Figure 29.13 A schematic representation of protein biosynthesis. The mRNA containing codon base sequences is read by tRNA containing complementary anticodon base sequences. Transfer RNA assembles the proper amino acids into position for incorporation into the growing peptide.

PROBLEM..

29.16 List codon sequences for these amino acids:

(a) Ala   (b) Phe   (c) Leu   (d) Tyr

PROBLEM..

29.17 List anticodon sequences on the tRNA's carrying the amino acids shown in Problem 29.16.

PROBLEM..
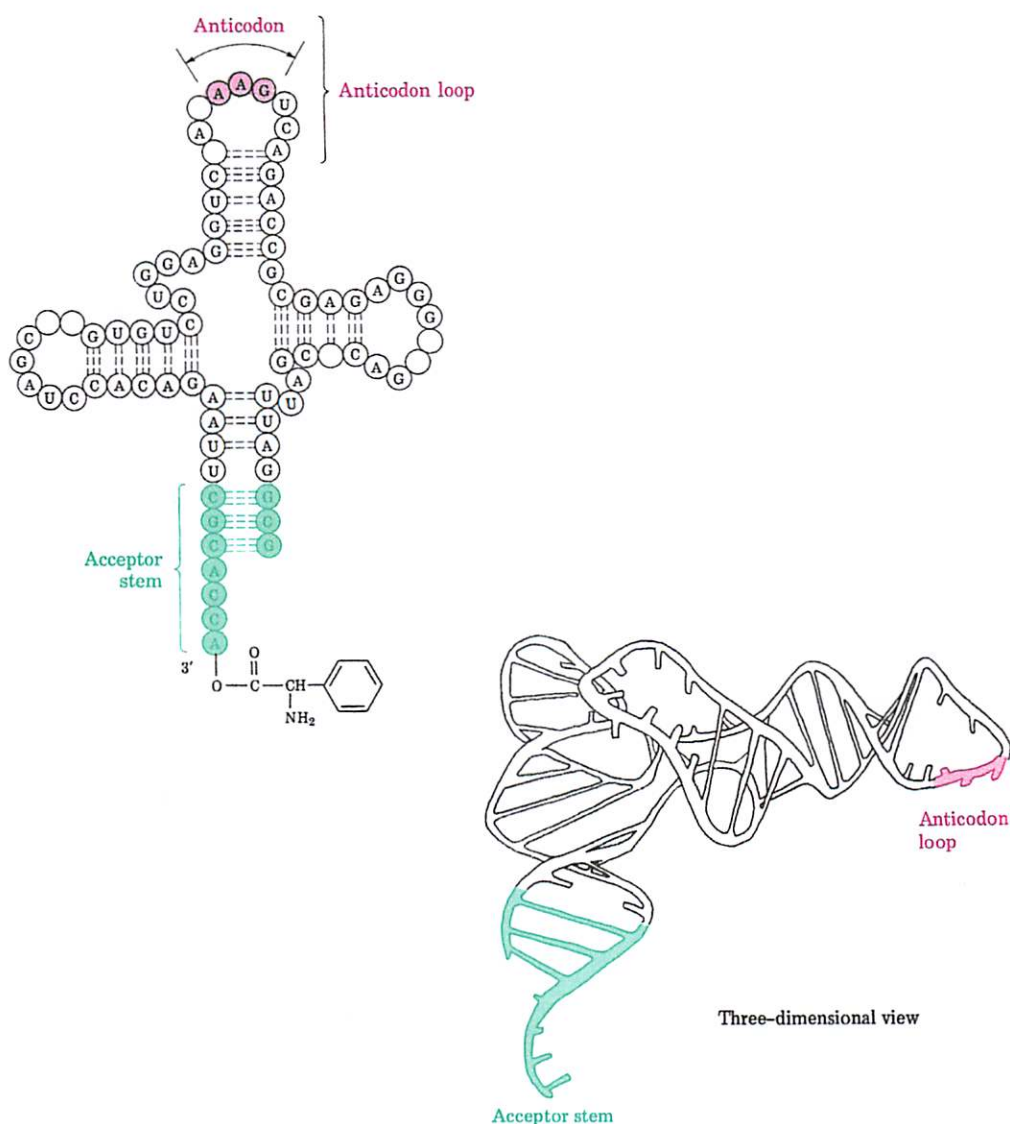
29.18 What amino acid sequence is coded for by the following mRNA base sequence?

