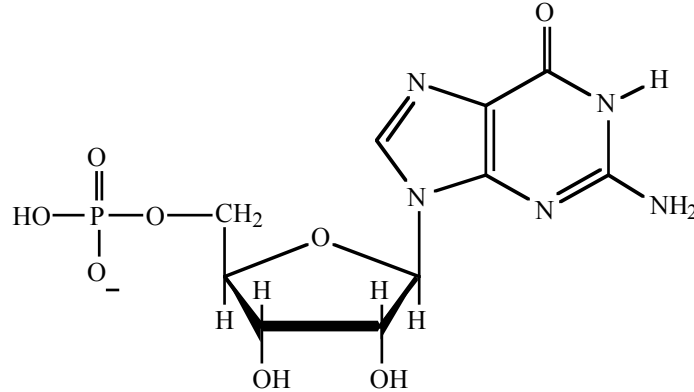


CHAPTER 16: ANSWERS TO SELECTED PROBLEMS

SAMPLE PROBLEMS (“Try it yourself”)

16.1 Connecting the base guanine (shown in Table 16.1) with ribose and phosphate gives the structure of GMP.



16.2 When we match each base in the original strand with its complement (A with T, C with G), we get the base sequence AAACGTTT. However, since the two strands run in opposite directions, this sequence is written from the 3' end to the 5' end. Turning the sequence around gives us **TTTGCAA** (which is the same as the sequence in the original strand!).

16.3 The RNA strand has the same sequence as the coding strand in the DNA molecule, except that RNA uses the base U instead of T. Therefore, the RNA base sequence is **ACAAUGG**.

16.4 We need to divide up the RNA bases into three-base codons:

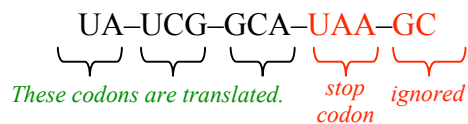


Then we use the genetic code (Table 16.4) to translate these codons. The amino acid sequence is **Gly – Arg – Pro**.

16.5 The last two amino acids are Ser–Ala (serine – alanine). Here are the base sequences in the DNA template strand and the mRNA:

<i>DNA coding strand:</i>	TATCGGCATAAGC
<i>DNA template strand:</i>	ATAGCCGTATTTCG
<i>mRNA:</i>	UAUCGGCAUAAGC

The mRNA contains the code for the end of a protein, so it must contain a stop codon. To translate the mRNA, we must first look for the stop codon, then work backward to divide the mRNA into codons. All of the bases after the stop codon are ignored. The only stop codon in the mRNA sequence is UAA, so the mRNA is read as follows



The last two codons that are translated are UCG and GCA. These correspond to the amino acids **Ser (serine) and Ala (alanine)**.

16.6 This is a substitution mutation, but we need to classify it further as either a silent mutation, a missense mutation, or a nonsense mutation. Let us compare how the original and mutated DNA molecules are transcribed and translated:

Original DNA coding strand: AAA

Mutated DNA coding strand: TAA

Original mRNA: AAA

Mutated RNA: UAA

Translation: Lys

Translation: stop codon

Since the mutation produces a stop codon, this is a **nonsense mutation**. It will result in a protein that is missing all of the amino acids starting from the mutation.

16.7 The new DNA sequence is ATCATTACG, and the corresponding mRNA sequence is AUCAUUACG. When we translate this mRNA, we get the amino acid sequence Ile – Ile – Thr. This mutation does not produce a frameshift, because all of the codons beyond the mutation remain unchanged. (Deletions and additions do not produce frameshifts when the number of bases removed or added is a multiple of three.)

END OF SECTION PROBLEMS

Section 16.1

16.1 The three components of a nucleotide are a five-carbon sugar, a phosphate group, and an organic base.

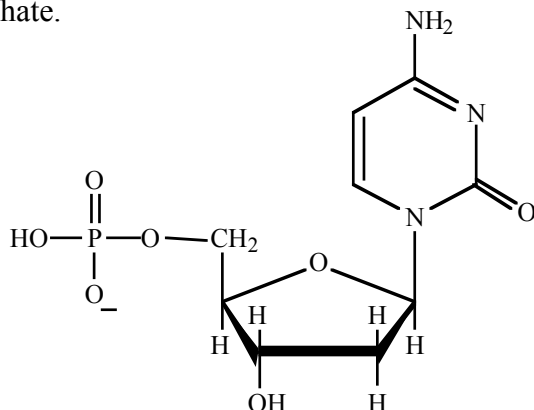
16.2 The base is attached to the 1' carbon atom in the sugar.

