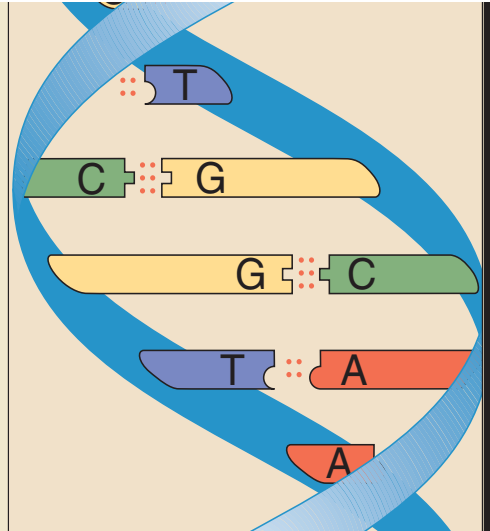


DNA and RNA

The Molecular Basis of Heredity



CHAPTER 7

Chapter Outline

7.1 The Main Idea: The Central Dogma

7.2 The Structure of DNA and RNA

7.3 DNA Replication

HOW SCIENCE WORKS 7.1: *Of Men (and Women!), Microbes, and Molecules*

7.4 DNA Transcription

Prokaryotic Transcription • Eukaryotic Transcription

outlooks 7.1: *Telomeres*

7.5 Translation, or Protein Synthesis

7.6 Alterations of DNA

7.7 Manipulating DNA to Our Advantage

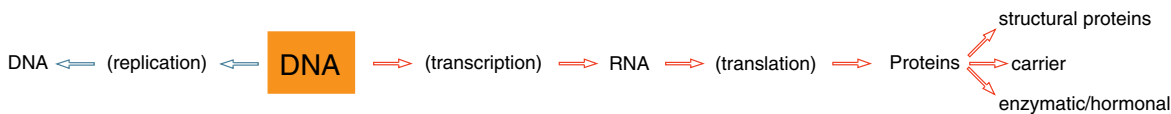
Genetic Engineering

HOW SCIENCE WORKS 7.2: *The PCR and Genetic Fingerprinting*

Key Concepts	Applications
Identify the chemical subunits of DNA, RNA, and protein.	<ul style="list-style-type: none"> Describe how DNA, RNA, and protein molecules differ chemically.
Understand how the packaging of DNA changes.	<ul style="list-style-type: none"> Distinguish among DNA, nucleoprotein, chromatin, and chromosomes. Identify how the cell uses DNA, nucleoprotein, chromatin, and chromosomes.
Understand the structure and function of DNA and RNA.	<ul style="list-style-type: none"> Know how DNA and RNA carry genetic information. Explain how DNA is able to make copies of itself.
Understand the process of transcription.	<ul style="list-style-type: none"> Explain how RNA is made by a cell from information in a DNA molecule.
Understand the process of translation.	<ul style="list-style-type: none"> Explain how a cell uses genetic information to make proteins. Explain the cellular organelles needed to make proteins.
Understand what a mutagenic agent is.	<ul style="list-style-type: none"> Explain how mutagenic agents can cause mutations in the genetic information. Explain how these mutations can cause a change in the whole organism.
Describe recombinant DNA processes.	<ul style="list-style-type: none"> Understand DNA technology and how it is used in forensics and medicine.

7.1 The Main Idea: The Central Dogma

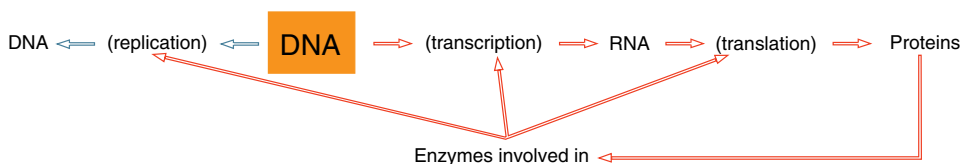
As scientists began to understand the chemical makeup of the **nucleic acids**, an attempt was made to understand how DNA and RNA relate to inheritance, cell structure, and cell activities. The concept that resulted is known as the *central dogma*, main belief, or “source of all information.” It is most easily written in this form:



What this concept map says is that at the center of it all is DNA, the genetic material of the cell and (going to the left) it is capable of reproducing itself, a process called **DNA replication**. Going to the right, DNA is capable of supervising the manufacture of RNA (a process known as **transcription**), which in turn is involved in the production of protein molecules, a process known as **translation**.

DNA replication occurs in cells in preparation for the cell division processes of mitosis and meiosis. Without replication, daughter cells would not receive the library of information required to sustain life. The transcription process results in the formation of a strand of RNA that is a copy of a segment of the DNA on which it is formed. Some of the RNA molecules become involved in various biochemical processes; others are used in the translation of the RNA information into proteins. Structural proteins are used by the cell as building materials (feathers, collagen, hair); while others are used to direct and control chemical reactions (enzymes or hormones) or carry molecules from place to place (hemoglobin).

Recall the roles enzymes play in metabolism (chapters 5 and 6). It is the processes of transcription and translation that result in the manufacture of all enzymes. Each unique enzyme molecule is made from a blueprint in the form of a DNA nucleotide sequence, or **gene**. Some of the thousands of enzymes manufactured in the cell are the tools required so that transcription and translation can take place. *The process of making enzymes is carried out by the enzymes made by the process!* Tools are made to make more tools! The same is true for DNA replication.



Enzymes made from the DNA blueprints by transcription and translation are used as tools to make exact copies of the genetic material! More blueprints are made so that future generations of cells will have the genetic materials necessary

to manufacture their own regulatory and structural proteins. Without DNA, RNA, and enzymes functioning in the proper manner, life as we know it would not occur.

DNA has four properties that enable it to function as genetic material. It is able to (1) *replicate* by directing the manufacture of copies of itself; (2) *mutate*, or chemically change, and transmit these changes to future generations; (3) *store* information that determines the characteristics of

cells and organisms; and (4) use this information to *direct* the synthesis of structural and regulatory proteins essential to the operation of the cell or organism.

7.2 The Structure of DNA and RNA

Nucleic acid molecules are enormous and complex polymers made up of monomers called **nucleotides**. Each nucleotide is composed of a sugar molecule (S) containing five carbon atoms, a phosphate group (P), and a molecule containing nitrogen that will be referred to as a **nitrogenous base** (B) (figure 7.1). It is possible to classify nucleic acids into two main groups based on the kinds of sugars and nitrogenous bases used in the nucleotides—that is, DNA and RNA.

In cells, DNA is the nucleic acid that functions as the original blueprint for the synthesis of proteins. It contains the sugar **deoxyribose**; phosphates; and adenine, guanine, cytosine, and thymine (A, G, C, T). RNA is a type of nucleic acid that is directly involved in the synthesis of protein. It contains the sugar **ribose**; phosphates; and **adenine, guanine, cytosine, and uracil** (A, G, C, U). There is no **thymine** (T) in RNA and no uracil in DNA.

DNA and RNA differ in one other respect. DNA is actually a double molecule. It consists of two flexible strands held together between their protruding bases. The two strands are twisted about each other in a coil or double helix (plural, helices) (figure 7.2). The two strands of the molecule are held together because they “fit” each other like two jigsaw puzzle pieces that interlock with one another and are

stabilized by weak chemical forces—hydrogen bonds. The four kinds of teeth always pair in a definite way: adenine (A) with thymine (T), and guanine (G) with cytosine (C). Notice that the large molecules (A and G) pair with the

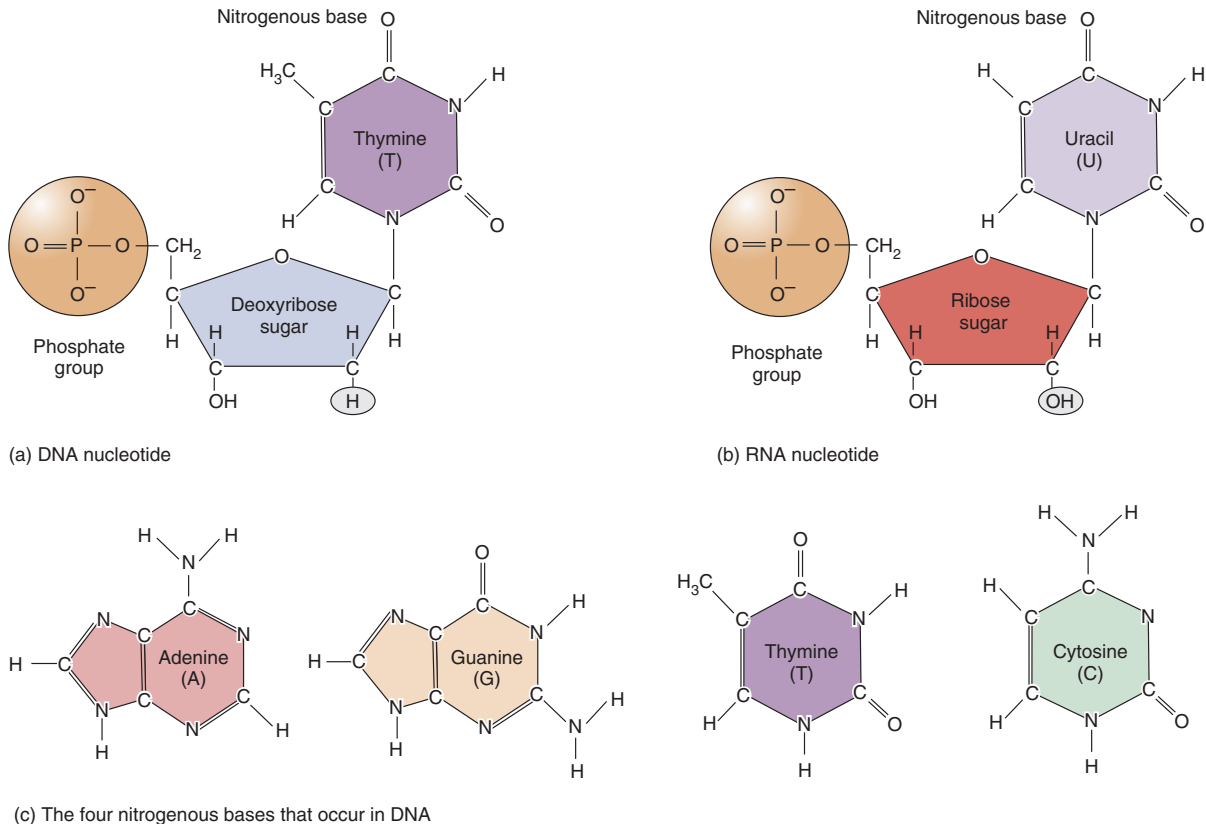


Figure 7.1

Nucleotide Structure

(a) The nucleotide is the basic structural unit of all nucleic acid molecules. A thymine nucleotide of DNA is comprised of phosphate, deoxyribose sugar, and the nitrogenous base, thymine (T). Notice in the nucleotides that the phosphate group is written in “shorthand” form as a P inside a circle. (b) The RNA uracil nucleotide is comprised of a phosphate, ribose sugar, and the nitrogenous base, uracil (U). Notice the difference between the sugars and how the bases differ from one another. (c) Using these basic components (phosphate, sugars, and bases) the cell can construct eight common types of nucleotides. Can you describe all eight?

small ones (T and C), thus keeping the two complementary (matched) strands parallel. The bases that pair are said to be **complementary bases** and this bonding pattern is referred to as the *base-pairing rule*. Three hydrogen bonds are formed between guanine and cytosine:



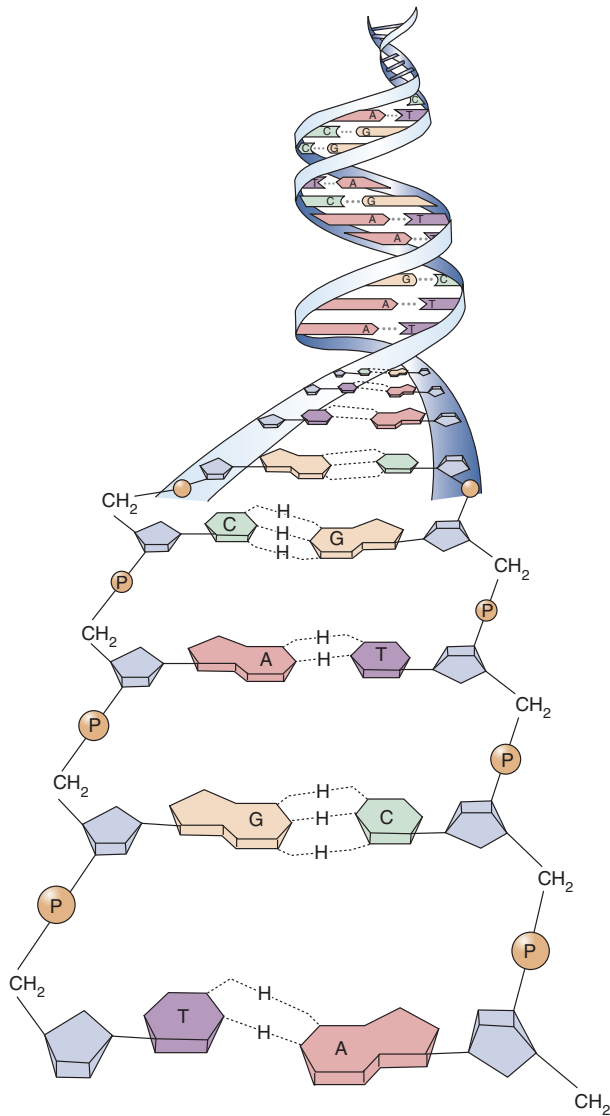
and two between adenine and thymine:



You can “write” a message in the form of a stable DNA molecule by combining the four different DNA nucleotides (A, T, G, C) in particular sequences. The four DNA nucleotides are being used as an alphabet to construct three-letter words. In order to make sense out of such a

code, it is necessary to read in one direction. Reading the sequence in reverse does not always make sense, just as reading this paragraph in reverse would not make sense (How Science Works 7.1).

The genetic material of humans and other eukaryotic organisms are *strands* of coiled double-stranded DNA, which has histone proteins attached along its length. These coiled DNA strands with attached proteins, which become visible during mitosis and meiosis, are called **nucleoproteins**, or **chromatin fibers**. The histone protein and DNA are not arranged randomly, but come together in a highly organized pattern. The double-stranded DNA spirals around repeating clusters of eight histone spheres. Histone clusters with their encircling DNA are called **nucleosomes** (figure 7.3a). When eukaryotic chromatin fibers coil into condensed, highly

**Figure 7.2****Double-Stranded DNA**

DeoxyriboNucleic Acid is a helical molecule. While the parts of each strand are held together by covalent bonds, the two parallel strands are interlinked by nitrogenous bases like jigsaw puzzle pieces. Hydrogen bonds help hold the two strands together.

knotted bodies, they are seen easily through a microscope after staining with dye. Condensed like this, a chromatin fiber is referred to as a **chromosome** (figure 7.3*b*). The genetic material in bacteria is also double-stranded DNA, but the ends of the molecule are connected to form a *loop* and

they do not form condensed chromosomes (figure 7.4). However, prokaryotic cells have an attached protein called *HU protein*. In certain bacteria, there is an additional loop of DNA called a *plasmid*. Plasmids are considered extra DNA because they appear not to contain genes that are required for the normal metabolism of the cell. However, they can play two important roles in bacteria that have them. Some plasmids have genes that enable the cell to resist certain antibiotics such as the penicillins. The gene may be for the production of the enzyme beta lactamase (formerly known as penicillinase), which is capable of destroying certain forms of penicillin. A second important gene enables the cell to become involved in *genetic recombination*, the transfer of genes from one cell (the donor) to another (the recipient). By transferring genes from one cell to another, cells that receive the genes can become genetically diverse and more likely to survive threatening environmental hazards.

Each chromatin strand is different because each strand has a different chemical code. Coded DNA serves as a central cell library. Tens of thousands of messages are in this storehouse of information. This information tells the cell such things as (1) how to produce enzymes required for the digestion of nutrients, (2) how to manufacture enzymes that will metabolize the nutrients and eliminate harmful wastes, (3) how to repair and assemble cell parts, (4) how to reproduce healthy offspring, (5) when and how to react to favorable and unfavorable changes in the environment, and (6) how to coordinate and regulate all of life's essential functions. If any of these functions are not performed properly, the cell may die. The importance of maintaining essential DNA in a cell becomes clear when we consider cells that have lost it. For example, human red blood cells lose their nuclei as they become specialized to carry oxygen and carbon dioxide throughout the body. Without DNA they are unable to manufacture the essential cell components needed to sustain themselves. They continue to exist for about 120 days, functioning only on enzymes manufactured earlier in their lives. When these enzymes are gone, the cells die. Because these specialized cells begin to die the moment they lose their DNA, they are more accurately called *red blood corpuscles (RBCs)*: "little dying red bodies."

7.3 DNA Replication

Because all cells must maintain a complete set of genetic material, there must be a doubling of DNA in order to have enough to pass on to the offspring. DNA replication is the process of duplicating the genetic material prior to its distribution to daughter cells. When a cell divides into two daughter cells, each new cell must receive a complete copy of the parent cell's genetic information, or it will not be able to manufacture all the proteins vital to its existence. Accuracy of duplication is also essential in order to guarantee the continued

HOW SCIENCE WORKS 7.1

Of Men (and Women!), Microbes, and Molecules



Microorganisms were very important in the research that led to our understanding of DNA, its structure and function. The better understanding of the microbe ushered in a period of rapid advancement in biology. A major contribution came in 1952, when Alfred Hershey and Martha Chase demonstrated, by using bacteria and viruses, that DNA is the controlling molecule of cells. Their work with the viruses that infect bacterial cells, bacteriophages, was so significant that the phage became a standard laboratory research organism. In 1953, just one year later, James D. Watson and Francis Crick used the information, and that of other researchers, to propose a double-helix molecular structure for DNA. Ten years later, Watson, Crick, and co-worker Maurice Wilkins shared a Nobel Prize for their work. In 1958, George Beadle and Edward Tatum won a Nobel Prize for

their discovery that genes operate by regulating specific chemical reactions in the cell, their "one gene—one enzyme" concept. The chemical reactions of the cell are controlled by the action of enzymes and it is the DNA that chemically codes the structure of those special protein molecules.

At first glance, some research by microbiologists may seem irrelevant or unrelated to everyday life. But it is a rare occasion when the results of such research do not make their way into our lives in some practical, beneficial form. The work of Watson, Crick, Beadle, and Tatum has been applied in hospitals and doctor's offices. Their basic research into DNA provided the information necessary to develop medicines that control disease-causing organisms and medicines that regulate basic metabolic processes in our bodies.

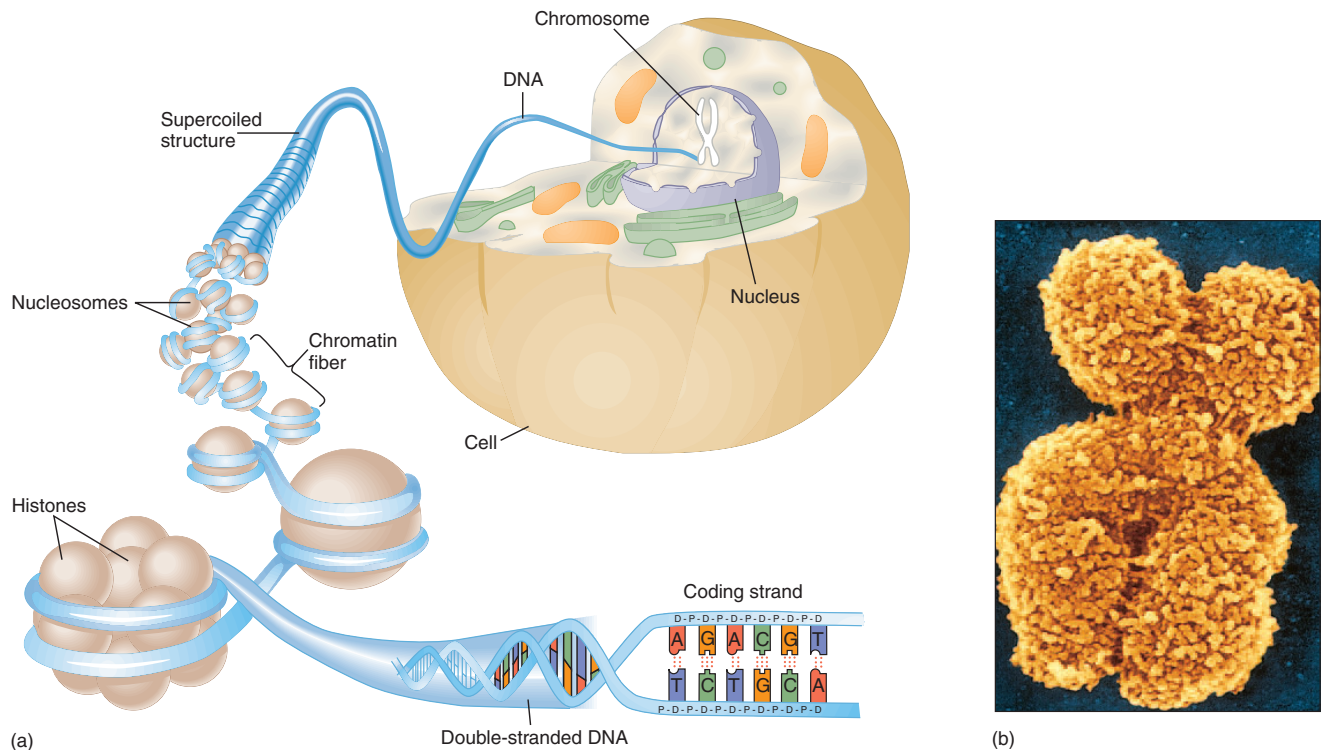


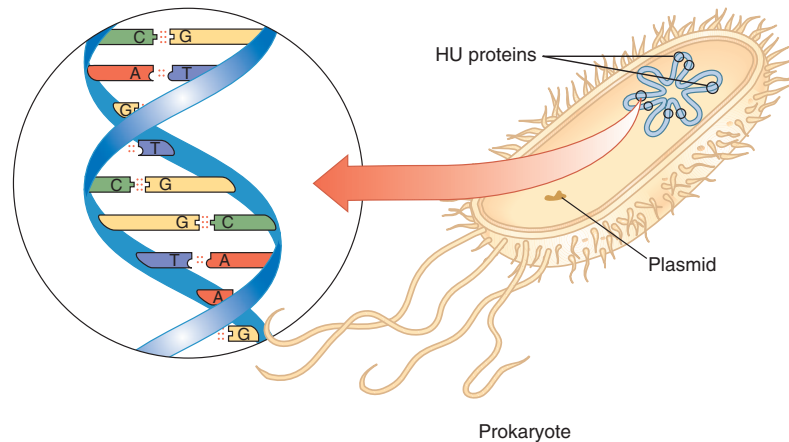
Figure 7.3

Eukaryotic DNA

(a) Eukaryotic cells contain double-stranded DNA in their nuclei, which takes the form of a three-dimensional helix. One strand is a chemical code (the coding strand) that contains the information necessary to control and coordinate the activities of the cell. The two strands fit together and are bonded by weak hydrogen bonds formed between the complementary, protruding nitrogenous bases according to the base-pairing rule. The length of a DNA molecule is measured in numbers of "base pairs"—the number of rungs on the ladder. (b) During certain stages in the reproduction of a eukaryotic cell, the nucleoprotein coils and "supercoils," forming tightly bound masses. When stained, these are easily seen through the microscope. In their supercoiled form, they are called chromosomes, meaning colored bodies.