CUU-AUG-GCU-UGG-CCC-UAA

PROBLEM..
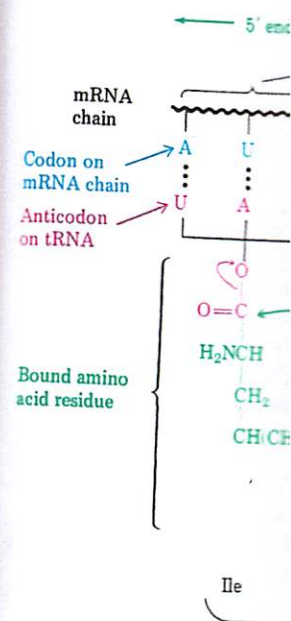
29.19 What anticodon sequences of tRNA's are coded for by the mRNA in Problem 29.18?

Figure 29.12 Structure of a tRNA molecule. The tRNA is a roughly cloverleaf-shaped molecule containing an anticodon triplet on one "leaf" and a covalently attached amino acid unit at its 3' end. The example shown is a yeast tRNA that codes for phenylalanine. The nucleotides not specifically identified are chemically modified analogs of the four normal nucleotides.

As each successive codon on mRNA is read, different tRNA's bring the correct amino acids into position for enzyme-mediated transfer to the growing peptide. When synthesis of the proper protein is completed, a "stop" codon signals the end, and the protein is released from the ribosome. The entire process of protein biosynthesis is illustrated schematically in Figure 29.13.

Figure 29.13 A schema
The mRNA containing co
containing complementar
assembles the proper ami
into the growing peptide.

re both strands are cop-
into mRNA. The strand
strand, and its comple-
te strand is transcribed.
and are complementary,
lecule are also comple-
e produced during tran-
: only difference is that
IA informational strand

cussed raises as many
here to unwind? Where
one start? How do the
mplate strand to begin
questions are extremely
the last decade is that
d **promoter sites** that
ries out RNA synthesis,
there are other base

nerged is that genes are
hain. Often a gene will
then be interrupted by
nd then take up again
nRNA molecule results
e remaining pieces are
0% of human DNA is
tually contains genetic

ine.

ing DNA base sequence

ct biosynthesis of the
by an organism. These
sses. The mechanics of
mRNA) and take place
sm of a cell that consist

of about 60% ribosomal RNA and 40% protein. On the ribosome, mRNA serves as a template to pass on the genetic information it has transcribed from DNA.

The specific ribonucleotide sequence in mRNA forms a "code" that determines the order in which different amino acid residues are to be joined. Each "word" or **codon** along the mRNA chain consists of a series of three ribonucleotides that is specific for a given amino acid. For example, the series cytosine–uracil–guanine (C-U-G) on mRNA is a codon directing incorporation of the amino acid leucine into the growing protein, and guanine–adenine–uracil (G-A-U) codes for aspartic acid. Of the $4^3 = 64$ possible triads of the four bases in RNA, 61 code for specific amino acids (certain amino acids are specified by more than one codon). In addition, 3 of the 64 codons specify chain termination. Table 29.3 shows the meaning of each codon.

TABLE 29.3 Codon Assignments of Base Triads

First base (5' end)	Second base	Third base (3' end)			
		U	C	A	G
U	U	Phe	Phe	Leu	Leu
	C	Ser	Ser	Ser	Ser
	A	Tyr	Tyr	Stop	Stop
	G	Cys	Cys	Stop	Trp
C	U	Leu	Leu	Leu	Leu
	C	Pro	Pro	Pro	Pro
	A	His	His	Gln	Gln
	G	Arg	Arg	Arg	Arg
A	U	Ile	Ile	Ile	Met
	C	Thr	Thr	Thr	Thr
	A	Asn	Asn	Lys	Lys
	G	Ser	Ser	Arg	Arg
G	U	Val	Val	Val	Val
	C	Ala	Ala	Ala	Ala
	A	Asp	Asp	Glu	Glu
	G	Gly	Gly	Gly	Gly

The code expressed in mRNA is read by transfer RNA (tRNA) in a process called **translation**. There are at least 60 different transfer RNA's, one for each of the codons in Table 29.3. Each specific tRNA acts as a carrier to bring a specific amino acid into place so that it can be transferred to the growing protein chain.