16.3 Thymine (T) is in DNA, but not in RNA. Uracil (U) is in RNA, but not in DNA.

16.4 Ribose (the sugar in RNA) has a hydroxyl group bonded to the 2' carbon. Deoxyribose (the sugar in DNA) has a hydrogen atom in place of the hydroxyl group.

16.5 Nucleotides contain the phosphate group, while nucleosides do not.

16.6 The structure of dCMP is shown below. This nucleotide is made from deoxyribose, cytosine, and phosphate.



16.7 This nucleotide contains ribose (note the OH group attached to the 2' carbon atom of the sugar), and it contains the base guanine (see Table 16.1), so it is GMP.

16.8 GMP contains the sugar ribose, while dGMP contains the sugar deoxyribose.

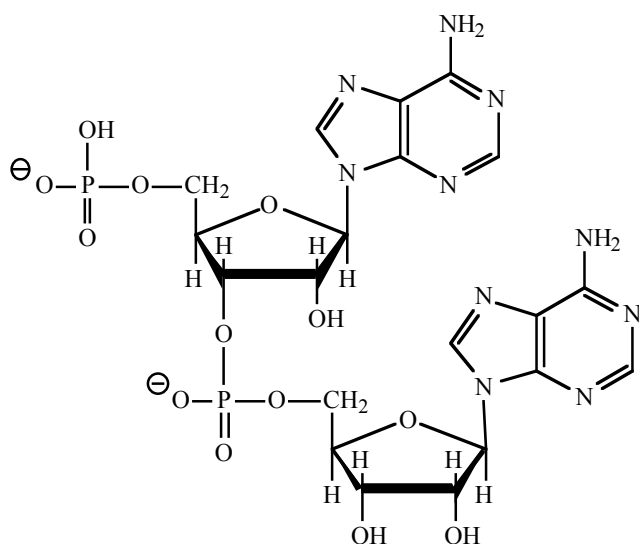
16.9 GMP contains one phosphate group bonded to ribose, while GDP and GTP contain chains of two or three phosphate groups, respectively.

Section 16.2

16.10 The phosphodiester group links the 5' carbon atom of one sugar to the 3' carbon atom of a second sugar.

16.11 The base is not part of the backbone. The backbone is the alternating chain of sugars and phosphates.

16.12 Use Figure 16.3 to guide you as you do this problem. Both bases are adenine, which is shown in Table 16.1. The structure of the dinucleotide is shown below.



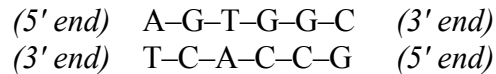
The dinucleotide that is formed from two molecules of AMP.

16.13 a) G forms a stable base pair with C (cytosine).
b) A forms a stable base pair with T (thymine).

16.14 The two DNA strands are held next to one another by hydrogen bonds between the complementary bases.

16.15 a) The base on the 5' end of this strand is A. (DNA strands are normally written with the 5' end on the left and the 3' end on the right.)

b) The base on the 5' end of the complementary strand is G. Here are the two strands, written to show how they complement one another:



c) The base sequence of the complementary strand is GCCACT (writing the sequence from the 5' end to the 3' end).

16.16 A histone is a protein that binds to DNA. DNA wraps itself around clusters of histones, as shown in Figure 16.8.

16.17 A chromosome is a DNA molecule, together with all of the proteins and RNA that bind to it. There is only one DNA molecule in a chromosome.

16.18 In the double helix structure, two DNA strands coil around one another. The bases in each strand face the other strand, and the backbones face outward.

16.19 In a eukaryotic cell, the DNA is located in the nucleus. RNA is distributed throughout the cell, but most of the RNA is located in the cytoplasm.

Section 16.3

16.20 DNA replication is the process in which a cell makes an exact copy of its DNA.

16.21 Most cells in the human body contain 46 chromosomes, of which 44 are autosomal chromosomes and two are sex chromosomes.

16.22 Building DNA, like all anabolic processes, requires energy. The cell gets the energy by breaking the bonds between the phosphate groups in the nucleoside triphosphates:



16.23 A primer is a short piece of RNA that is complementary to a DNA sequence. In DNA replication, each new DNA strand starts with a primer, which is made by an enzyme called primase.

16.24 DNA ligase removes the RNA primers, replaces them with DNA nucleotides, and seals the gaps between the newly-made pieces of DNA.