Figure 7.4**Prokaryotic DNA**

The nucleic acid of prokaryotic cells (the bacteria) does not have the histone protein; rather, it has proteins called HU proteins. In addition, the ends of the giant nucleoprotein molecule overlap and bind with one another to form a loop. The additional small loop of DNA is the plasmid, which contains genes that are not essential to the daily life of the cell.



existence of that type of cell. Should the daughters not receive exact copies, they would most likely die.

1. The DNA replication process begins as an enzyme breaks the attachments between the two strands of DNA. In eukaryotic cells, this occurs in hundreds of different spots along the length of the DNA (figure 7.5a).
2. Moving along the DNA, the enzyme “unzips” the halves of the DNA (figure 7.5b and c), and a new nucleotide pairs with its complementary base and is covalently bonded between the sugar and phosphate to the new backbone (figure 7.5c and d).
3. Proceeding in opposite directions on each side, the enzyme **DNA polymerase** moves down the length of the DNA, attaching new DNA nucleotides into position (figure 7.5d–g).
4. The enzyme that speeds the addition of new nucleotides to the growing chain works along with another enzyme to make sure that no mistakes are made. If the wrong nucleotide appears to be headed for a match, the enzyme will reject it in favor of the correct nucleotide (figure 7.5d). If a mistake is made and a wrong nucleotide is paired into position, specific enzymes have the ability to replace it with the correct one.
5. Replication proceeds in both directions, appearing as “bubbles” (figure 7.5e).
6. The complementary molecules pair with the exposed nitrogenous bases of both DNA strands (figure 7.5f).
7. Once properly aligned, a bond is formed between the sugars and phosphates of the newly positioned nucleotides. A strong sugar and phosphate backbone is formed in the process (figure 7.5g).
8. This process continues until all the replication “bubbles” join (figure 7.5b). Figure 7.6 summarizes this process.

A new complementary strand of DNA forms on each of the old DNA strands, resulting in the formation of two double-stranded DNA molecules. In this way, the exposed

nitrogenous bases of the original DNA serve as a **template**, or pattern, for the formation of the new DNA. As the new DNA is completed, it twists into its double-helix shape.

The completion of the DNA replication process yields two double helices that are identical in their nucleotide sequences. Half of each is new, half is the original parent DNA molecule. The DNA replication process is highly accurate. It has been estimated that there is only one error made for every 2×10^9 nucleotides. A human cell contains 46 chromosomes consisting of about 3,000,000,000 (3 billion) base pairs. This averages to about five errors per cell! Don’t forget that this figure is an estimate. Whereas some cells may have five errors per replication, others may have more, and some may have no errors at all. It is also important to note that some errors may be major and deadly, whereas others are insignificant. Because this error rate is so small, DNA replication is considered by most to be essentially error-free. Following DNA replication, the cell now contains twice the amount of genetic information and is ready to begin the process of distributing one set of genetic information to each of its two daughter cells.

The distribution of DNA involves splitting the cell and distributing a set of genetic information to the two new daughter cells. In this way, each new cell has the necessary information to control its activities. The mother cell ceases to exist when it divides its contents between the two smaller daughter cells (see figure 3.22).

A cell does not really die when it reproduces itself; it merely starts over again. This is called the *life cycle* of a cell. A cell may divide and redistribute its genetic information to the next generation in a number of ways. These processes will be dealt with in detail in chapters 8 and 9.

7.4 DNA Transcription

DNA functions in the manner of a reference library that does not allow its books to circulate. Information from the originals must be copied for use outside the library. The second

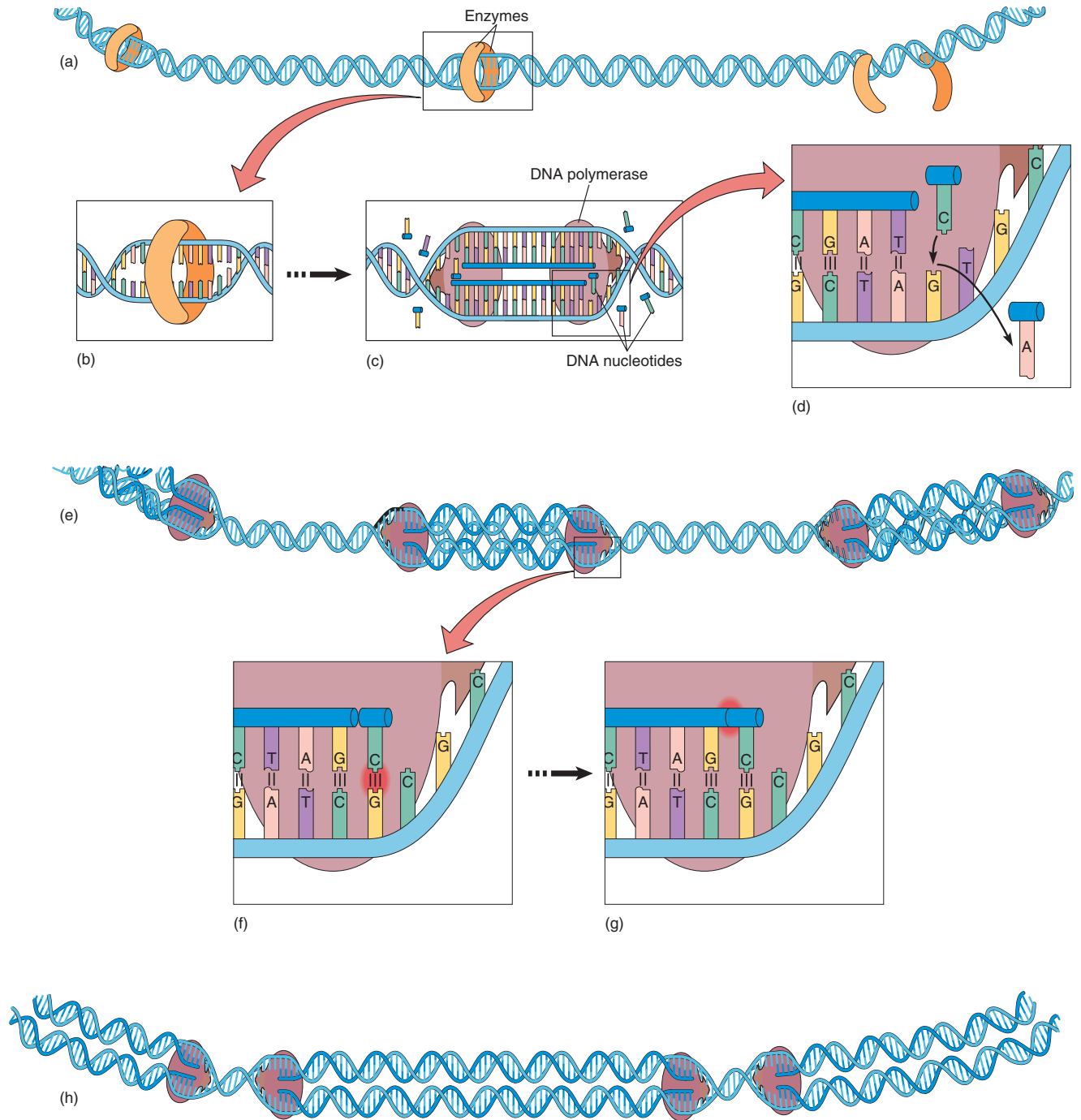


Figure 7.5

DNA Replication

These illustrations summarize the basic events that occur during the replication of DNA.

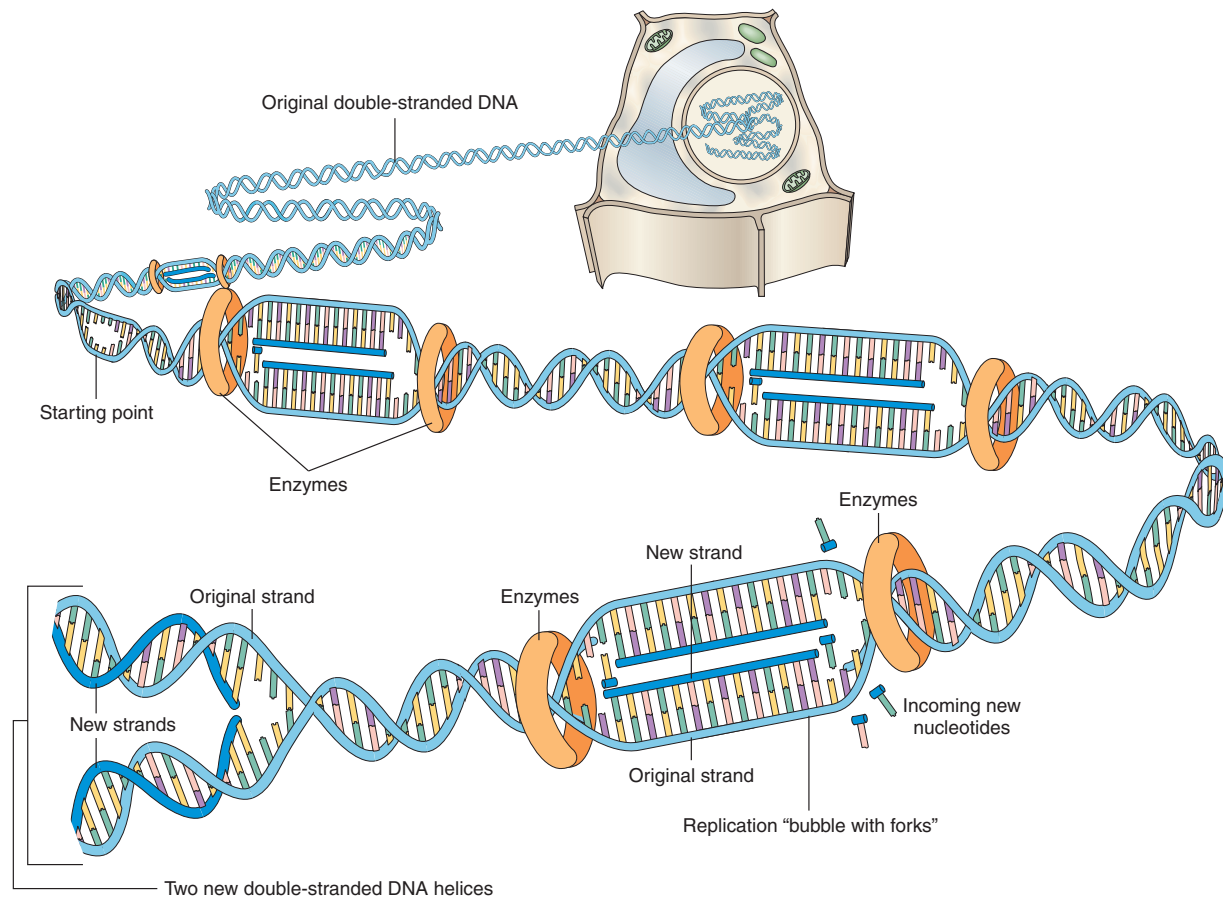


Figure 7.6

DNA Replication Summary

In eukaryotic cells, the “unzipping” enzymes attach to the DNA at numerous points, breaking the bonds that bind the complementary strands. As the DNA replicates, numerous replication “bubbles” and “forks” appear along the length of the DNA. Eventually all the forks come together, completing the replication process.

OUTLOOKS 7.1**Telomeres**

The ends of a chromosome contain a special sequence of nucleotides called **telomeres**. In humans these chromosome “caps” contain the nucleotide base pair sequence

TTAGGG
AATCCC

repeated many times over. Telomeres are very important segments of the chromosome. They are required for chromosome replication, they protect the chromosome from being destroyed by dangerous DNAase enzymes and keep chromosomes from

bonding end to end. Evidence shows that the loss of telomeres is associated with cell “aging,” whereas their maintenance has been linked to cancer. Every time a cell reproduces itself, it loses telomeres because the enzyme *telomerase* is not normally produced in normal differentiated cells. However, cancer cells appear to be “immortal” as a result of their production of this enzyme. This enables them to maintain, if not increase, the number of telomeres from one cell generation to the next. Telomerase activity is critical to the continued reproduction of tumor cells.



major function of DNA is to make these single-stranded, complementary RNA copies of DNA. This operation is called transcription (*scribe* = to write), which means to transfer data from one form to another. In this case, the data is copied from DNA language to RNA language. The same base-pairing rules that control the accuracy of DNA replication apply to the process of transcription. Using this process, the genetic information stored as a DNA chemical code is carried in the form of an RNA copy to other parts of the cell. It is RNA that is used to guide the assembly of amino acids into structural and regulatory proteins. Without the process of transcription, genetic information would be useless in directing cell functions. Although many types of RNA are synthesized from the genes, the three most important are *messenger RNA (mRNA)*, *transfer RNA (tRNA)*, and *ribosomal RNA (rRNA)*. Refer to figure 3.23 for an overview of this process.