A typical tRNA is roughly the shape of a cloverleaf, as shown in Figure 29.12. It consists of about 70–100 ribonucleotides and is bonded to a specific amino acid by an ester linkage through the free 3'-hydroxyl on ribose at the 3' end of the tRNA. Each tRNA also contains in its structure a segment called an **anticodon**, a sequence of three ribonucleotides complementary to the codon sequence. For example, the codon sequence C-U-G present on mRNA is read by a leucine-bearing tRNA having the complementary anticodon base sequence G-A-C.
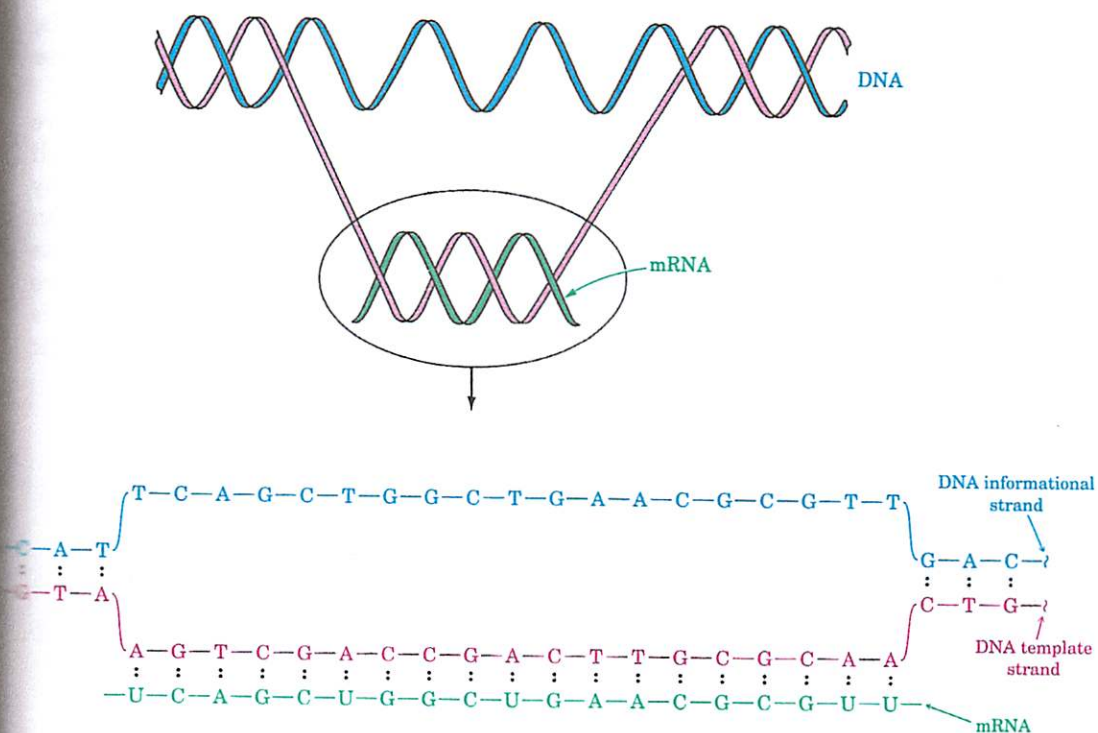
Messenger RNA (mRNA) carries genetic messages from DNA to *ribosomes*, small granular particles in the cytoplasm of a cell where protein synthesis takes place.

Ribosomal RNA (rRNA) complexed with protein provides the physical makeup of the ribosomes.

Transfer RNA (tRNA) transports specific amino acids to the ribosomes where they're joined together to make proteins.

Molecules of RNA are synthesized in the nucleus of the cell by **transcription** of DNA. A portion of the DNA double helix unwinds, and the bases of the two strands are exposed. Ribonucleotides line up in the proper order by hydrogen-bonding to their complementary bases on DNA, bond formation occurs in the $5' \rightarrow 3'$ direction, and the completed RNA molecule then unwinds from DNA and migrates from the nucleus (Figure 29.11).

DNA

mRNA

T—C—A—G—C—T—G—G—C—T—G—A—A—C—G—C—G—T—T   DNA informational strand

C—A—T
G—T—A

G—A—C—
C—T—G—

A—G—T—C—G—A—C—C—G—A—C—T—T—G—C—G—C—A—A   DNA template strand

—U—C—A—G—C—U—G—G—C—U—G—A—A—C—G—C—G—U—U—   mRNA

Figure 29.11 Biosynthesis of RNA using a DNA segment as template.