16.25 Option B is correct. Each of the two new DNA molecules contains one of the original strands and one new strand.

16.26 DNA polymerase makes one mistake for every 100,000 nucleotides. The cell reduces this error rate in two ways. First, it uses “proof-reading” enzymes that remove mismatched nucleotides and replace them with the correct nucleotides during replication. Second, it uses repair enzymes that locate and repair sections of damaged DNA.

Section 16.4

16.27 Transcription is the process in which a cell makes a molecule of RNA, using a DNA strand as a template.

16.28 Statement “a” is correct.

16.29 Option A is correct. The two DNA strands re-form their hydrogen bonds after transcription, and the RNA is released as a single strand.

16.30 A gene is a section of DNA that is transcribed as a single RNA molecule.

16.31 The template strand binds to the RNA during transcription.

16.32 The RNA sequence is AACCUUG. Remember that the RNA is the complement of the template strand, which is in turn the complement of the coding strand.

Coding strand (DNA): (5' end) AACCTTG (3' end)

Template strand (DNA): (3' end) TTGGAAC (5' end)

RNA strand: (5' end) AACCUUG (3' end)

16.33 Both transfer RNA and ribosomal RNA are originally made as parts of a larger RNA molecule. During processing, enzymes remove the extra nucleotides. Transfer RNA and ribosomal RNA differ in that transfer RNA is modified after the extra RNA is removed; three extra nucleotides are added to the 3' end of the tRNA, and several of the bases are chemically modified.

16.34 Introns are sections in the interior of a messenger RNA molecule that do not code for amino acids. The introns are removed and broken down during mRNA processing.

16.35 a) Messenger RNA b) Transfer RNA c) Messenger RNA

Section 16.5

16.36 Translation is the process in which the cell builds a polypeptide, using the sequence of bases in mRNA to determine the correct order of the amino acids.

16.37 A codon is a sequence of three bases in a messenger RNA molecule. Codons are the information units of mRNA; each codon (except the stop codons) corresponds to a single amino acid.

16.38 A stop codon signals the end of a polypeptide chain. When the ribosome reaches a stop codon, it stops translation and releases the completed polypeptide.

16.39 AUG is the codon for the amino acid methionine, and it is the start codon. Translation always starts at an AUG codon (but only the first AUG in a messenger RNA is a start signal; any other AUG codons simply mean “put a methionine here”).

16.40 The amino acid sequence is Asn–Arg–Leu (asparagine–arginine–leucine).

- 16.41 a) Two codons correspond to aspartic acid (GAC and GAU).
b) Methionine (Met) and tryptophan (Trp) have only one codon apiece.

16.42 Since this mRNA contains the code for the beginning of the polypeptide, it must contain a start codon (AUG), and translation begins with the start codon. (All bases before the start codon are ignored.) In this case, the start codon is bases 3, 4 and 5, so we divide up the mRNA into codons as follows:

C–A – **A–U–G** – U–U–G – G–C–A – U–A–C – G–?–?

Then we translate these codons, starting with AUG. The first three amino acids are Met, Leu, and Ala (methionine, leucine, and alanine).

16.43 Since this mRNA contains the code for the end of the polypeptide, it must contain a stop codon (UAA, UAG or UGA). All bases after the stop codon are ignored. In this case, the stop codon is bases 12, 13 and 14 (UGA). We work backward from this sequence to divide up the mRNA into codons:

?–C–G – C–A–G – A–G–A – G–A–C – **U–G–A** – C–U–A

Then we translate the last three codons before AUG. The last three amino acids are Gln, Arg, and Asp (glutamine, arginine, and aspartic acid).

- 16.44 a) The mRNA base sequence is ACAUCGUUC.
b) The amino acid sequence is Thr–Ser–Phe (threonine–serine–phenylalanine).

Section 16.6

16.45 Ribosomes are the parts of a cell that build proteins. They are made from RNA and proteins.

16.46 Transfer RNA bonds to an amino acid, carries it to the ribosome, and binds to a mRNA codon so the amino acid can be added to a growing protein. Transfer RNA ensures that each codon is matched with the corresponding amino acid during translation.

16.47 An anticodon is a three-base sequence in a transfer RNA molecule. The anticodon forms hydrogen bonds to the complementary mRNA codon during translation.

- 16.48 a) Transfer RNA forms a covalent bond to an amino acid.
b) The covalent bond links the tRNA to the carboxylic acid group in the amino acid.
c) The 3' end of the tRNA bonds to the amino acid. This end is called the acceptor stem.

