ANSWERS TO PROBLEMS ON MOLECULAR BIOLOGY, PROTEIN SYNTHESIS, AND LIFE CYCLES

1. c.

2. d. The G+C fraction may be different for different DNAs, although it is a very crude way of distinguishing DNAs. This fraction varies from as low as 20% to as high as 80% among different bacteria; among eukaryotes, it is generally around 50%.

3. a. fmet-arg-leu-ser-pro-val
   b. Seven bases in 7 positions are different. There are no amino acid differences. This is an example of “degeneracy”, which means that two or more codons can code for the same amino acid.
   c. Three bases in two codons are different. Two amino acids are different. This is an example of two “mis-sense” mutations, in which codon meanings are changed.
   d. One base in one position is different. The amino acid chain 4) lacks most of the amino acids in 2), because the base change produced a new termination codon.
   e. Sequence 5) has an additional A after the seventh base. This addition changes the third codon and the codons that follow, because it changes the “reading frame” (the way that bases fit into codons). Thus it changes all the corresponding amino acids. Note that the deletion of one (or two) base would have the same effect.

4. The mRNA would have the following sequence, which bases above and below one another represent alternatives.

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AUG GCU CCU CCU UUA UGG AUG GGU ...
 A A A A
 G G G CUU G
 C C C A C
 G
 C
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The total degeneracy is quantified by the number of possible mRNAs, which in this case is 4x4x4x6x4=1536. Any mRNA with one of the possible sequences would give the appropriate amino acid sequence and would be a real mRNA.