Some sample Molecular Biology problems for Bio 110, part 1

This document contains some sample problems to give you practice analyzing nucleic acids. Remember: if there is a term or concept you aren’t familiar with, you can always look it up! An answer key is provided in a separate document, but you should give these problems your best effort BEFORE looking at the answers.

A few multiple choice problems for you to try; these are end-of-chapter problems from Campbell’s *Biology*; they focus on DNA replication and transcription.

**Question 1:**

A biochemist isolates and purifies various molecules needed for DNA replication. When she adds some DNA, replication occurs, but each DNA molecule consists of a normal strand paired with numerous segments of DNA a few hundred nucleotides long. What has she probably left out of the mixture?

1. DNA polymerase
2. DNA ligase
3. nucleotides
4. Okazaki fragments
5. primase

**Question 2:**

What is the basis for the difference in how the leading and lagging strands of DNA molecules are synthesized?

* 1. The origins of replication occur only at the 5' end.
	2. Helicases and single-strand binding proteins work at the 5' end.
	3. DNA polymerase can join new nucleotides only to the 3' end of a growing strand.
	4. DNA ligase works only in the 3' → 5' direction.
	5. Polymerase can work on only one strand at a time.

**Question 3:**

In analyzing the number of different bases in a DNA sample, which result would be consistent with the base-pairing rules?

* 1. A = G
	2. A + G = C + T
	3. A + T = G + T
	4. A = C
	5. G = T

**Question 4:**

The elongation of the leading strand during DNA synthesis:

1. progresses away from the replication fork
2. occurs in the 3' → 5' direction
3. produces Okazaki fragments.
4. depends on the action of DNA polymerase.
5. does not require a template strand.

**Question 5:**

Which of the following is **not** true about **both** DNA replication and transcription?

1. The newly synthesized nucleic acid is built in a 5’ to 3’ direction.
2. A polymerase catalyzes the attachment of new nucleotides on the growing chain.
3. The DNA double helix must be unwound.
4. The newly synthesized nucleic acid is complementary to the template.
5. Primers are required to initiate nucleic acid synthesis.

**Question 6:**

A part of the promoter, called the TATA box, is said to be highly conserved in evolution. Which of the following might explain this observation?

1. The sequence of the TATA box evolves very rapidly.
2. The sequence of the TATA box does not mutate.
3. Mutation in the TATA box is selected against.
4. The TATA box is found in many, but not all, promoters.
5. The TATA box is a transcribed portion of the gene.

**Question 7**:

In eukaryotic cells, transcription cannot begin until:

1. the two DNA strands have completely separated and exposed the promoter.
2. several transcription factors have bound to the promoter.
3. the 5' caps are removed from the mRNA
4. the DNA introns are removed from the template.
5. DNA nucleases have isolated the transcription unit.

**Question 8:**

Which of the following is *not* true of RNA processing?

1. Exons are cut out before mRNA leaves the nucleus.
2. Nucleotides may be added at both ends of the RNA.
3. Ribozymes may function in RNA splicing.
4. RNA splicing can be catalyzed by spliceosomes.
5. A primary transcript is often much longer than the final RNA molecule that leaves the nucleus.

And a non-multiple choice central dogma question…

**Question 9**: This problem focuses on understanding complementarity of base pairing and polarity in double-stranded nucleic acids.

The sequence below represents a short RNA.

5’--A U U A G G C C G A U A C G A U U A C C—3’

Using this sequence, write out the sequence of the double stranded DNA molecule from which this RNA was derived. Be sure to label the 5’ and 3’ ends of both strands of the DNA molecule. In addition, label the appropriate DNA strands as “template” and “non-template”.