The conversion of the information contained in a DNA segment into proteins begins with the synthesis of mRNA molecules that contain anywhere from several hundred to several thousand ribonucleotides, depending on the size of the protein to be made. Each of the 100,000 or so proteins in the human body is synthesized from a different mRNA that has been transcribed from a specific gene on DNA.
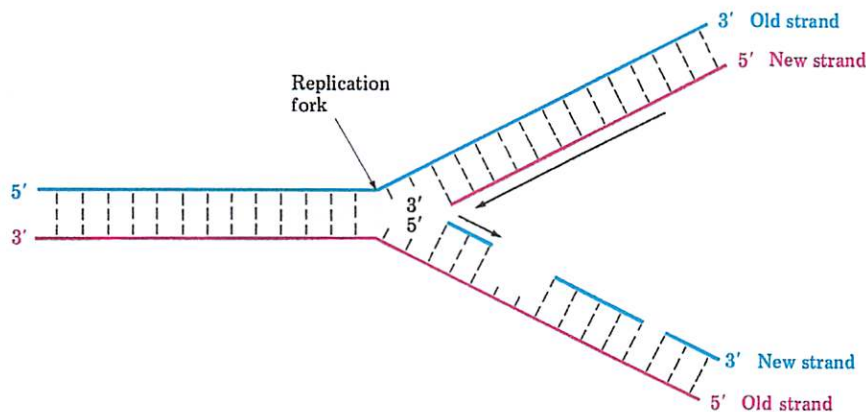
Figure 29.10 Replication of DNA. Both new DNA strands are synthesized in a 5′ → 3′ direction. The original strand whose 3′ end is near the point of unraveling is replicated smoothly, but the original strand whose 5′ end is near the unraveling point is replicated in small pieces that are later joined. The arrowheads are at the growing ends of the chains.

molecules, their base sequence is faithfully copied during replication. The copying process takes only minutes, and it's been estimated that an error occurs only about once each 10 billion to 100 billion bases.

29.14   Structure and Synthesis of RNA: Transcription

RNA is structurally similar to DNA. Both are sugar–phosphate polymers and both have heterocyclic bases attached. The only differences are that RNA contains ribose rather than deoxyribose and uracil rather than thymine. Uracil in RNA forms strong hydrogen bonds to its complementary base, adenine, just as thymine does in DNA.
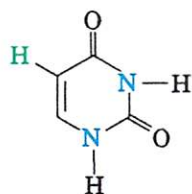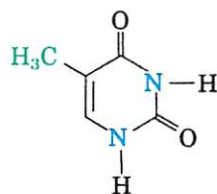
Uracil (in RNA)   Thymine (in DNA)

There are three major kinds of ribonucleic acid, each of which serves a specific function. All three kinds of RNA are structurally similar to DNA, but they're much smaller molecules than DNA and they remain single stranded, rather than double stranded like DNA.
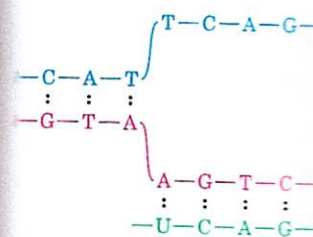
Mess
somes
synth

Ribos
maker

Trans
where

Molec
scription
bases of th
order by I
formation
then unwi

T—C—A—G—
—C—A—T
: : :
—G—T—A
A—G—T—C—
: : : :
—U—C—A—G—

Figure 29.11   Biosynthes
template.

