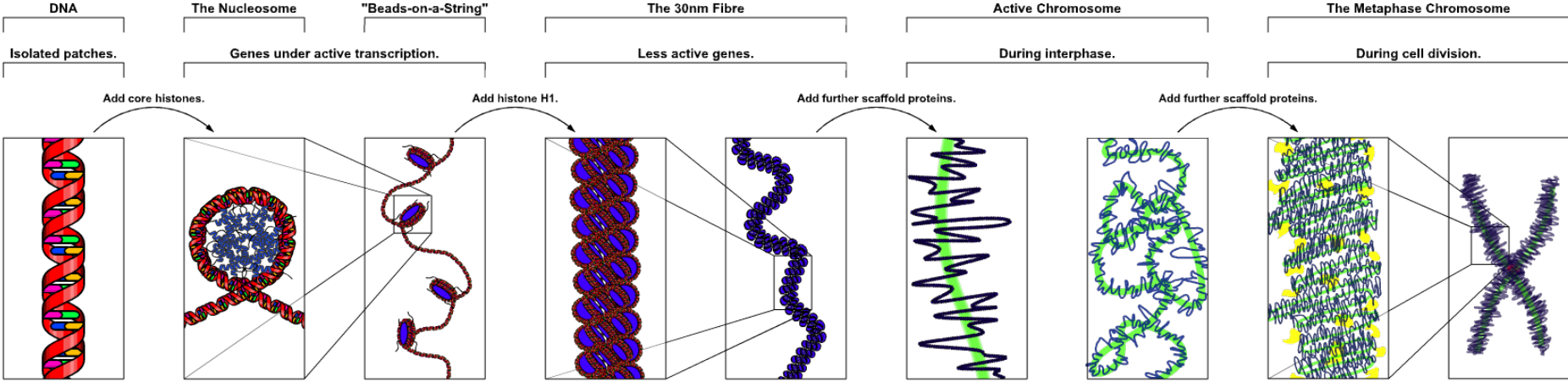


The major structures in DNA compaction



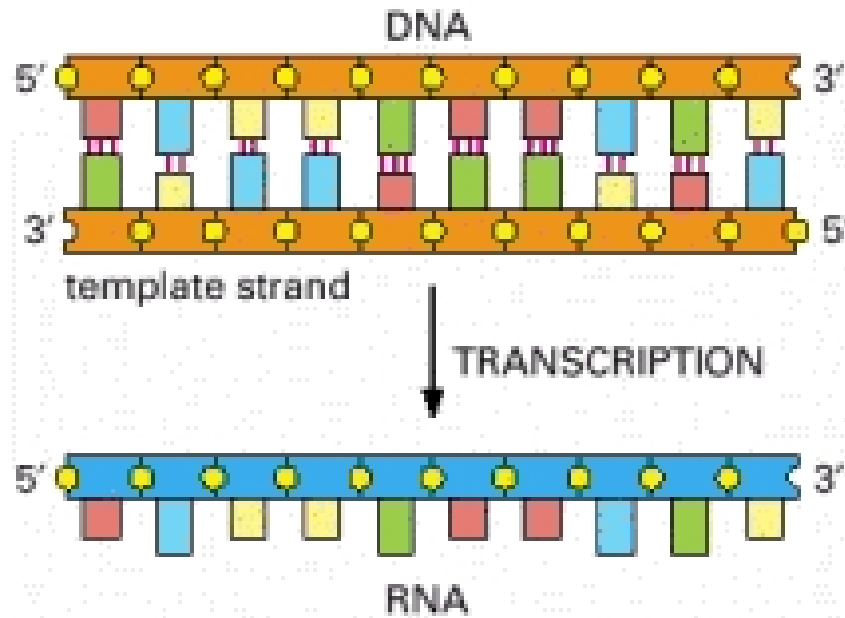


Figure 6-7

DNA transcription produces a single-stranded RNA molecule that is complementary to one strand of DNA