16.49 Aminoacyl-tRNA synthetase forms the bond between a tRNA molecule and the corresponding amino acid.

16.50 Two codons fit into a ribosome.

16.51 First, the tRNA (with its amino acid) moves into the ribosome and binds to the mRNA codon. Next, the bond between the previous tRNA and the growing polypeptide is broken, and

the polypeptide is attached to the new amino acid. Third, the previous tRNA leaves the ribosome, and the ribosome moves along the mRNA. After this cycle, the next amino acid can be added, using the same sequence of reactions. (See Figure 16.21.)

16.52 Our bodies break down four molecules of ATP when we add one amino acid to a polypeptide during translation.

Section 16.7

16.53 The four common categories of mutations are substitutions, additions, deletions, and recombinations.

16.54 Recombination mutations are a normal part of a cell's activities.

16.55 Additions and deletions (choices “b” and “c”) can produce a frameshift.

16.56 a) This is a missense mutation. The corresponding mRNA codons are also GAA and GAC, which in turn correspond to the amino acids Glu (glutamic acid) and Asp (aspartic acid). Therefore, the mutation has exchanged one amino acid for another.

b) This is a silent mutation. The corresponding mRNA codons are also GAA and GAG, both of which correspond to glutamic acid. Therefore, the mutation did not have any effect on the protein.

c) This is a nonsense mutation. The corresponding mRNA codons are GAA and UAA. GAA corresponds to glutamic acid, but UAA is a stop codon.

16.57 a) The mRNA sequence that corresponds to this coding strand is AAACAUAAGUUG. Translating this mRNA gives us the amino acid sequence Lys–His–Lys–Leu.

b) The new DNA coding strand is AAACGTAAGTTG, and the corresponding mRNA is AAACGUAAGUUG. Translating this mRNA gives us the amino acid sequence Lys–Arg–Lys–Leu.

c) The new DNA coding strand is AAACATTAAGTTG, and the corresponding mRNA is AAACAUAAGUUG. Translating this mRNA gives us the amino acid sequence Lys–His. (Note that the third codon is a stop codon, so only the first two codons are translated!)

16.58 Choice “a” is correct. When we replace one DNA base pair by another, this mutation usually affects only one amino acid. In contrast, adding or removing a base pair affects all of the amino acids beyond the mutation, resulting in a completely different amino acid sequence in the protein.

16.59 A mutagen is any chemical that causes DNA mutations, normally by damaging the DNA.

16.60 Each cell in an embryo will divide into many cells as the embryo develops. Therefore, any mutation in the DNA of an embryonic cell will be passed on to all of the descendants of that cell. If the mutation is harmful, it may kill the embryo, or it may produce a birth defect. In an adult, by contrast, mutations affect far fewer cells, and the surrounding cells can easily carry out the function of the mutated cell.