The cor
proteins beg
where from
on the size
the human I
scribed from

Figure 29.9   Addition of a new nucleotide to a growing DNA strand.
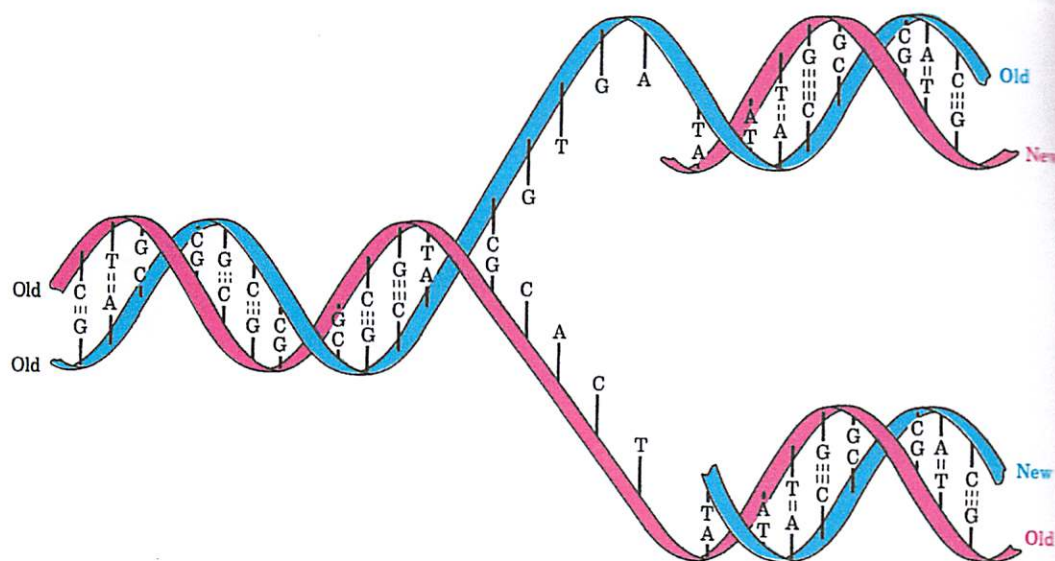
Figure 29.8 Schematic representation of DNA replication.

separate; a new hand forms inside the glove; and a new glove forms around the hand. Two identical copies now exist where only one existed before.

The process by which the individual nucleotides are joined to create new DNA strands involves many steps and many different enzymes. Addition of new nucleotide units to the growing chain is catalyzed by the enzyme *DNA polymerase* and has been shown to occur by addition of a 5'-mononucleotide triphosphate to the free 3'-hydroxyl group of the growing chain, as indicated in Figure 29.9.

Both of the new DNA strands are synthesized in the same 5'-to-3' direction, which implies that the two strands can't be synthesized in exactly the same way. Since the two complementary DNA strands are lined up in opposite directions, one strand must have its 3' end near the point of unraveling (the **replication fork**) while the other strand has its 5' end near the replication fork. What evidently happens is that the complement of the original 3' → 5' strand is synthesized smoothly and in a single piece, but the complement of the original 5' → 3' strand is synthesized discontinuously in small pieces that are then linked at a later point by DNA ligase enzymes (Figure 29.10).

It's difficult to conceive of the magnitude of the replication process. The nucleus of a human cell contains 46 chromosomes (23 pairs), each of which consists of one very large DNA molecule. Each chromosome, in turn, is made up of several thousand DNA segments called *genes*, and the sum of all genes in a human cell (the *genome*) is estimated to be approximately 3 billion base pairs. A single DNA chain might have a length of over 12 cm and contain up to 250 million pairs of bases. Regardless of the size of these enormous
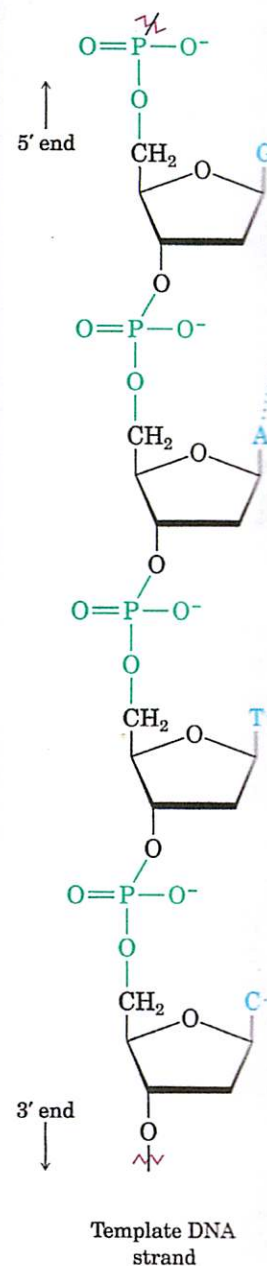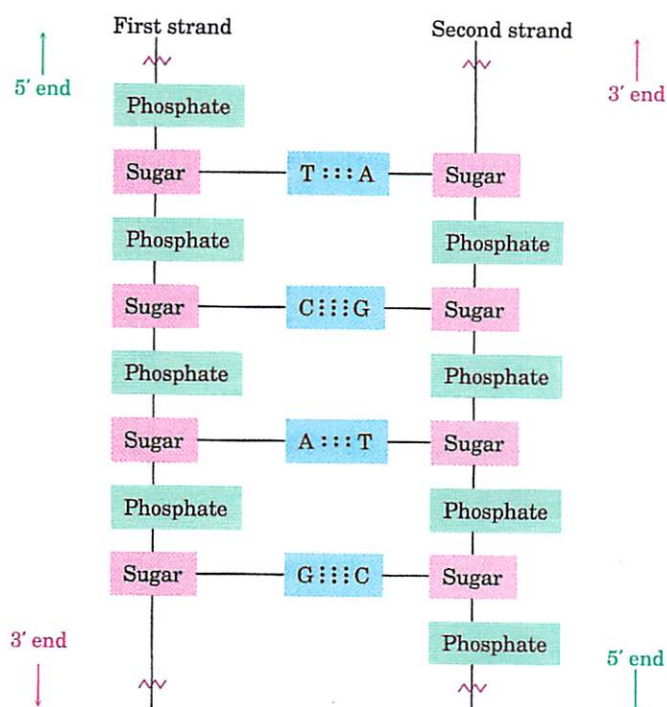