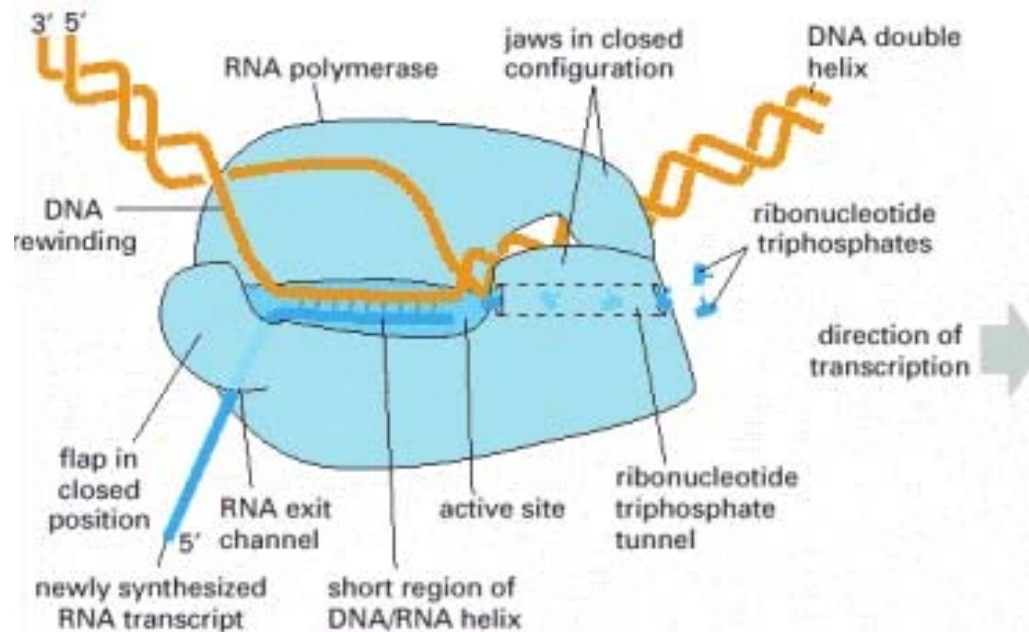
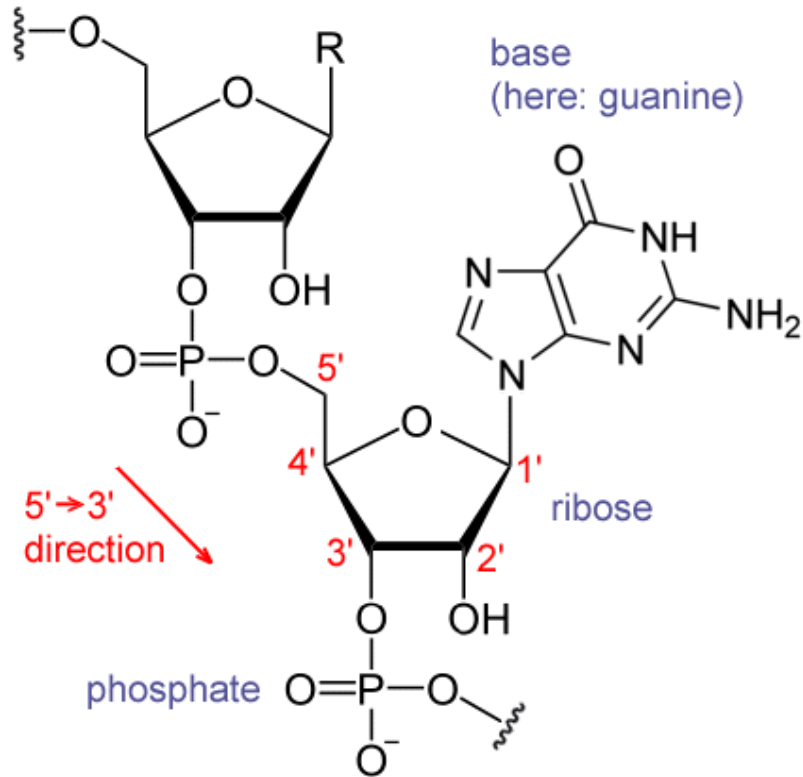