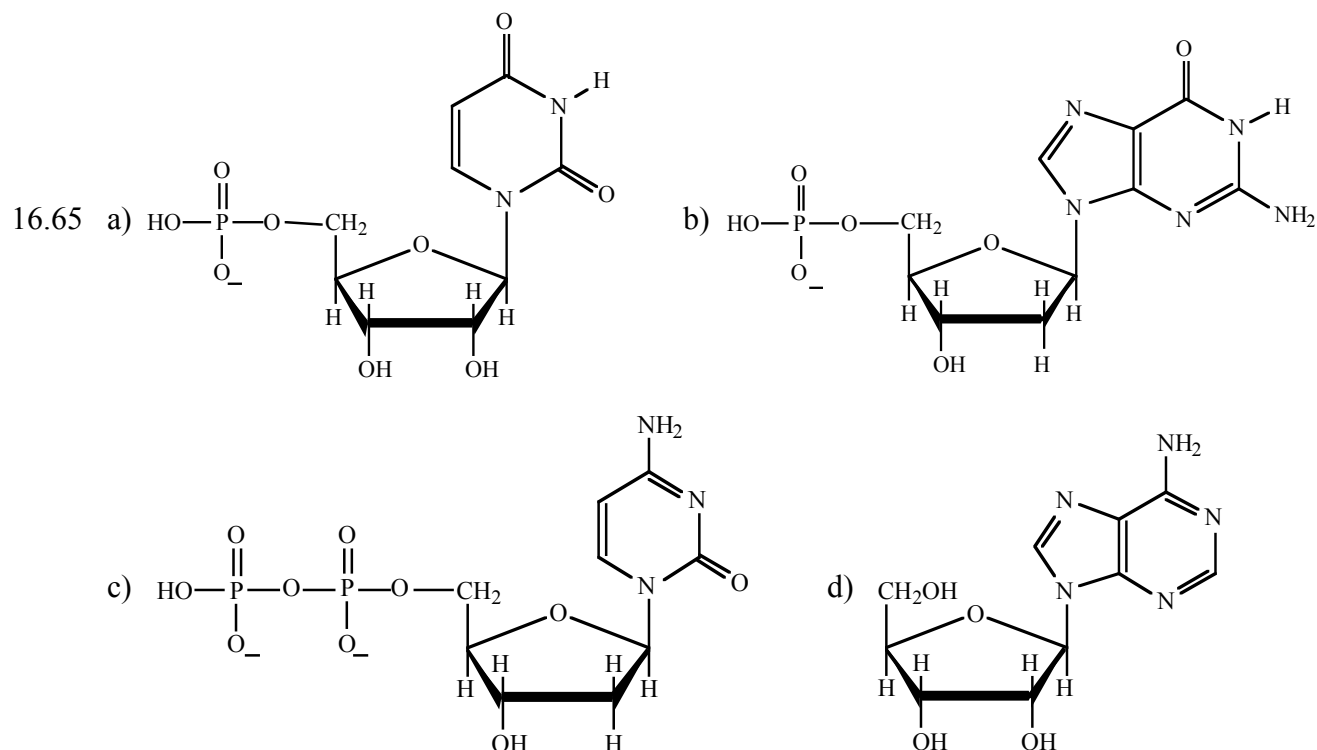
16.61 If a cell in an embryo undergoes a mutation that is not harmful, the person that develops from the embryo will be healthy, but all of the descendants of the original mutated cell will carry the mutation. As a result, the person will be a mixture of two types of cells, one of which has the mutation while the other does not. Such a person is a genetic mosaic.

16.62 In an autosomal genetic disorder, the mutation is in one of the autosomes. Autosomal disorders are equally likely to affect men and women. In a sex-linked genetic disorder, the mutation is in a sex chromosome. Sex-linked disorders affect men more often than women.

16.63 Many (if not all) cancers are caused by mutations in the DNA that controls how and when cells divide. Mutagens increase the number of mutations in this DNA, so they increase the likelihood that a person will develop cancer.

16.64 A mutation can be beneficial to an organism in a variety of ways. It may result in a protein that carries out its function better, or it may produce a protein that carries out some new function that helps the organism survive.

CUMULATIVE PROBLEMS (Odd-numbered problems only)



16.67 a) The four bases that occur in RNA are adenine, cytosine, guanine, and uracil (A, C, G and U).

b) In RNA, A and U form a complementary base pair, and C and G form the other complementary base pair.

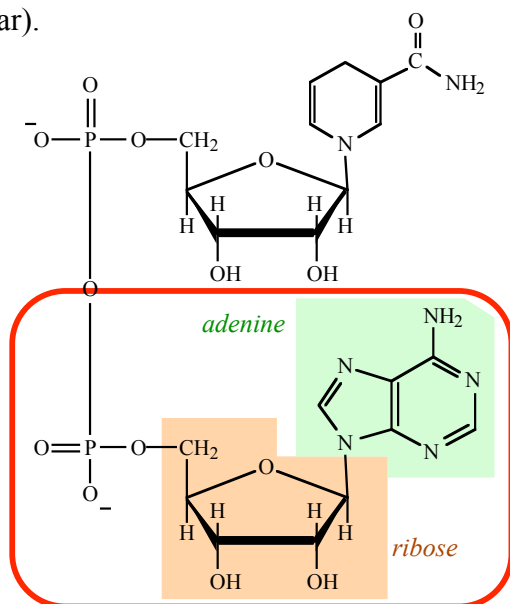
16.69 This molecule contains deoxyribose, thymine, and three phosphate groups, so its abbreviation is dTTP (short for **d**eoxy**t**hymidine **t**ri**p**hosphate).

16.71 a) The sugar is ribose (because it has an OH group on the 2' carbon of each sugar). The bases are uracil, adenine, and guanine, reading from top to bottom.

b) This is a molecule of RNA, because it contains ribose.

c) The base sequence UAG. We start with the upper nucleotide, because this is the 5' end of the chain.