Transcription begins in a way that is similar to DNA replication. The double-stranded DNA is separated by an enzyme, exposing the nitrogenous-base sequences of the two strands. However, unlike DNA replication, transcription occurs only on one of the two DNA strands, which serves as a template, or pattern, for the synthesis of RNA (figure 7.7). This side is also referred to as the **coding strand** of the DNA. But which strand is copied? Where does it start and when does it stop? Where along the sequence of thousands of nitrogenous bases does the chemical code for the manufacture of a particular enzyme begin and where does it end? If transcription begins randomly, the resulting RNA may not be an accurate copy of the code, and the enzyme product may be useless or deadly to the cell. To answer these questions, it is necessary to explore the nature of the genetic code itself.

We know that genetic information is in chemical-code form in the DNA molecule. When the coded information is used or *expressed*, it guides the assembly of particular amino acids into structural and regulatory polypeptides and proteins. If DNA is molecular language, then each nucleotide in this language can be thought of as a letter within a four-letter alphabet. Each word, or code, is always three letters (nucleotides) long, and only three-letter words can be written. A **DNA code** is a triplet nucleotide sequence that codes for 1 of the 20 common amino acids. The number of codes in this language is limited because there are only four different nucleotides, which are used only in groups of three. The order of these three letters is just as important in DNA language as it is in our language. We recognize that CAT is not the same as TAC. If all the possible three-letter codes were written using only the four DNA nucleotides for letters, there would be a total of 64 combinations.

$$4^3 = 4 \times 4 \times 4 = 64$$

When codes are found at a particular place along a coding strand of DNA, and the sequence has meaning, the sequence is a gene. “Meaning” in this case refers to the fact that the gene can be transcribed into an RNA molecule, which in turn may control the assembly of individual amino acids into a polypeptide.

Prokaryotic Transcription

Each bacterial gene is made of attached nucleotides that are transcribed in order into a single strand of RNA. This RNA molecule is used to direct the assembly of a specific sequence of amino acids to form a polypeptide. This system follows the pattern of:

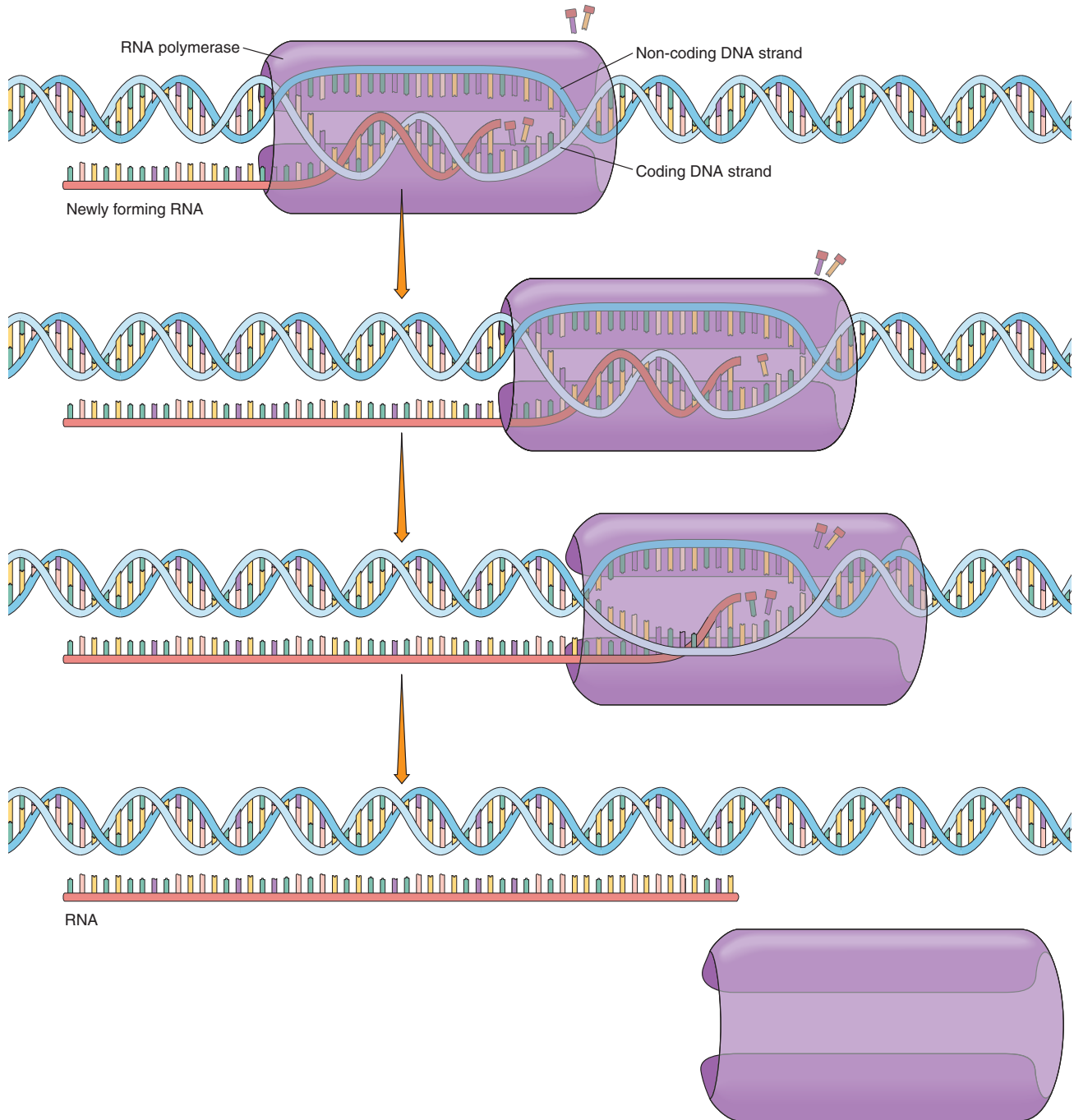
one DNA gene → one RNA → one polypeptide

The beginning of each gene on a DNA strand is identified by the presence of a region known as the **promoter**, just ahead of an **initiation code** that has the base sequence TAC. The gene ends with a terminator region, just in back of one of three possible **termination codes**—ATT, ATC, or ACT. These are the “start reading here” and “stop reading here” signals. The actual genetic information is located between initiation and termination codes:

promoter::initiator code::::gene::::terminator code::terminator region

When a bacterial gene is transcribed into RNA, the DNA is “unzipped,” and an enzyme known as **RNA polymerase** attaches to the DNA at the promoter region. It is from this region that the enzymes will begin to assemble RNA nucleotides into a complete, single-stranded copy of the gene, including initiation and termination codes. Triplet RNA nucleotide sequences complementary to DNA codes are called **codons**. Remember that there is no thymine in RNA molecules; it is replaced with uracil. Therefore the initiation code in DNA (TAC) would be base-paired by RNA polymerase to form the RNA codon AUG. When transcription is complete, the newly assembled RNA is separated from its DNA template and made available for use in the cell; the DNA recoils into its original double-helix form. In summary (see figure 7.7):

1. The process begins as one portion of the enzyme RNA polymerase breaks the attachments between the two strands of DNA; the enzyme “unzips” the two strands of the DNA.
2. A second portion of the enzyme RNA polymerase attaches at a particular spot on the DNA called the start code. It proceeds in one direction along one of the two DNA strands, attaching new RNA nucleotides into position until it reaches a stop code. The enzymes then assemble RNA nucleotides into a complete, single-stranded RNA copy of the gene. There is no thymine in RNA molecules; it is replaced by uracil. Therefore, the start code in DNA (TAC) would be paired by RNA polymerase to form the RNA codon AUG.
3. The enzyme that speeds the addition of new nucleotides to the growing chain works along with another enzyme to make sure that no mistakes are made.
4. When transcription is complete, the newly assembled RNA is separated from its DNA template and made available for use in the cell; the DNA recoils into its original double-helix form.

**Figure 7.7****Transcription of an RNA Molecule**

This summary illustrates the basic events that occur during the transcription of one side (the coding strand) of double-stranded DNA. The enzyme attaches to the DNA at a point that allows it to separate the complementary strands. As this enzyme, RNA polymerase, moves down the DNA, new complementary RNA nucleotides are base-paired on one of the exposed strands and linked together, forming a new strand that is complementary to the nucleotide sequence of the DNA. The newly formed (transcribed) RNA is then separated from its DNA complement. Depending on the DNA segment that has been transcribed, this RNA molecule may be a messenger RNA (mRNA), a transfer RNA (tRNA), a ribosomal RNA (rRNA), or an RNA molecule used for other purposes within the cell.

As previously mentioned, three general types of RNA are produced by transcription: messenger RNA, transfer RNA, and ribosomal RNA. Each kind of RNA is made from a specific gene and performs a specific function in the synthesis of polypeptides from individual amino acids at ribosomes. **Messenger RNA (mRNA)** is a mature, straight-chain copy of a gene that describes the exact sequence in which amino acids should be bonded together to form a polypeptide.

Transfer RNA (tRNA) molecules are responsible for picking up particular amino acids and transferring them to the ribosome for assembly into the polypeptide. All tRNA molecules are shaped like cloverleaves. This shape is formed when they fold and some of the bases form hydrogen bonds that hold the molecule together. One end of the tRNA is able to attach to a specific amino acid. Toward the midsection of the molecule, a triplet nucleotide sequence can base-pair with a codon on mRNA. This triplet nucleotide sequence on tRNA that is complementary to a codon of mRNA is called an **anticodon**. **Ribosomal RNA (rRNA)** is a highly coiled molecule and is used, along with protein molecules, in the manufacture of all ribosomes, the cytoplasmic organelles where tRNA, mRNA, and rRNA come together to help in the synthesis of proteins.

Eukaryotic Transcription

The transcription system is different in eukaryotic cells. A eukaryotic gene begins with a promoter region and an initiation code and ends with a termination code and region. However, the intervening gene sequence contains patches of nucleotides that apparently have no meaning but do serve important roles in maintaining the cell. If they were used in protein synthesis, the resulting proteins would be worthless. To remedy this problem, eukaryotic cells prune these segments from the mRNA after transcription. When such *split genes* are transcribed, RNA polymerase synthesizes a strand of pre-mRNA that initially includes copies of both *exons* (meaningful mRNA coding sequences) and *introns* (meaning-

less mRNA coding sequences). Soon after its manufacture, this pre-mRNA molecule has the meaningless introns clipped out and the exons spliced together into the final version, or *mature mRNA*, which is used by the cell (figure 7.8). In humans, it has been found that the exons of a single gene may be spliced together in three different ways resulting in the production of three different mature messenger RNAs. This means that a single gene can be responsible for the production of three different proteins. Learning this information has lead geneticists to revise their estimate of the total number of genes found in the human genome from 100,000 to an estimated 30,000.

7.5 Translation, or Protein Synthesis

The mRNA molecule is a coded message written in the biological world's universal nucleic acid language. The code is read in one direction starting at the initiator. The information is used to assemble amino acids into proteins by a process called translation. The word *translation* refers to the fact that nucleic acid language is being changed to protein language. To translate mRNA language into protein language, a dictionary is necessary. Remember, the four letters in the nucleic acid alphabet yield 64 possible three-letter words. The protein language has 20 words in the form of 20 common amino acids (table 7.1). Thus, there are more than enough nucleotide words for the 20 amino acid molecules because each nucleotide triplet codes for an amino acid.

