Proteins and Their Translation

BASIC PROBLEMS

1.

3´ CGT ACC ACT GCA 5´	DNA double helix (transcribed strand)
5´ GCA TGG TGA CGT 3´	DNA double helix
5´ GCA UGG UGA CGU 3´	mRNA transcribed
3´ CGU ACC ACU GCA 5´	appropriate tRNA anticodon
NH_3 - Ala - Trp - (stop) - COOH	amino acids incorporated

2. **a. and b.** 5´UUG GGA AGC 3´

c. and d. Assuming the reading frame starts at the first base:

NH_3 - Leu - Gly - Ser - COOH

For the bottom strand, the mRNA is 5´GCU UCC CAA 3´ and assuming the reading frame starts at the first base, the corresponding amino acid chain is NH_3 - Ala - Ser - Gln - COOH.

3. (5) With an insertion, the reading frame is disrupted. This will result in a drastically altered protein from the insertion to the end of the protein (which may be much shorter or longer than wild type because of altered stop signals).

6. There are three codons for isoleucine: 5´ AUU 3´, 5´ AUC 3´, and 5´ AUA 3´. Possible anticodons are 3´ UAA 5´ (complementary), 3´ UAG 5´ (complementary), and 3´ UAI 5´ (wobble). 5´ UAU 3´, although complementary, would also base-pair with 5´ AUG 3´ (methionine) due to wobble and therefore would not be an acceptable alternative.

8. The codon for amber is UAG. Listed below are the amino acids that would have been needed to be inserted to continue the wild-type chain and their codons:

glutamine	CAA, CAG*
lysine	AAA, AAG*
glutamic acid	GAA, GAG*
tyrosine	UAU*, UAC*
tryptophan	UGG*
serine	AGU, AGC, UCU, UCC, UCA, UCG*

In each case, the codon marked by an asterisk would require a single base change to become UAG.

9. **a.** The codons for phenylalanine are UUU and UUC. Only the UUU codon can exist with randomly positioned A and U. Therefore, the chance of UUU is $(1/2)(1/2)(1/2) = 1/8$.

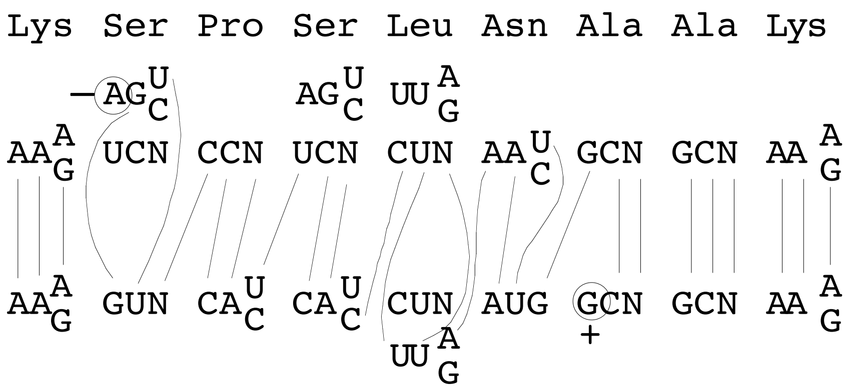
b. The codons for isoleucine are AUU, AUC, and AUA. AUC cannot exist. The probability of AUU is $(1/2)(1/2)(1/2) = 1/8$, and the probability of AUA is $(1/2)(1/2)(1/2) = 1/8$. The total probability is thus $1/4$.

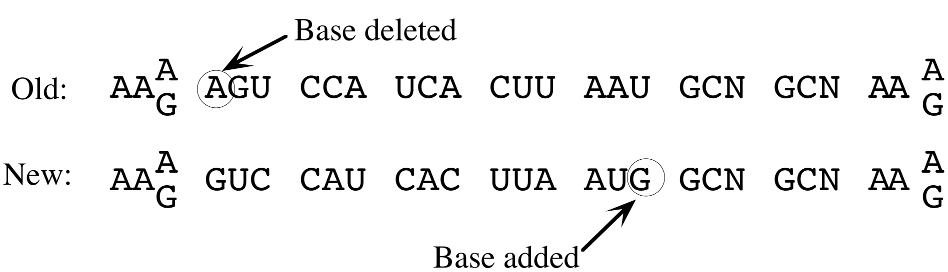
c. The codons for leucine are UUA, UUG, CUU, CUC, CUA, and CUG, of which only UUA can exist. It has a probability of $(1/2)(1/2)(1/2) = 1/8$.

d. The codons for tyrosine are UAU and UAC, of which only UAU can exist. It has a probability of $(1/2)(1/2)(1/2) = 1/8$.

20. Initiaton of translation in eukaryotes requires initiation factors (eIF4a, b, and G) that associate with the 5´ cap of the mRNA. Because prokaryotic mRNAs are not capped, translation would not initiate.

24. **a. and b.** The goal of this type of problem is to align the two sequences. You are told that there is a single nucleotide addition and single nucleotide deletion, so look for single base differences that effect this alignment. These should be located where the protein sequence changes (i.e., between Lys-Ser and Asn-Ala). Remember also that the genetic code is redundant. (N = any base)





29. **a. and b.** The sequence of double-stranded DNA is as follows:

5´–TAC ATG ATC ATT TCA CGG AAT TTC TAG CAT GTA–3´

3´—ATG TAC TAG TAA AGT GCC TTA AAG ATC GTA CAT—5´

First look for stop codons. Next look for the initiating codon, AUG (3´—TAC—5´ in DNA). Only the upper strand contains the necessary codons.

DNA	3´ TAC GAT CTT TAA GGC ACT 5´
RNA	5´ AUG CUA GAA AUU CCG UGA 3´
protein	Met Leu Glu Ile Pro stop

The DNA strand is read from right to left as written in your text and is written above in reverse order from your text.

c. Remember that polarity must be taken into account. The inversion is

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DNA 5´ TAC ATG CTA GAA ATT CCG TGA AAT GAT CAT GTA 3´
RNA 3´         —GAU CUU UAA GGC ACU UUA CUA GUA—    5´
amino acids     HOOC  7   6   5   4   3   2   1 —NH3
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d.

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DNA   3´ATG TAC TAG TAA AGT GCC TTA AAG ATC GTA CAT 5´
mRNA  5´UAC AUG AUC AUU UCA CGG AAU UUC UAG 3´
                 1   2   3   4   5   6   7   stop
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Codon 4 is 5´—UCA—3´, which codes for Ser. Anticodon 4 would be 3´—AGU—5´ (or 3´—AGI—5´ given wobble).