16.73 The common nucleotide is circled below. This nucleotide contains adenine (the base) and ribose (the sugar).



16.75 There are 44 autosomal chromosomes in a typical cell in the human body.

16.77 a) The mRNA has the sequence AAUCAAGGC. Messenger RNA has the same sequence as the coding strand in DNA, except that U is substituted for T.

b) The mRNA has the sequence GCCUUGAUU. The bases in messenger RNA are the complements of the bases in the template strand. Remember that complementary strands run in opposite directions (the 5' end of one strand is paired with the 3' end of the other).

DNA template: (5' end) AATCAAGGC (3' end)

mRNA: (3' end) UUAGUCCG (5' end)

To write the mRNA in the normal direct (5' to 3'), you simply reverse the order of the mRNA bases.

16.79 Introns are sections in the interior of a messenger RNA molecule that do not code for amino acids. The introns are removed and broken down during mRNA processing.

16.81 The amino acid sequence is Met-Val-His-Leu-Thr-Pro. First, you must determine the base sequence in the messenger RNA that corresponds to this coding DNA strand.

DNA coding strand: (5' end) ACACCATGGTGCATCTGACTCCT (3' end)
 DNA template strand: (3' end) TGTGGTACCACGTAGACTGAGGA (5' end)
 messenger RNA: (5' end) ACACCAUGGUGCAUCUGACUCCU (3' end)

Next, you must locate the start codon in the mRNA.

ACACCAUGGUGCAUCUGACUCCU

Finally, you translate the mRNA, starting with the start codon and ignoring all of the bases before the start codon.

AUG - GUG - CAU - CUG - ACU - CCU
 Met - Val - His - Leu - Thr - Pro

16.83 a) This is similar to problem 16.81. First, you must determine the base sequence in the messenger RNA that corresponds to this coding DNA strand.

DNA coding strand: (5' end) GGCCACAAGTATCACTAAGCTCGCT (3' end)
 DNA template strand: (3' end) CCGGGTGTTCATAGTGATTTCGAGCGA (5' end)
 messenger RNA: (5' end) GGCCACAAGUAUCACUAAGCUCGCU (3' end)

Next, you must locate a stop codon in the mRNA. The only stop codon in this piece of mRNA is UAA.

GGCCACAAGUAUCACUAAGCUCGCU

The stop codon UAA corresponds to the DNA bases TAA in the coding strand.

b) The last amino acids in the protein are Ala-His-Lys-Tyr-His. You must translate the mRNA working backward from the stop codon. Ignore all of the bases after the stop codon. (The stop codon is not translated either.)

??G - GCC - CAC - AAG - UAU - CAC - UAA
 ? - Ala - His - Lys - Tyr - His

16.85 The mRNA could contain all of the possible codons that contain only A's and C's. Therefore, the polypeptide could contain any amino acid whose codon is made up of only A's and C's. The possible amino acids and their corresponding codons are:

lysine (AAA) asparagine (AAC) threonine (ACA and ACC)
 glutamine (CAA) histidine (CAC) proline (CCA and CCC)

16.87 The possible lysine codons are AAA and AAG. The possible asparagine codons are AAC and AAU. Therefore, there are four possible mRNA sequences:

AAAAAC AAAAAU AAGAAC AAGAAU

16.89 The phosphate groups in DNA are negatively charged, so the positive magnesium ions are strongly attracted to them.

16.91 The DNA double helix contains two long chains of nucleotides, each of which spirals around the other. The bases face one another, and the hydrogen bonds between bases hold the two chains next to one another. The phosphate-sugar backbone faces outward.

16.93 An activated nucleotide is a nucleotide that contains three phosphate groups rather than just one. Breaking the bonds between phosphate groups supplies the energy that the cell needs to build DNA.

16.95 a) Helicase unwinds the double helix and pulls the two chains away from one another, so new DNA strands can be built using the existing base sequences as templates.

b) DNA polymerase builds the new DNA chains from activated nucleotides, using the existing chains as templates.

16.97 Proof-reading enzymes find mismatched base pairs, remove the mismatched nucleotide, and replace it with the correct nucleotide. This makes DNA replication more accurate.

16.99 Chargaff's Rule is related to the way that DNA bases pair with one another in the double helix. A always pairs with T, so the number of A's equals the number of T's. Likewise, C always pairs with G, so the number of C's equals the number of G's. Therefore, the total number of A's and G's must always equal the total number of C's and T's.

Here is a numerical example to help you see how this works...

Say a piece of DNA contains 100 A's. Then it must also contain 100 T's, since A always pairs with T.