Figure 29.9 Addition of strand.

Figure 29.7 Complementarity in base pairing in the DNA double helix as shown by this computer-generated structure. The sugar–phosphate backbone runs along the outside of the helix, while the amine bases hydrogen-bond to one another on the inside.

Notice in Figure 29.7 that the two strands of the double helix coil such that two kinds of "grooves" result, a **major groove** that's 12 Å wide and a **minor groove** that's 6 Å wide. The major groove is slightly deeper than the minor groove, and both are lined by potential hydrogen-bond donors and acceptors. Thus, a variety of molecules are able to *intercalate*, or fit into one of the grooves between the strands. A large number of cancer-causing and cancer-preventing agents are thought to function by interacting with DNA in this way.

PROBLEM...

29.13   What sequence of bases on one strand of DNA is complementary to the following sequence on another strand?

G-G-C-T-A-A-T-C-C-G-T

....

29.12   Nucleic

A DNA m
mation, w
together i
on to futu
informatio
message a
    What
that the fi
the proper
the inform
of individu
make a sp
the right
genetic inf
for carryin

Replication

    Three
informatio

1. Re
    ma
    offs

2. Tr
    tai
    the

3. Tr
    dec

29.13   Replicatic

The Watson
it also provi
exact copies
process that
separate an
an exactly c
begin to gro
and two new
    Crick d
DNA strand

In 1953, James Watson[1] and Francis Crick[2] made their now classic proposal for the secondary structure of DNA. According to the Watson–Crick model, DNA consists of two polynucleotide strands coiled around each other in a **double helix**. The two strands run in opposite directions and are held together by hydrogen bonds between specific pairs of bases. Adenine (A) and thymine (T) form strong hydrogen bonds to each other but not to C or G. Similarly, guanine (G) and cytosine (C) form strong hydrogen bonds to each other but not to A or T.

(Guanine) G : : : : : : C (Cytosine)

(Adenine) A : : : : : : T (Thymine)
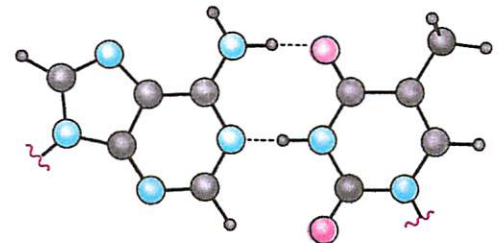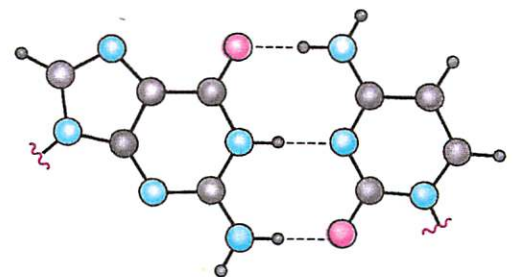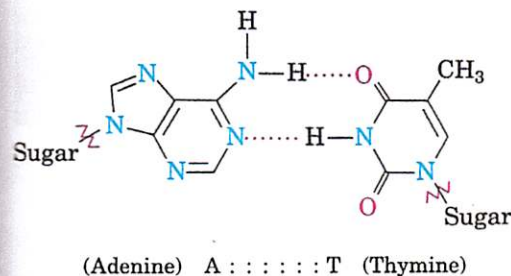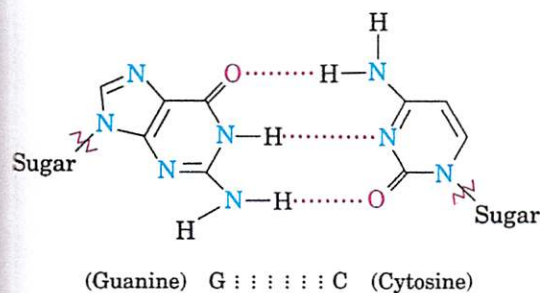
The two strands of the DNA double helix aren't identical; rather, they're complementary. Whenever a C base occurs in one strand, a G base occurs opposite it in the other strand. When an A base occurs in one strand, a T appears opposite it in the other strand. This complementary pairing of bases explains why A and T, and C and G, are always found in equal amounts. Figure 29.7 illustrates this base pairing, showing how the two complementary strands are coiled into the double helix. X-ray measurements show that the DNA double helix is 20 Å wide, that there are exactly 10 base pairs in each full turn, and that each turn is 34 Å in height.