Figure 6-8

DNA is transcribed by the enzyme RNA polymerase

The [RNA polymerase](#) (*pale blue*) moves stepwise along the DNA, unwinding the DNA helix at its [active site](#). As it progresses, the polymerase adds [nucleotides](#) (here, *small “T” shapes*) one by one to the RNA chain at the polymerization site using an exposed DNA strand as a [template](#). The RNA [transcript](#) is thus a single-stranded [complementary](#) copy of one of the two DNA strands. The polymerase has a rudder (see [Figure 6-11](#)) that displaces the newly formed RNA, allowing the two strands of DNA behind the polymerase to rewind. A short region of DNA/RNA helix (approximately nine [nucleotides](#) in length) is therefore formed only transiently, and a “window” of DNA/RNA helix therefore moves along the DNA with the polymerase. The incoming [nucleotides](#) are in the form of ribonucleoside triphosphates (ATP, UTP, CTP, and GTP), and the energy stored in their phosphate-phosphate bonds provides the driving force for the polymerization [reaction](#) (see [Figure 5-4](#)). (Adapted from a figure kindly supplied by Robert Landick.)

Ribonucleic acid (RNA)



RNA can perform many functions for example:

Messenger RNA (mRNA) is translated into amino acid chains.

Transfer RNA (tRNA) carries amino acids to the ribosome.

Small interfering RNA (siRNA) regulates gene function.

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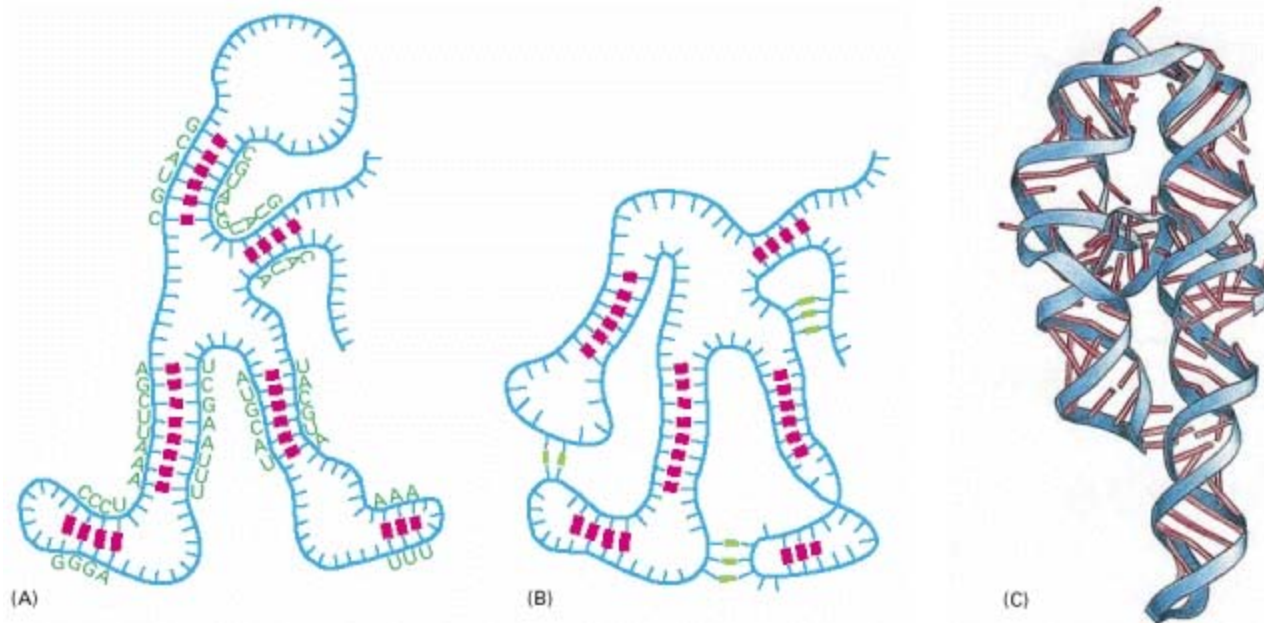