Say this same piece of DNA contains 75 C's. Then it must also contain 75 G's, since C always pairs with G.

$$\text{Total number of A's plus G's} = 100 + 75 = 175$$

$$\text{Total number of T's plus C's} = 100 + 75 = 175$$

16.101 a) Replication is the process in which a cell makes a copy of all of its DNA. Replication allows all of the genetic instructions in a cell to be passed on to the descendants of that cell.

b) Transcription is the process in which a cell makes RNA, using a section of DNA as a template. Transcription allows a cell to make all of the various types of RNA that it needs. Transcription is also the starting step of protein synthesis.

16.103 A gene is a section of a DNA molecule that is transcribed as a single unit. A chromosome is an entire DNA molecule, along with all of the protein and RNA that is bound to it.

16.105 The anticodon binds to the codon in mRNA, allowing the tRNA to match its amino acid with the correct codon.

16.107 a) Transfer RNA b) Ribosomal RNA c) Messenger RNA

16.109 The enzyme that builds RNA moves from the 3' end of the DNA to the 5' end. (See Figure 16.13.)

16.111 The tRNA that binds to AUG cannot also bind to AUA. You can tell by looking at the genetic code: AUG and AUA correspond to different amino acids, so the same tRNA cannot bind to both codons.

16.113 a) The amino acid sequence is Ile–Val–Phe–Pro.

b) All of these amino acids are hydrophobic (see Table 13.1), so this section of the polypeptide is hydrophobic.

c) These amino acids should be on the inside of the protein, away from the water that surrounds most proteins.

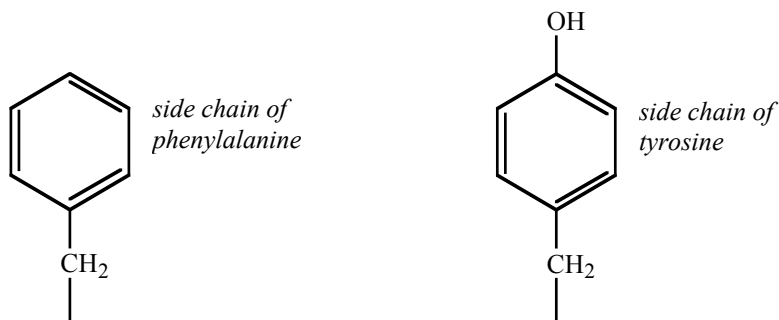
16.115 We don't need 61 different types of tRNA because several types of tRNA can bind to more than one mRNA codon. For example, the tRNA that binds to UUG also binds to UUA, so we only need one tRNA to translate these two codons.

16.117 We break down 4 molecules of ATP when we add one amino acid to a polypeptide, so we must break down $150 \times 4 = 600$ molecules of ATP.

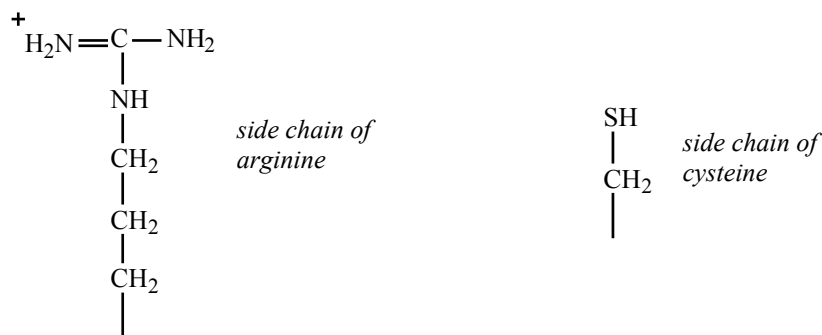
16.119 Before you answer this question, you must work out the effect of each mutation on the amino acid sequence of factor VIII.

Mutation number	Effect on the coding DNA strand	Effect on the mRNA	Effect on the protein
1	TAT → TTT	UAU → UUU	Tyr → Phe
2	CGC → TGC	CGC → UGC	Arg → Cys
3	CGA → TGA	CGA → UGA	Arg → <i>stop codon</i>

Mutation #1 replaces tyrosine with phenylalanine. The side chains of these two amino acids are similar sizes, but tyrosine is polar while phenylalanine is nonpolar.



Mutation #2 replaces arginine with cysteine. The side chains of these amino acids are very different: arginine is basic and is ionized at pH 7, while cysteine is only weakly polar.



Mutation #3 eliminates arginine and all of the amino acids beyond arginine.

