first 25 bases following transcription.

b) What are the first 5 amino acids of the resulting protein?

c) Finish translating the following mRNA sequence.

```
   1
5′ AUA UUU AUG CAU GGG ACU UAU AGC GAU AGC UAC UAA CAU AAG 3′
   ile phe met ___ ___ ___ ___ ___ ___ ___ ___ ___ ___ ___
```

d) The organism that makes the above RNA sequence is exposed to a mutagen. What does a mutagen do?

e) For each of the following mutations, identify the type of mutation (insertion, deletion, point, or silent) that occurred in the DNA and the affect on the resulting protein. Consider each mutation independently.

i) C10 → A10

ii) A40 → U40

iii) T12 → C12

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Question 1,continued

f) You purify protein made from different mutant organisms. Each new protein sequence results from a single change (insertion, deletion, or substitution) in the sequence given. Modify the DNA sequence given such that it would encode each new protein.

i) Ile Phe Met His Gly Thr Tyr Ser Glu Ser Tyr

5′ AUA UUU AUG CAU GGG ACU UAU AGC GAU AGC UAC UAA CAU AAG 3′

ii) Ile Phe Met Gln Trp Asp Leu

5′ AUA UUU AUG CAU GGG ACU UAU AGC GAU AGC UAC UAA CAU AAG 3′

Question 2

You are studying replication in your favorite bacteria when you notice the replication fidelity has decreased by a factor of 100.

a) You suspect this is caused by a mutation in the gene for the replicative enzyme. Circle the activity that you suspect is altered and results in this decrease in fidelity.

5' → 3' polymerase	5' → 3' exonuclease	3' → 5' exonuclease
mismatch repair	helicase	ligase

b) You purify the above protein and find that it is approximately half the size you expect it to be given DNA sequence data. Explain what kind of mutation could cause this result.

c) Your roommate in course 5 has designed a unique amino acid and creates a tRNA charged with this new amino acid. This new tRNA recognizes the codon 5' UGA 3'. You add this charged tRNA to the replication deficient mutant cells from above and find that now the fidelity is increased. Speculate why the addition of the novel tRNA results in this increased fidelity.

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Question 3

Martians, tired of hiding from our spacecraft, send their own spacecraft to Earth with some single-celled Martian organisms. They are willing to give these to NASA on the condition that we leave Mars alone.

Instead of having only 4 bases, their DNA has 8 different bases: B, C, D, E, W, X, Y, and Z. Chemical analysis of a single-celled Martian organism reveals that its genome is composed of:

B: 13% C: 7% D: 13% E: 19% W: 19% X: 11% Y: 7% Z: 11%

a) Identify which bases pair with each other.

b) Martian DNA replicates in a manner analogous to that seen with earthly DNA. Given this Draw a replication fork and label the following:

leading strand
lagging strand
RNA primer
2 Okazaki fragments
5' and 3' ends (10 total)