Table 7.2 is an amino acid–mRNA nucleic acid dictionary. Notice that more than one mRNA codon may code for the same amino acid. Some would contend that this is needless repetition, but such “synonyms” can have survival value. If, for example, the gene or the mRNA becomes damaged in a way that causes a particular nucleotide base to change to another type, the chances are still good that the proper amino acid will be read into its proper position. But not all such changes can be compensated for by the codon system,

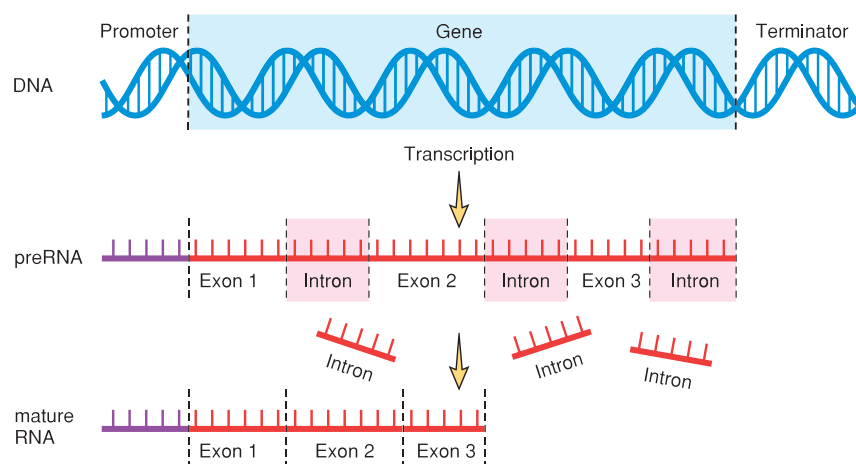


Figure 7.8

Transcription of mRNA in Eukaryotic Cells

This is a summary of the events that occur in the nucleus during the manufacture of mRNA in a eukaryotic cell. Notice that the original nucleotide sequence is first transcribed into an RNA molecule that is later “clipped” and then rebonded to form a shorter version of the original. It is during this time that the introns are removed.

Table 7.1

THE 20 COMMON AMINO ACIDS AND THEIR ABBREVIATIONS

These are the 20 common amino acids used in the protein synthesis operation of a cell. Each has a known chemical structure.

Amino Acid	Three-Letter Abbreviation	Amino Acid	Three-Letter Abbreviation
alanine	Ala	leucine	Leu
arginine	Arg	lysine	Lys
asparagine	ASN	methionine	Met
aspartic acid	Asp	phenylalanine	Phe
cysteine	Cys	proline	Pro
glutamic acid	Glu	serine	Ser
glutamine	Gln	threonine	Thr
glycine	Gly	tryptophan	Trp
histidine	His	tyrosine	Tyr
isoleucine	Ile	valine	Val

Table 7.2

AMINO ACID–mRNA NUCLEIC ACID DICTIONARY

		Second letter				
		U	C	A	G	
First letter	U	UUU } Phe UUC } UUA } Leu UUG }	UCU } Ser UCC } UCA } UCG }	UAU } Tyr UAC } UAA } Stop UAG } Stop	UGU } Cys UGC } UGA } Stop UGG } Try	U C A G
	C	CUU } Leu CUC } CUA } CUG }	CCU } Pro CCC } CCA } CCG }	CAU } His CAC } CAA } Gln CAG }	CGU } Arg CGC } CGA } CGG }	U C A G
	A	AUU } Ile AUC } AUA } Met or start AUG }	ACU } Thr ACC } ACA } ACG }	AAU } ASN AAC } AAA } Lys AAG }	AGU } Ser AGC } AGA } Arg AGG }	U C A G
	G	GUU } Val GUC } GUA } GUG }	GCU } Ala GCC } GCA } GCG }	GAU } Asp GAC } GAA } Glu GAG }	GGU } Gly GGC } GGA } GGG }	U C A G
						Third letter

and an altered protein may be produced (figure 7.9). Changes can occur that cause great harm. Some damage is so extensive that the entire strand of DNA is broken, resulting in improper **protein synthesis**, or a total lack of synthesis. Any change in DNA is called a **mutation**.

The construction site of the protein molecules (i.e., the translation site) is on the ribosome, a cellular organelle that serves as the meeting place for mRNA and the tRNAs that carry amino acid building blocks. Ribosomes can be found free in the cytoplasm or attached to the ER (endoplasmic

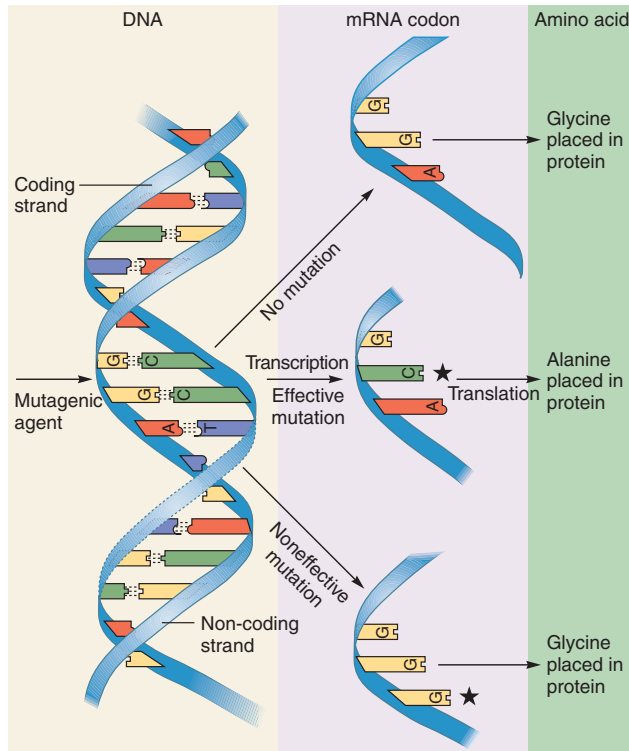


Figure 7.9

Noneffective and Effective Mutation

A nucleotide substitution changes the genetic information only if the changed codon results in a different amino acid being substituted into a protein chain. This feature of DNA serves to better ensure that the synthesized protein will be functional.

reticulum). Proteins destined to be part of the cell membrane or packaged for export from the cell are synthesized on ribosomes attached to the endoplasmic reticulum. Proteins that are to perform their function in the cytoplasm are synthesized on unattached or free ribosomes.

Figure 7.10 is a sequence illustrating the events of translation. Go directly to figure 7.10 and follow steps 1–14 before returning to this place in the text. Thus, the mRNA moves through the ribosomes, its specific codon sequence allowing for the chemical bonding of a specific sequence of amino acids. Remember that the DNA originally determined the sequence of bases in the RNA.

Each protein has a specific sequence of amino acids that determines its three-dimensional shape. This shape determines the activity of the protein molecule. The protein may be a structural component of a cell or a regulatory protein, such as an enzyme. Any changes in amino acids or their order changes the action of the protein molecule. The protein insulin, for example, has a different amino acid sequence than the digestive enzyme trypsin. Both proteins are essential to human life and must be produced constantly and accurately. The amino acid sequence of each is determined by a different gene. Each gene is a particular sequence of DNA nucleotides. Any alteration of that sequence can directly alter the protein structure and, therefore, the survival of the organism.

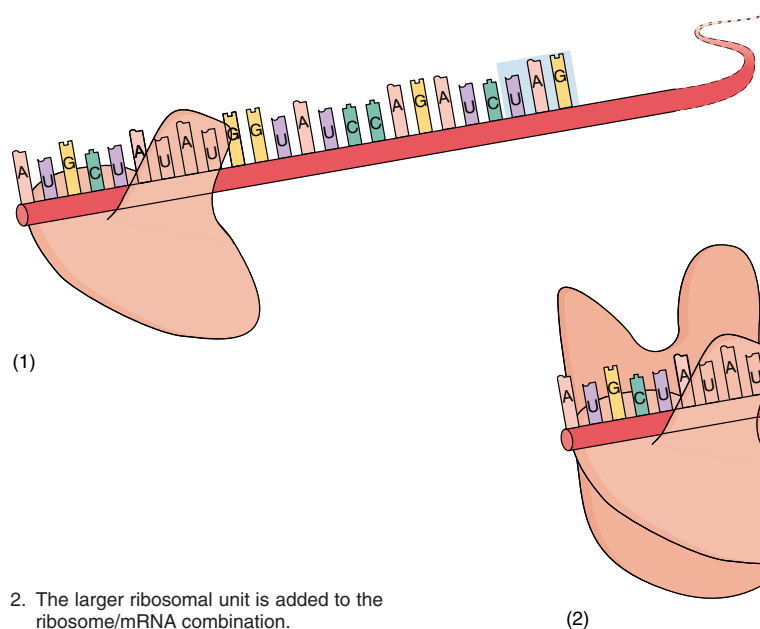


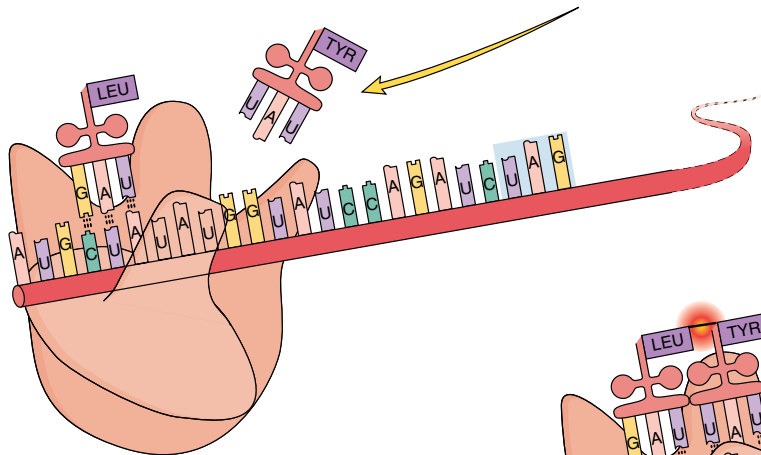
Figure 7.10

Basic Steps of Translation

1. An mRNA molecule is placed in the small portion of a ribosome so that six nucleotides (two codons) are locked into position.

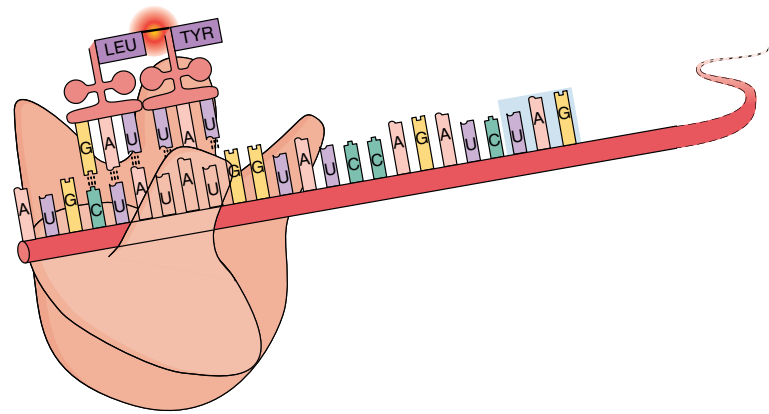
2. The larger ribosomal unit is added to the ribosome/mRNA combination.

(2)



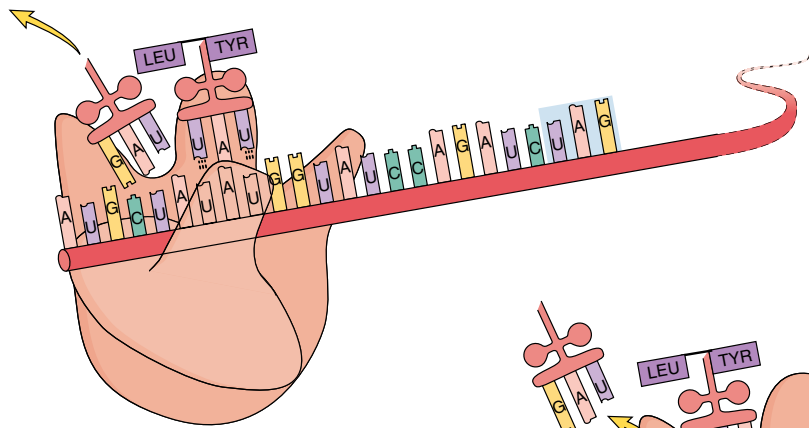
(3)

3. A tRNA with bases that match the second mRNA codon attaches to the mRNA. The tRNA is carrying a specific amino acid. Once attached, a second tRNA carrying another specific amino acid moves in and attaches to its complementary mRNA codon right next to the first tRNA/amino acid complex.