Figure 6-6

RNA can fold into specific structures

RNA is largely single-stranded, but it often contains short stretches of [nucleotides](#) that can form conventional [base-pairs](#) with [complementary](#) sequences found elsewhere on the same [molecule](#). These interactions, along with additional “nonconventional” [base-pair](#) interactions, allow an RNA [molecule](#) to fold into a three-dimensional structure that is [determined](#) by its sequence of [nucleotides](#). (A) Diagram of a folded RNA structure showing only conventional [base-pair](#) interactions; (B) structure with both conventional (*red*) and nonconventional (*green*) [base-pair](#) interactions; (C) structure of an actual RNA, a portion of a group 1 [intron](#) (see [Figure 6-36](#)). Each conventional [base-pair](#) interaction is indicated by a “rung” in the [double helix](#). [Bases](#) in other configurations are indicated by broken rungs.

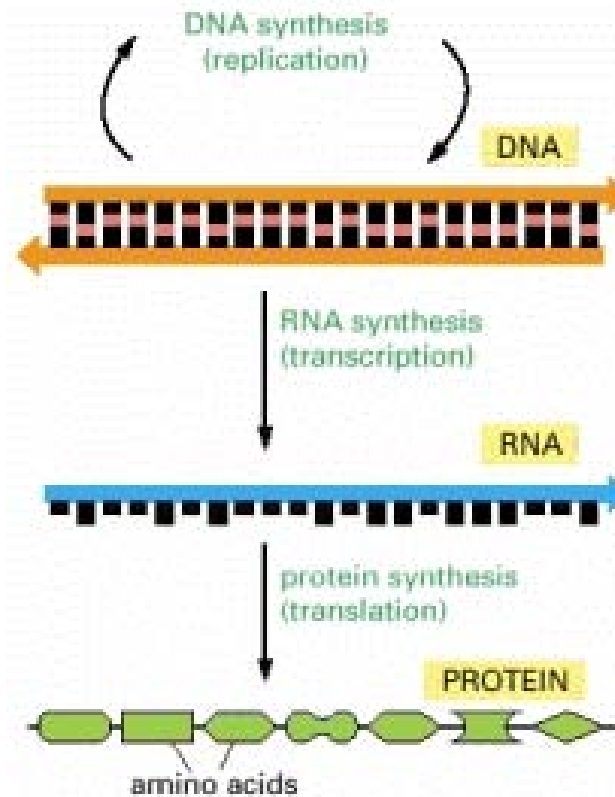
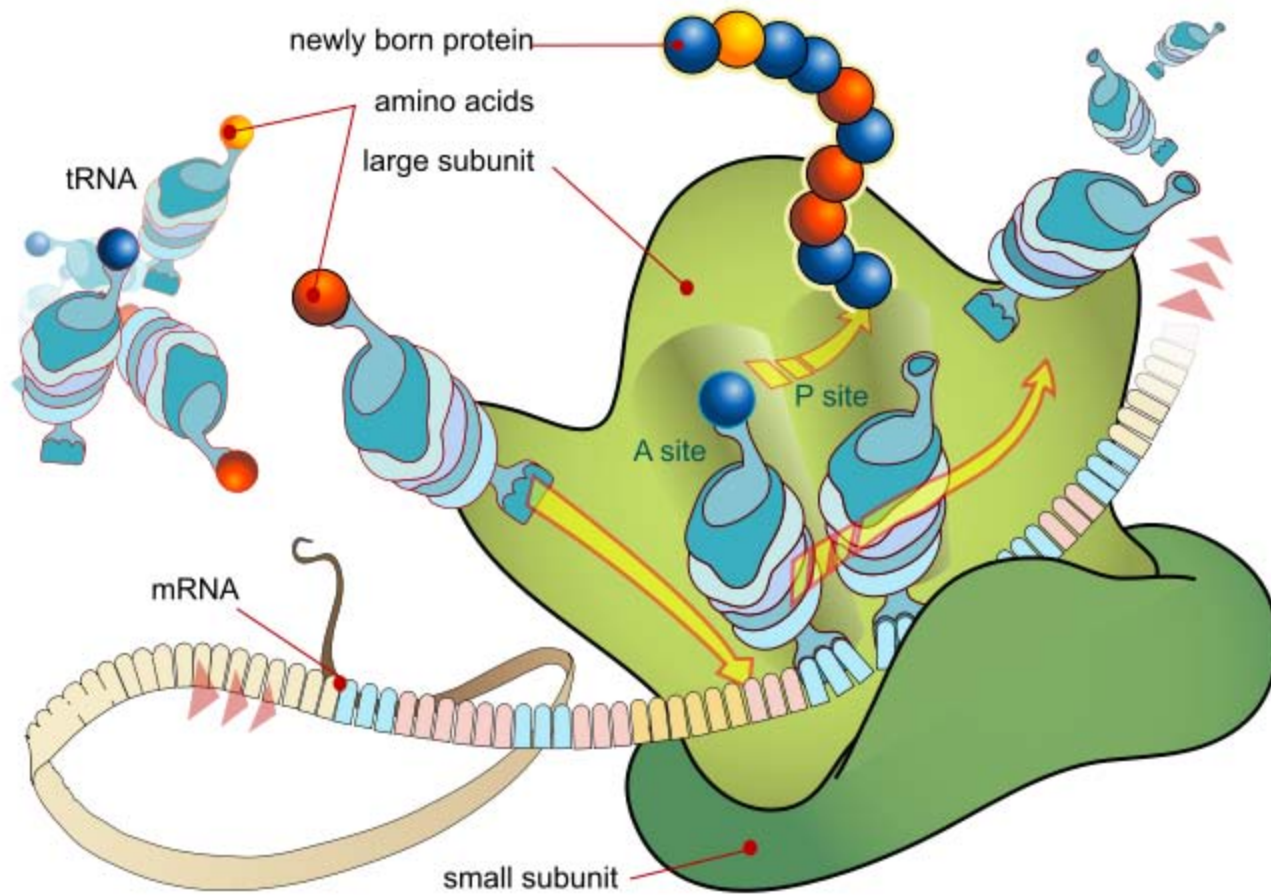