A helpful mnemonic device to remember the nature of the hydrogen bonding between the four DNA bases is the simple phrase "Pure silver taxi."

| Pure	Silver	Taxi
Pur	Ag	TC
The purine bases,	A and G,	hydrogen-bond to T and C.

[1]James Dewey Watson (1928–); b. Chicago, Ill.; Ph.D. Indiana; professor, Harvard University; Nobel Prize in medicine (1960).

[2]Francis H. C. Crick (1916–); b. England; Ph.D. Cambridge; professor, Cambridge University; Nobel Prize in medicine (1960).

29.10   2'-Deoxythymidine exists largely in the lactam form rather than in the tautomeric lactim form. Explain.

Lactam form   Lactim form
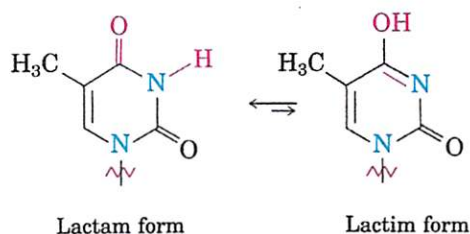
29.10   Structure of DNA

Nucleotides join together in DNA by forming a phosphate ester bond between the 5'-phosphate component of one nucleotide and the 3' hydroxyl on the sugar component of another nucleotide (Figure 29.6). One end of the nucleic acid polymer has a free hydroxyl at C3' (called the **3' end**), and the other end has a phosphoric acid residue at C5' (the **5' end**).
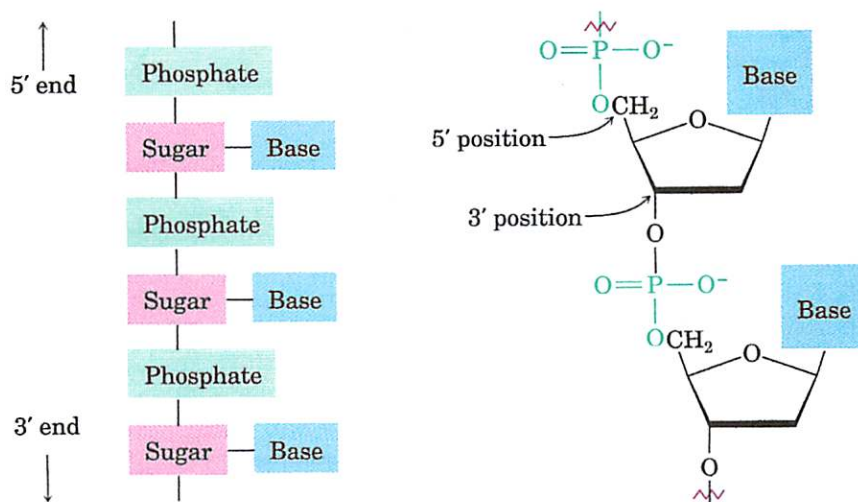
**Figure 29.6**   Generalized structure of DNA.

Just as the structure of a protein depends on the sequence in which individual amino acid residues are connected, the structure of a nucleic acid depends on the sequence of individual nucleotides. To carry the analogy further, just as a protein has a polyamide backbone with different side chains attached to it, a nucleic acid has an alternating sugar–phosphate backbone with different amine bases attached.