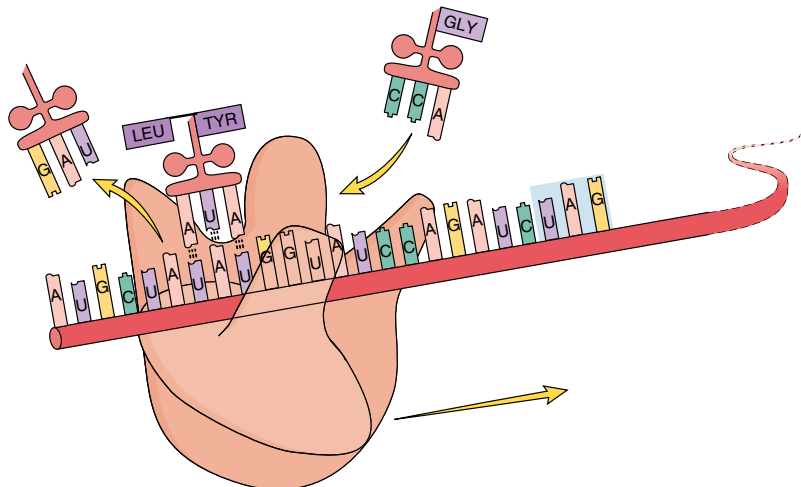
(4)

4. The two tRNAs properly align their two amino acids so that they may be chemically attached to one another.



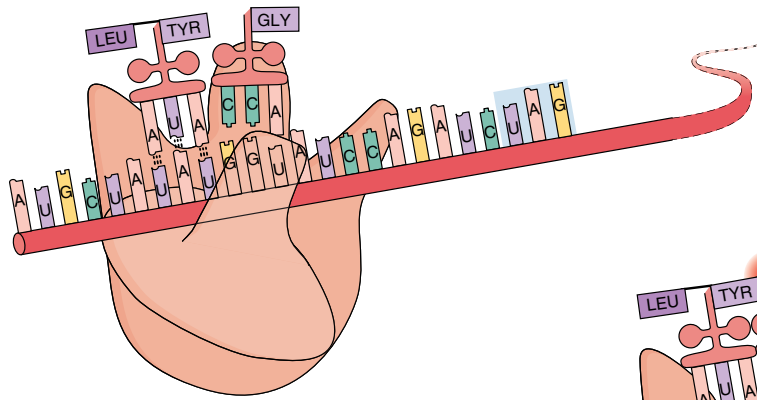
(5)

5. Once the two amino acids are connected to one another by a covalent peptide bond, the first tRNA detaches from its amino acid and mRNA codon and leaves.



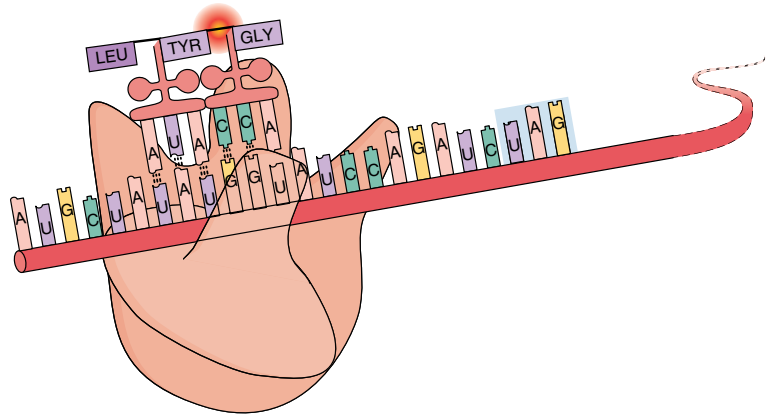
(6)

6. The ribosome moves along the mRNA to the next codon (the first tRNA is set free to move through the cytoplasm to attach to and transfer another amino acid).



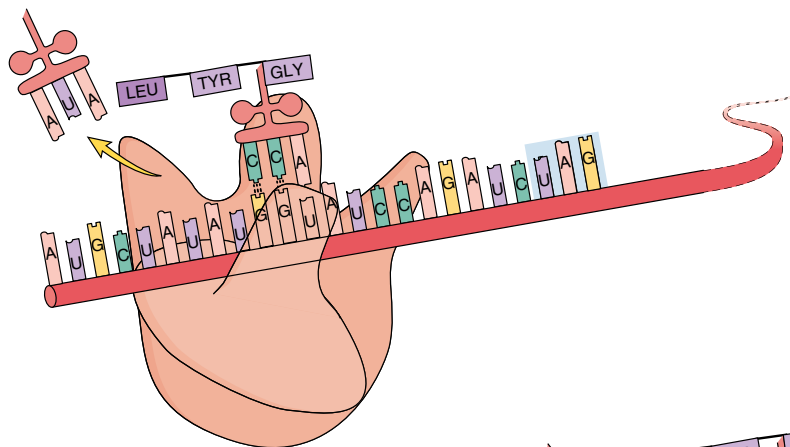
(7)

7. The next tRNA/amino acid unit enters the ribosome and attaches to its codon next to the first set of amino acids.



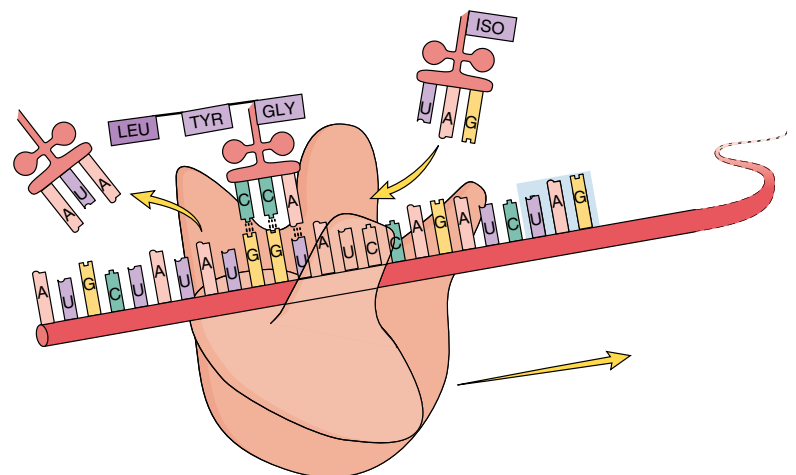
(8)

8. The tRNAs properly align their amino acids so that they may be chemically attached to one another, forming a chain of three amino acids.



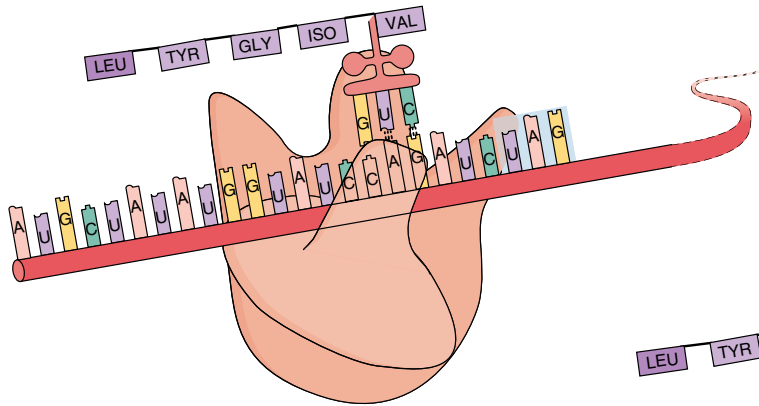
(9)

9. Once three amino acids are connected to one another, the second tRNA is released from its amino acid and mRNA (this tRNA is set free to move through the cytoplasm to attach to and transfer another amino acid).



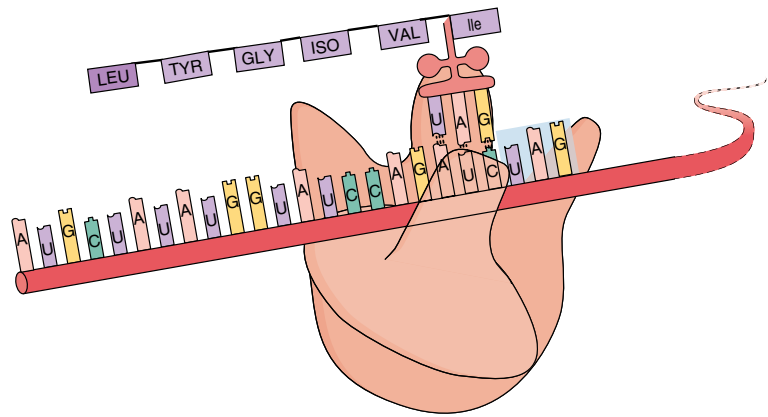
(10)

10. The ribosome moves along the mRNA to the next codon and the fourth tRNA arrives.



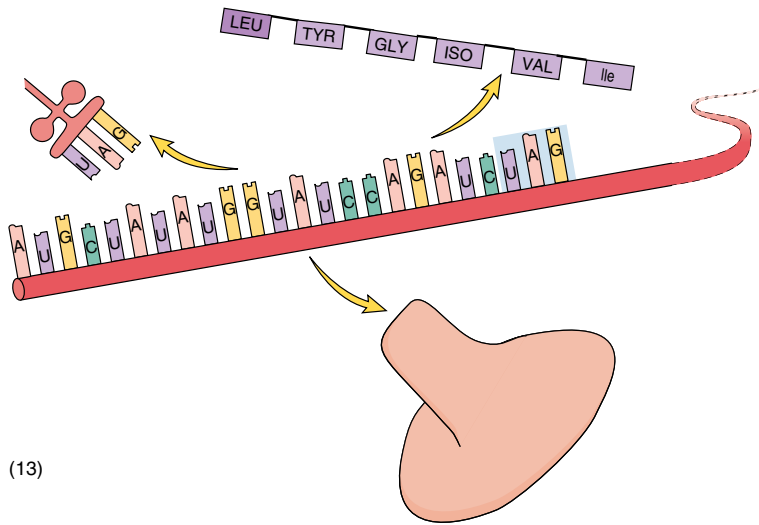
11. This process repeats until all the amino acids needed to form the protein have attached to one another in the proper sequence. This amino acid sequence was encoded by the DNA gene.

(11)



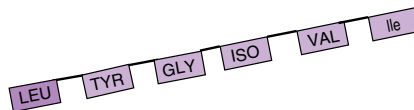
12. Once the final amino acid is attached to the growing chain of amino acids, all the molecules (mRNA, tRNA, and newly formed protein) are released from the ribosome. The stop mRNA codon signals this action.

(12)



13. The ribosome is again free to become involved in another protein-synthesis operation.

(13)



14. The newly synthesized chain of amino acids (the new protein) leaves the ribosome to begin its work. However, the protein may need to be altered by the cell before it will be ready for use.

(14)

7.6 Alterations of DNA

Several kinds of changes to DNA may result in mutations. Phenomena that are either known or suspected causes of DNA damage are called **mutagenic agents**. Agents known to cause damage to DNA are certain viruses (e.g., papillomavirus), weak or “fragile” spots in the DNA, X radiation (X rays), and chemicals found in foods and other products such as nicotine in tobacco. All have been studied extensively and there is little doubt that they cause mutations. **Chromosomal aberrations** is the term used to describe major changes in DNA. Four types of aberrations include inversions, translocations, duplications, and deletions. An *inversion* occurs when a chromosome is broken and this piece becomes reattached to its original chromosome but in reverse order. It has been cut out and flipped around. A *translocation* occurs when one broken segment of DNA becomes integrated into a different chromosome. *Duplications* occur when a portion of a chromosome is replicated and attached to the original section in sequence. *Deletion* aberrations result when the broken piece becomes lost or is destroyed before it can be reattached.