Figure 1-4

From DNA to protein

Genetic information is read out and put to use through a two-step process. First, in *transcription*, segments of the DNA sequence are used to guide the synthesis of [molecules](#) of RNA. Then, in *translation*, the RNA [molecules](#) are used to guide the synthesis of [molecules](#) of [protein](#).



The ribosome (green) translates mRNA into an amino acid sequence

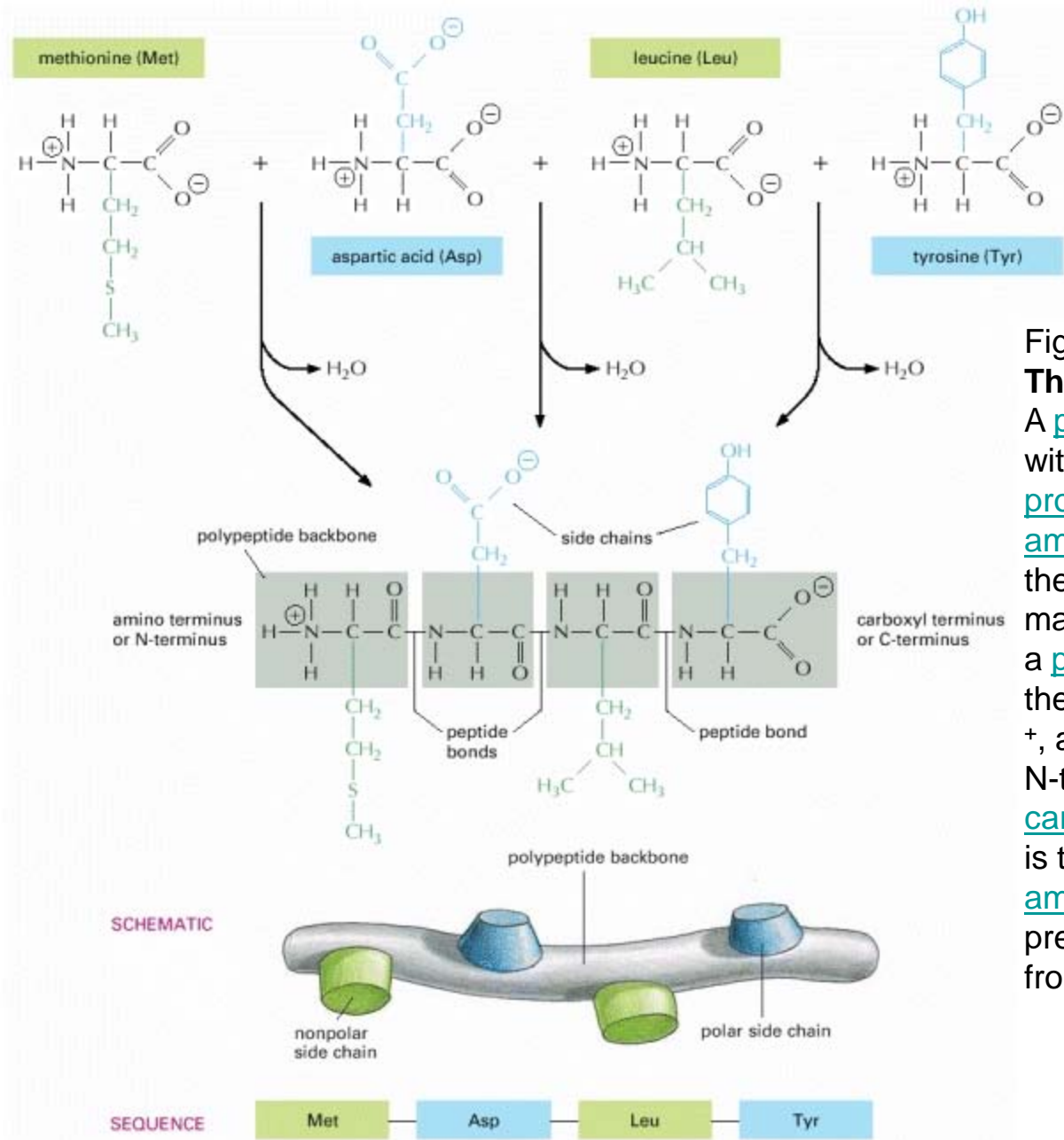


Figure 3-2

The structural components of a protein

A protein consists of a polypeptide backbone with attached side chains. Each type of protein differs in its sequence and number of amino acids; therefore, it is the sequence of the chemically different side chains that makes each protein distinct. The two ends of a polypeptide chain are chemically different: the end carrying the free amino group (NH_3^+ , also written NH_2) is the amino terminus, or N-terminus, and that carrying the free carboxyl group (COO^- , also written $COOH$) is the carboxyl terminus or C-terminus. The amino acid sequence of a protein is always presented in the N-to-C direction, reading from left to right.

AMINO ACID		SIDE CHAIN		AMINO ACID		SIDE CHAIN	
Aspartic acid	Asp	D	negative	Alanine	Ala	A	nonpolar
Glutamic acid	Glu	E	negative	Glycine	Gly	G	nonpolar
Arginine	Arg	R	positive	Valine	Val	V	nonpolar
Lysine	Lys	K	positive	Leucine	Leu	L	nonpolar
Histidine	His	H	positive	Isoleucine	Ile	I	nonpolar
Asparagine	Asn	N	uncharged polar	Proline	Pro	P	nonpolar
Glutamine	Gln	Q	uncharged polar	Phenylalanine	Phe	F	nonpolar
Serine	Ser	S	uncharged polar	Methionine	Met	M	nonpolar
Threonine	Thr	T	uncharged polar	Tryptophan	Trp	W	nonpolar
Tyrosine	Tyr	Y	uncharged polar	Cysteine	Cys	C	nonpolar

┌ POLAR AMINO ACIDS ───────────┐
┌ NONPOLAR AMINO ACIDS ───────────┐

Figure 3-3

The 20 amino acids found in proteins

Both three-letter and one-letter abbreviations are listed. As shown, there are equal numbers of polar and nonpolar side chains. For their atomic structures, see Panel 3-1 (pp. 132–133).