Deoxyribonucleotides
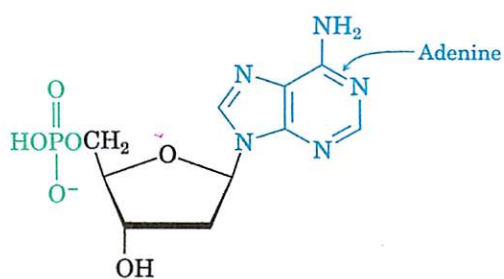
2'-Deoxyadenosine 5'-phosphate
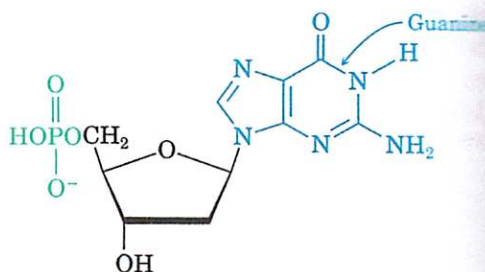
2'-Deoxyguanosine 5'-phosphate
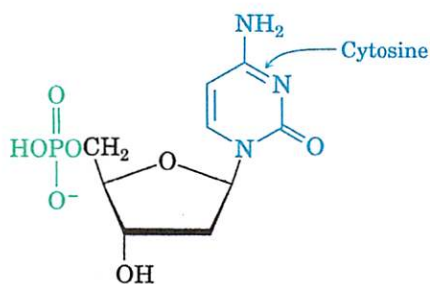
2'-Deoxycytidine 5'-phosphate
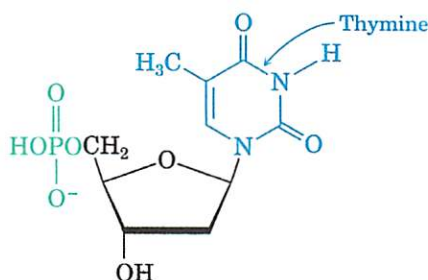
2'-Deoxythymidine 5'-phosphate

Ribonucleotides
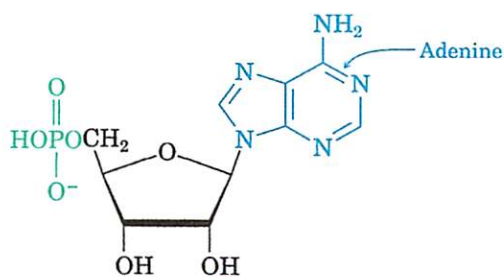
Adenosine 5'-phosphate
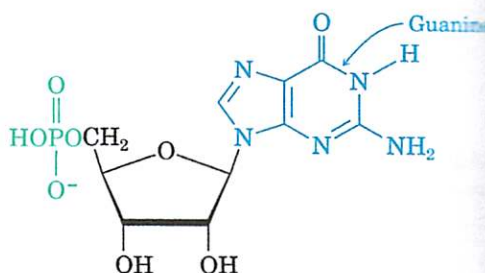
Guanosine 5'-phosphate
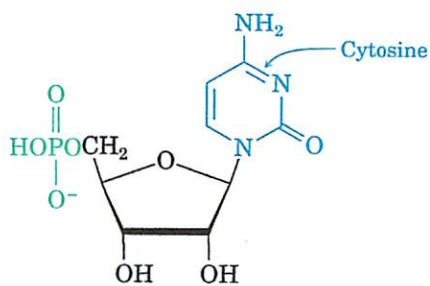
Cytidine 5'-phosphate
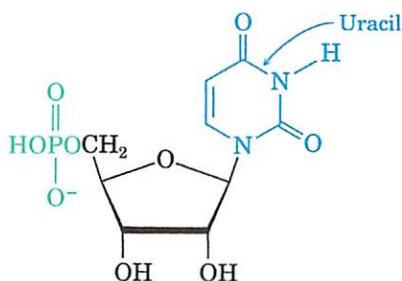
Uridine 5'-phosphate

Figure 29.5 Structures of the four deoxyribonucleotides and the four ribonucleotides.

PROBLEM..............

29.10 2'-Deoxyth
lactim form

29.10   Structur

Nucleotid
the 5'-phc
sugar com
acid polyr
end has a

5' end

3' end

Figure 29.

Just
individua
depends
further, j
attached
with diffe