In some individuals, a single nucleotide of the gene may be changed. This type of mutation is called a **point mutation**. An example of the effects of altered DNA may be seen in human red blood cells. Red blood cells contain the oxygen-transport molecule, hemoglobin. Normal hemoglobin molecules are composed of 150 amino acids in four chains—two alpha and two beta. The nucleotide sequence of the gene for the beta chain is known, as is the amino acid sequence for this chain. In normal individuals, the sequence begins like this:

Val-His-Leu-Thr-Pro-Glu-Glu-Lys . . .

The result of this mutation is a new amino acid sequence in all the red blood cells:

Val-His-Leu-Thr-Pro-Val-Glu-Lys . . .

This single nucleotide change (known as a *missense point mutation*), which causes a single amino acid to change, may seem minor. However, it is the cause of **sickle-cell anemia**, a disease that affects the red blood cells by changing them from a circular to a sickle shape when oxygen levels are low (figure 7.11). When this sickling occurs, the red blood cells do not flow smoothly through capillaries. Their irregular shapes cause them to clump, clogging the blood vessels. This prevents them from delivering their oxygen load to the oxygen-demanding tissues. A number of physical disabilities may result, including physical weakness, brain damage, pain and stiffness of the joints, kidney damage, rheumatism, and, in severe cases, death.

Other mutations occur as a result of changing the number of nucleotide bases in a gene. **Transposons** or “jumping genes” are segments of DNA capable of moving from one

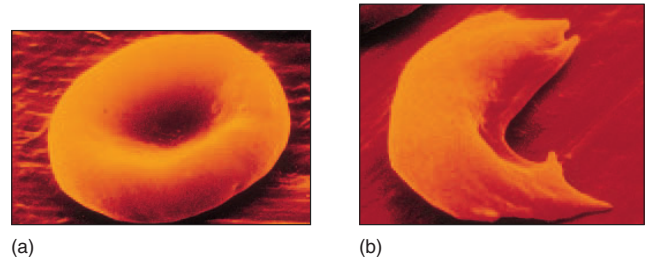


Figure 7.11

Normal and Sickled Red Blood Cells

(a) A normal red blood cell is shown in comparison with (b) a cell having the sickle shape. This sickling is the result of a single amino acid change in the hemoglobin molecule.

chromosome to another. When the jumping gene is spliced into its new location, it alters the normal nucleotide sequence, causing normally stable genes to be misread during transcription. The result may be a mutant gene. It is estimated that 10% of all human genes are transposons. Transposons can alter the genetic activity of a cell when it leaves its original location, stop transcription of the gene they “jump” into, or change the reading of codons from their normal sequence. For example, one person who developed hemophilia (“bleeders disease”) did so as a result of a transposon “jumping” into the gene that was responsible for producing a specific clotting factor, factor VIII.

Changes in the structure of DNA may have harmful effects on the next generation if they occur in the sex cells. Some damage to DNA is so extensive that the entire strand of DNA is broken, resulting in the synthesis of abnormal proteins or a total lack of protein synthesis. A number of experiments indicate that many street drugs such as LSD (lysergic acid diethylamide) are mutagenic agents and cause DNA to break. Abnormalities have also been identified that are the result of changes in the number or sequence of bases. One way to illustrate these various kinds of mutations is seen in table 7.3.

A powerful new science of gene manipulation, **biotechnology**, suggests that, in the future, genetic diseases may be controlled or cured. Since 1953, when the structure of the DNA molecule was first described, there has been a rapid succession of advances in the field of genetics. It is now possible to transfer DNA from one organism to another. This has made possible the manufacture of human genes and gene products by bacteria.

Figure 7.12 is a summary of the protein-synthesis process beginning with the formation of the various forms of RNA as copies of coding sections of DNA.

Table 7.3**TYPES OF CHROMOSOMAL MUTATIONS**

A sentence comprised of three-letter words can provide an analogy to the effect of mutations on a gene's nucleotide sequence.

Normal Sequence	THE ONE BIG FLY HAD ONE RED EYE
Kind of Mutation	Sequence Change
Missense	THQ ONE BIG FLY HAD ONE RED EYE
Nonsense	THE ONE BIG
Frameshift	THE ONE QBI GFL YHA DON ERE DEY
Deletion	THE ONE BIG HAD ONE RED EYE
Duplication	THE ONE BIG FLY FLY HAD ONE RED EYE
Insertion	THE ONE BIG WET FLY HAD ONE RED EYE
Expanding mutation:	
Parents	THE ONE BIG FLY HAD ONE RED EYE
Children	THE ONE BIG FLY FLY FLY HAD ONE RED EYE
Grandchildren	THE ONE BIG FLY FLY FLY FLY FLY FLY HAD ONE RED EYE

7.7 Manipulating DNA to Our Advantage

Biotechnology includes the use of a method of splicing genes from one organism into another, resulting in a new form of DNA called **recombinant DNA**. Organisms with these genetic changes are referred to as **genetically modified (GMO)** or **transgenic organisms**. These organisms or their offspring have been engineered so that they contain genes from at least one unrelated organism such as a virus, plant, or other animal. This process is accomplished using enzymes that are naturally involved in the DNA-replication process and others naturally produced by bacteria. When genes are spliced from different organisms into host cells, the host cell replicates these new, “foreign” genes and synthesizes proteins encoded by them. Gene splicing begins with the laboratory isolation of DNA from an organism that contains the desired gene; for example, from human cells that contain the gene for the manufacture of insulin. If the gene is short enough and its base sequence is known, it may be synthesized in the laboratory from separate nucleotides. If the gene is too long and complex, it is cut from the chromosome with enzymes called *restriction endonucleases*. They are given this name because these enzymes (*-ases*) only cut DNA (*nucle-*) at certain base sequences (restricted in their action) and work inside (*endo-*) the DNA. These particular enzymes act like

molecular scissors that do not cut the DNA straight across, but in a zig-zag pattern that leaves one strand slightly longer than its complement. The short nucleotide sequence that sticks out and remains unpaired is called a *sticky end* because it can be reattached to another complementary strand. DNA segments have been successfully cut from rats, frogs, bacteria, and humans.

This isolated gene with its “sticky end” is spliced into microbial DNA. The host DNA is opened up with the proper restriction endonuclease and ligase (i.e., tie together) enzymes that are used to attach the sticky ends into the host DNA. This gene-splicing procedure may be performed with small loops of bacterial DNA that are not part of the main chromosome. These small DNA loops are called *plasmids*. Once the splicing is completed, the plasmids can be inserted into the bacterial host by treating the cell with special chemicals that encourage it to take in these large chunks of DNA. A more efficient alternative is to splice the desired gene into the DNA of a bacterial virus so that it can carry the new gene into the bacterium as it infects the host cell. Once inside the host cell, the genes may be replicated, along with the rest of the DNA to clone the “foreign” gene, or they may begin to synthesize the encoded protein.

As this highly sophisticated procedure has been refined, it has become possible to quickly and accurately splice genes from a variety of species into host bacteria, making possible the synthesis of large quantities of medically important products. For example, recombinant DNA procedures are responsible for the production of human insulin, used in the control of diabetes; interferon, used as an antiviral agent; human growth hormone, used to stimulate growth in children lacking this hormone; and somatostatin, a brain hormone also implicated in growth. Over 200 such products have been manufactured using these methods.

The possibilities that open up with the manipulation of DNA are revolutionary (How Science Works 7.2). These methods enable cells to produce molecules that they would not normally make. Some research laboratories have even spliced genes into laboratory-cultured human cells. Should such a venture prove to be practical, genetic diseases such as sickle-cell anemia could be controlled. The process of recombinant DNA gene splicing also enables cells to be more efficient at producing molecules that they normally synthesize. Some of the likely rewards are (1) production of additional, medically useful proteins; (2) mapping of the locations of genes on human chromosomes; (3) more complete understanding of how genes are regulated; (4) production of crop plants with increased yields; and (5) development of new species of garden plants.

The discovery of the structure of DNA nearly 50 years ago seemed very far removed from the practical world. The importance of this “pure” or “basic” research is just now being realized. Many companies are involved in recombinant DNA research with the aim of alleviating or curing disease.

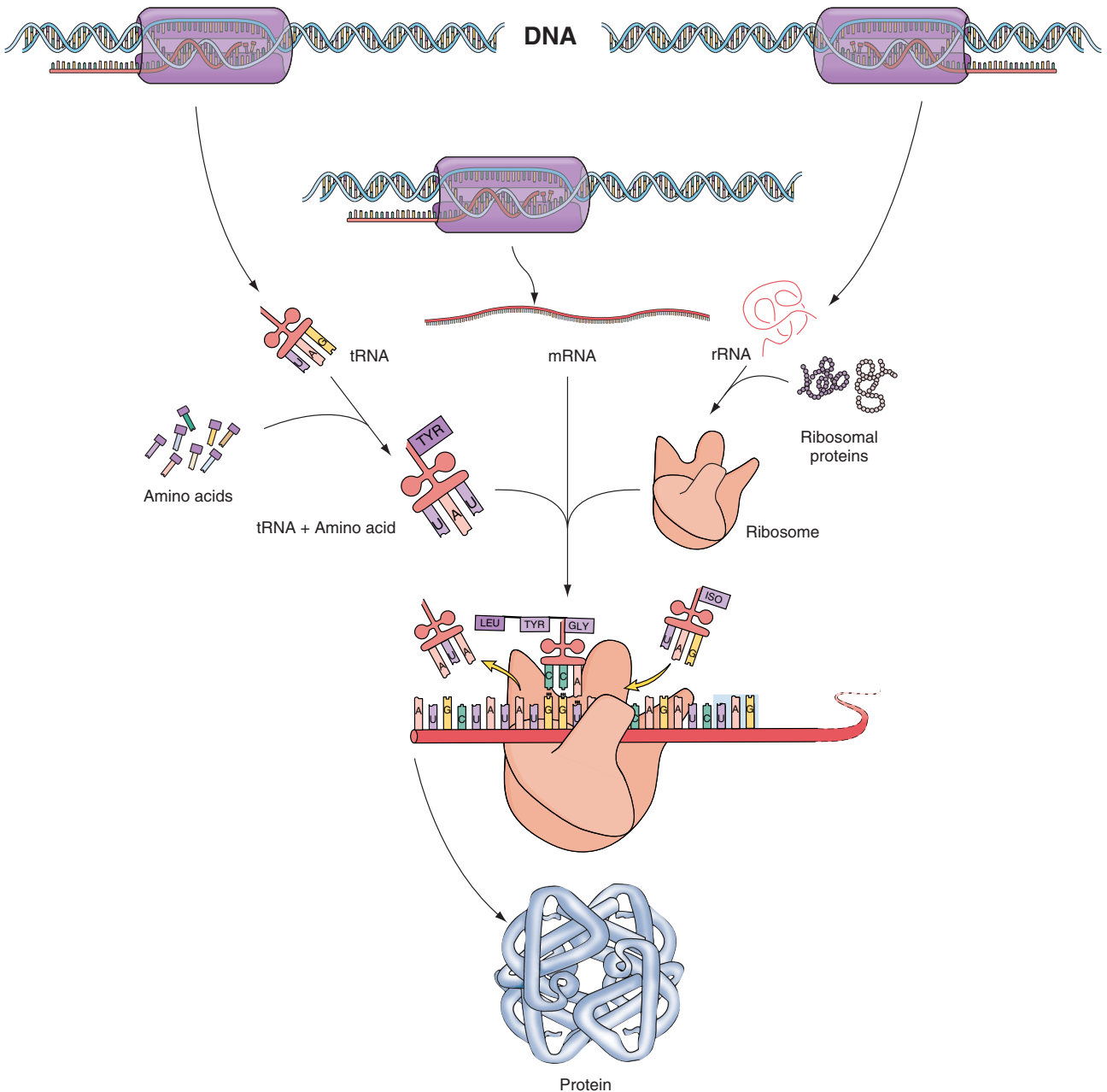


Figure 7.12

Protein Synthesis

There are several steps involved in protein synthesis. (1) mRNA, tRNA, and rRNA are manufactured from genes at various points on the DNA using the transcription process; (2) the mRNA enters the cytoplasm and attaches to rRNA-containing ribosomes; (3) tRNA molecules carry various amino acids to the ribosome and positions them in the order specified based on the mRNA codon sequence in the translation operation; (4) the amino acids are combined by dehydration synthesis to form a protein; (5) when complete, the mRNA and tRNA are released from the ribosome to be reused to synthesize other protein molecules.