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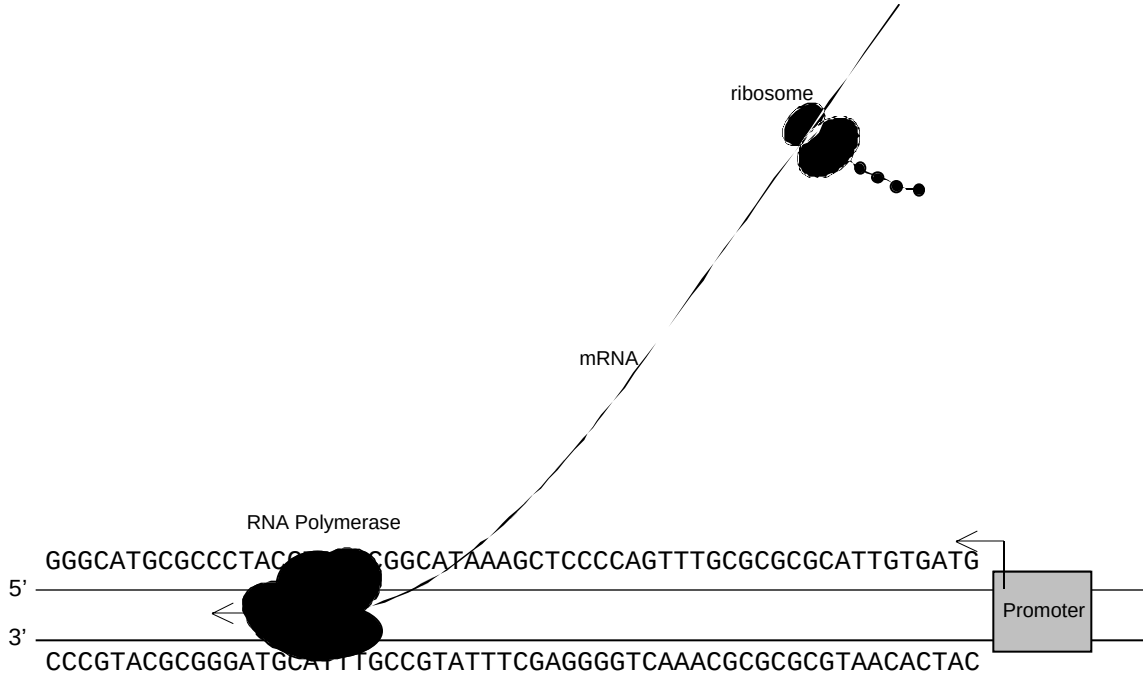
Question 4



a) On the above graphic…

i) Label the N (amino) termini of the protein being made.

ii) Box the 3 bases encoding the first amino acid of the protein being made.

iii) Circle the part of the schematic where tRNAs would bind.

b) Draw the tRNA encoding trp, include the sequence for the anticodon. Be sure to label the 5' and 3' ends.

c) Would a substitution within a codon for trp always change the resulting protein sequence? Explain your answer.

d) Would a substitution within a codon for thr always change the resulting protein sequence? Explain your answer.

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	U		C		A		G		
U	UUU	**phe (F)**	UCU	**ser (S)**	UAU	**tyr (Y)**	UGU	**cys (C)**	U
	UUC	**phe**	UCC	**ser**	UAC	**tyr**	UGC	**cys**	C
	UUA	**leu (L)**	UCA	**ser**	**UAA**	**STOP**	**UGA**	**STOP**	A
	UUG	**leu**	UCG	**ser**	**UAG**	**STOP**	UGG	**trp (W)**	G
C	CUU	**leu**	CCU	**pro (P)**	CAU	**his (H)**	CGU	**arg (R)**	U
	CUC	**leu**	CCC	**pro**	CAC	**his**	CGC	**arg**	C
	CUA	**leu**	CCA	**pro**	CAA	**gln (Q)**	CGA	**arg**	A
	CUG	**leu**	CCG	**pro**	CAG	**gln**	CGG	**arg**	G
A	AUU	**ile (I)**	ACU	**thr (T)**	AAU	**asn (N)**	AGU	**ser (S)**	U
	AUC	**ile**	ACC	**thr**	AAC	**asn**	AGC	**ser**	C
	AUA	**ile**	ACA	**thr**	AAA	**lys (K)**	AGA	**arg (R)**	A
	AUG	**met (M)**	ACG	**thr**	AAG	**lys**	AGG	**arg**	G
G	GUU	**val (V)**	GCU	**ala (A)**	GAU	**asp (D)**	GGU	**gly (G)**	U
	GUC	**val**	GCC	**ala**	GAC	**asp**	GGC	**gly**	C
	GUA	**val**	GCA	**ala**	GAA	**glu (E)**	GGA	**gly**	A
	GUG	**val**	GCG	**ala**	GAG	**glu**	GGG	**gly**	G