Mutation #3 has the most severe effect on factor VIII, so it should produce an inactive version of this protein. Mutation #2 should also have a significant impact on the activity of factor VIII, because the replacement of arginine with cysteine eliminates an ion pair. Mutation #1 should have the least impact on the activity of factor VIII. Therefore, the correct matching is:

Mutation #1 – description “c”

Mutation #2 – description “b”

Mutation #3 – description “a”

16.121 a) As in Problem 16.119, you should start by working out the effect of each mutation on the amino acid sequence of factor VIII.

Mutation number	Effect on the coding DNA strand	Effect on the mRNA	Effect on the protein
1	GTT → GAT	GUU → GAU	Val → Asp
2	GTC → GAC	GUC → GAC	Val → Asp

Both of these mutations substitute an aspartic acid for a valine, leaving the rest of the primary structure unchanged.

b) Mutation #1 affects an amino acid in the active site of factor VIII. We can tell because mutation #1 has a much more severe impact on the activity of factor VIII than mutation #2 does. Any mutation that affects the amino acids around the active site changes the shape of the active site, making the protein unable to bind correctly to its normal substrates. Mutations that affect other amino acids can also have a dramatic effect on the activity of a protein, but they often have a minor effect, because they do not necessarily affect the shape of the active site.

16.123 a) There are a lot of possibilities here, because we can replace any of the three bases in the original DNA sequence (CGA).

Changing the first base can produce three new sequences: AGA, GGA, and TGA.

Changing the second base can produce three new sequences: CAA, CCA, and CTA.

Changing the third base can produce three new sequences: CGC, CGG, and CGT.

To do parts b, c and d, look at all nine possible mutations, their effect on the mRNA, and their effect on the amino acid sequence.

Change in the DNA coding strand	Change in the mRNA	Change in the protein	Type of mutation
CGA → AGA	CGA → AGA	Arg → Arg	silent
CGA → GGA	CGA → GGA	Arg → Gly	missense
CGA → TGA	CGA → UGA	Arg → <i>stop codon</i>	nonsense
CGA → CAA	CGA → CAA	Arg → Gln	missense
CGA → CCA	CGA → CCA	Arg → Pro	missense
CGA → CTA	CGA → CUA	Arg → Leu	missense
CGA → CGC	CGA → CGC	Arg → Arg	silent
CGA → CGG	CGA → CGG	Arg → Arg	silent
CGA → CGT	CGA → CGU	Arg → Arg	silent

To answer the remaining parts of this problem, simply count up the number of each type of mutation.

- b) Four of these are silent mutations.
- c) Four of these are missense mutations.
- d) One of these is a nonsense mutation.

16.125 It is possible to have an addition mutation that does not produce a frameshift. If you add three bases to the coding strand (or any multiple of three), you will not produce a frameshift. (The resulting protein will have one or more extra amino acids at the point of the mutation, but all of the subsequent amino acids will be correct.)

16.127 The skin is the part of the body that is exposed to ultraviolet radiation from the sun. Normally, skin cells can repair most of the DNA damage that is caused by ultraviolet radiation, but in people with XP, this is not possible. Therefore, the DNA in their skin cells suffers a large number of mutations. Some of these mutations affect the regions of DNA that control cell division, and when enough of these regions are damaged, the cell becomes cancerous.

16.129 Cells cannot survive if they cannot carry out the citric acid cycle, because the citric acid cycle is involved in all catabolic pathways. Therefore, the cell that suffers this mutation dies. Adults have many cells that can take over the function of the dead cell, so they do not suffer any ill effects. However, an embryo has few cells, and each cell will give rise to a very large number of cells as the embryo develops into a baby. The embryo may not be able to replace the dead cell, so a major part of the embryo will not develop, killing the embryo.

16.131 An error that occurs during replication has a greater impact than an error that occurs during transcription. Any error that occurs during replication changes the genetic instructions in the cell that receives the mutated DNA, and that mutation is in turn passed on to all descendants of the cell. By contrast, an error that occurs during transcription affects a piece of RNA. Cells transcribe their genes many times, so a piece of RNA that contains incorrect information can be replaced quickly.

16.133 A cell in Flora's body underwent a recombination mutation, moving one of the two genes (A or B) to a different chromosome. This cell then gave rise to an egg that contained only one of the two chromosomes (the one that contained gene A). This egg was fertilized and became Nancy. (*Note: egg and sperm cells only contain 23 chromosomes rather than the usual 46. They are formed when a cell divides without replicating its DNA. Half of the chromosomes end up in one egg or sperm cell, and the other half end up in the other egg or sperm cell.*)