HOW SCIENCE WORKS 7.2



The PCR and Genetic Fingerprinting

In 1989, the American Association for the Advancement of Science named DNA polymerase Molecule of the Year. The value of this enzyme in the polymerase chain reaction (PCR) is so great that it could not be ignored. Just what is the PCR, how does it work, and what can you do with it?

The PCR is a laboratory procedure for copying selected segments of DNA. A single cell can provide enough DNA for analysis and identification! Having a large number of copies of a “target sequence” of nucleotides enables biochemists to more easily work with DNA. This is like increasing the one “needle in the haystack” to such large numbers (100 billion in only a matter of hours) that they’re not hard to find, recognize, and work with. The types of specimens that can be used include semen, hair, blood, bacteria, protozoa, viruses, mummified tissue, and frozen cells. The process requires the DNA specimen, free DNA nucleotides, synthetic “primer” DNA, DNA polymerase, and simple lab equipment, such as a test tube and a source of heat.

Having decided which target sequence of nucleotides (which “needle”) is to be replicated, scientists heat the specimen of DNA to separate the coding and non-coding strands. Molecules of synthetic “primer” DNA are added to the specimen. These primer molecules are specifically designed to attach to the ends of the target sequence. Next, a mixture of triphosphorylated nucleotides is added so that they can become the newly replicated DNA. The presence of the primer, attached to the DNA and added nucleotides, serves as the substrate for the DNA polymerase. Once added, the polymerase begins making its way down the length of the DNA from one attached primer end to the other. The enzyme bonds the new DNA nucleotides to the strand, replicating the molecule as it goes. It stops when it reaches the other end, having produced a new copy of the target sequence. Because the DNA polymerase will continue to operate as long as enzymes and substrates are available, the process continues, and in a short time there are billions of small pieces of DNA, all replicas of the target sequence.

So what, you say? Well, consider the following. Using the PCR, scientists have been able to:

1. More accurately diagnose such diseases as sickle-cell anemia, cancer, Lyme disease, AIDS, and Legionnaires disease
2. Perform highly accurate tissue typing for matching organ-transplant donors and recipients
3. Help resolve criminal cases of rape, murder, assault, and robbery by matching suspect DNA to that found at the crime scene
4. Detect specific bacteria in environmental samples
5. Monitor the spread of genetically engineered microorganisms in the environment
6. Check water quality by detecting bacterial contamination from feces
7. Identify viruses in water samples
8. Identify disease-causing protozoa in water
9. Determine specific metabolic pathways and activities occurring in microorganisms
10. Determine races, distribution patterns, kinships, migration patterns, evolutionary relationships, and rates of evolution of long-extinct species
11. Accurately settle paternity suits
12. Confirm identity in amnesia cases
13. Identify a person as a relative for immigration purposes
14. Provide the basis for making human antibodies in specific bacteria
15. Possibly provide the basis for replicating genes that could be transplanted into individuals suffering from genetic diseases
16. Identify nucleotide sequences peculiar to the human genome (an application currently underway as part of the Human Genome Project)

Genetic Engineering

The field of **bioengineering** is advancing as quickly as is the electronics industry. The first bioengineering efforts focused on developing genetically altered or modified (GM) crops that had improvements over past varieties, such as increased resistance to infectious plant disease. This was primarily accomplished through selective breeding and irradiation of cells to produce desirable mutations. The second wave of research involved directly manipulating DNA using the more sophisticated techniques of recombinant DNA technology such as the PCR, genetic fingerprinting, and cloning. Genetic engineers identify and isolate sequences of nucleotides from a living or dead cell and install it into another living cell. Once these new genes have been installed, they begin to

undergo transcription resulting in the production of a protein “foreign” to that organism, and undertake DNA replication passing that “foreign gene” down through the generations. There are several steps involved in generating GM organisms: (1) locating the desired gene in a donor organism, (2) isolating that gene, (3) modifying that gene to a more desirable form if necessary, (4) amplifying or replicating that gene using PCR (polymerase chain reaction) techniques, and (5) introducing the gene into the recipient cell. This has resulted in improved food handling and processing, such as slower ripening in tomatoes. Currently, crops are being genetically manipulated to manufacture large quantities of specialty chemicals such as antibiotics, steroids, and other biologically useful organic chemicals.

Although some of these chemicals have been produced in small amounts from genetically engineered microorganisms, crops such as turnips, rice, soybeans, potatoes, cotton, corn, and tobacco can generate tens or hundreds of kilograms of specialty chemicals per year. Many of these GM crops also have increased nutritional value and yet can be cultivated using traditional methods. Such crops have the potential of supplying the essential amino acids, fatty acids, and other nutrients now lacking in the diets of people in underdeveloped or developing nations. Researchers have also shown, for example, that turnips can produce interferon (an antiviral agent), tobacco can create antibodies to fight human disease, oilseed rape plants can serve as a source of human brain hormones, and potatoes can synthesize human serum albumin that is indistinguishable from the genuine human blood protein. The work of genetic engineers may sound exciting and positive, but many ethical questions must be addressed. In small groups, identify and discuss five ethical issues associated with bioengineering.

Another genetic engineering accomplishment has been *genetic fingerprinting*. Using this technique it is possible to show the nucleotide sequence differences among individuals since no two people have the same nucleotide sequences. While this sounds like an easy task, the presence of many millions of base pairs in a person's chromosomes makes this process time-consuming and impractical. Therefore, scientists don't really do a complete fingerprint but focus only on certain shorter, repeating patterns in the DNA. By focusing on these shorter repeating nucleotide sequences, it is possible to determine whether samples from two individuals have these same repeating segments. Genetic engineers use a small number of sequences that are known to vary a great deal among individuals, and compare those to get a certain probability of a match. The more similar the sequences the more likely the two samples are from the same person. The less similar the sequences the less likely the two samples are from the same person. In criminal cases, DNA samples from the crime site can be compared to those taken from suspects. If there is a high number of short repeating sequence matches, it is highly probable that the suspect was at the scene of the crime and may be the guilty party. This same procedure can also be used to confirm the identity of a person as in cases of amnesia, murder, or accidental death.

SUMMARY

The successful operation of a living cell depends on its ability to accurately reproduce genes and control chemical reactions. DNA replication results in an exact doubling of the genetic material. The process virtually guarantees that identical strands of DNA will be passed on to the next generation of cells.

The enzymes are responsible for the efficient control of a cell's metabolism. However, the production of protein molecules is

under the control of the nucleic acids, the primary control molecules of the cell. The structure of the nucleic acids DNA and RNA determine the structure of the proteins, whereas the structure of the proteins determines their function in the cell's life cycle. Protein synthesis involves the decoding of the DNA into specific protein molecules and the use of the intermediate molecules, mRNA and tRNA, at the ribosome. Errors in any of the codons of these molecules may produce observable changes in the cell's functioning and lead to cell death.

Methods of manipulating DNA have led to the controlled transfer of genes from one kind of organism to another. This has made it possible for bacteria to produce a number of human gene products.

THINKING CRITICALLY

An 18-year-old college student reported that she had been raped by someone she identified as a "large, tanned white man." A student in her biology class fitting that description was said by eyewitnesses to have been, without a doubt, in the area at approximately the time of the crime. The suspect was apprehended and upon investigation was found to look very much like someone who lived in the area and who had a previous record of criminal sexual assaults. Samples of semen from the woman's vagina were taken during a physical exam after the rape. Cells were also taken from the suspect. He was brought to trial but found to be innocent of the crime based on evidence from the criminal investigations laboratory. His alibi that he had been working alone on a research project in the biology lab held up. Without PCR genetic fingerprinting, the suspect would surely have been wrongly convicted, based solely on circumstantial evidence provided by the victim and the "eyewitnesses."

Place yourself in the position of the expert witness from the criminal laboratory who performed the PCR genetic fingerprinting tests on the two specimens. The prosecuting attorney has just asked you to explain to the jury what led you to the conclusion that the suspect could not have been responsible for this crime. Remember, you must explain this to a jury of twelve men and women who in all likelihood have little or no background in the biological sciences. Please, tell the whole truth and nothing but the truth.

CONCEPT MAP TERMINOLOGY

Construct a concept map to show relationships among the following concepts.

- base pairing
- complementary bases
- DNA polymerase
- DNA repair
- mutation
- replication
- template

KEY TERMS

adenine	deoxyribose	nitrogenous base	RNA polymerase
anticodon	DNA code	nucleic acids	sickle-cell anemia
bioengineering	DNA polymerase	nucleoproteins	telomeres
biotechnology	DNA replication	nucleosomes	termination code
chromatin fibers	gene	nucleotide	thymine
chromosomal aberrations	genetically modified organism (GMO)	point mutation	transcription
chromosome	guanine	promoter	transfer RNA (tRNA)
coding strand	initiation code	protein synthesis	transgenic organisms
codon	messenger RNA (mRNA)	recombinant DNA	translation
complementary base	mutagenic agent	ribonucleic acid (RNA)	transposons
cytosine	mutation	ribose	uracil
deoxyribonucleic acid (DNA)		ribosomal RNA (rRNA)	

e—LEARNING CONNECTIONS www.mhhe.com/enger10

Topics	Questions	Media Resources
7.1 The Main Idea: The Central Dogma		Quick Overview <ul style="list-style-type: none"> The flow of genetic information Key Points <ul style="list-style-type: none"> The main idea: The central dogma
7.2 The Structure of DNA and RNA	<ol style="list-style-type: none"> What are the differences among a nucleotide, a nitrogenous base, and a codon? What are the differences between DNA and RNA? 	Quick Overview <ul style="list-style-type: none"> Nucleic acids and genetic information Key Points <ul style="list-style-type: none"> The structure of DNA and RNA
7.3 DNA Replication	<ol style="list-style-type: none"> Why is DNA replication necessary? What is DNA polymerase and how does it function? 	Quick Overview <ul style="list-style-type: none"> Using templates to copy information Key Points <ul style="list-style-type: none"> DNA replication
7.4 DNA Transcription	<ol style="list-style-type: none"> What is RNA polymerase and how does it function? How does DNA replication differ from the manufacture of an RNA molecule? If a DNA nucleotide sequence is CATAAAGCA, what is the mRNA nucleotide sequence that would base-pair with it? 	Quick Overview <ul style="list-style-type: none"> A working copy Key Points <ul style="list-style-type: none"> DNA transcription
7.5 Translation, or Protein Synthesis	<ol style="list-style-type: none"> What amino acids would occur in the protein chemically coded by the sequence of nucleotides in the question directly preceding this one? List the sequence of events that takes place when a DNA message is translated into protein. How do tRNA, rRNA, and mRNA differ in function? 	Quick Overview <ul style="list-style-type: none"> Reading RNA to make a protein Key Points <ul style="list-style-type: none"> Translation or protein synthesis
7.6 Alterations of DNA	<ol style="list-style-type: none"> Both chromosomal and point mutations occur in DNA. In what ways do they differ? How is this related to recombinant DNA? 	Quick Overview <ul style="list-style-type: none"> Implications of errors in DNA Key Points <ul style="list-style-type: none"> Alterations of DNA
7.7 Manipulating DNA to Our Advantage		Quick Overview <ul style="list-style-type: none"> Custom DNA Key Points <ul style="list-style-type: none"> Manipulating DNA to our advantage