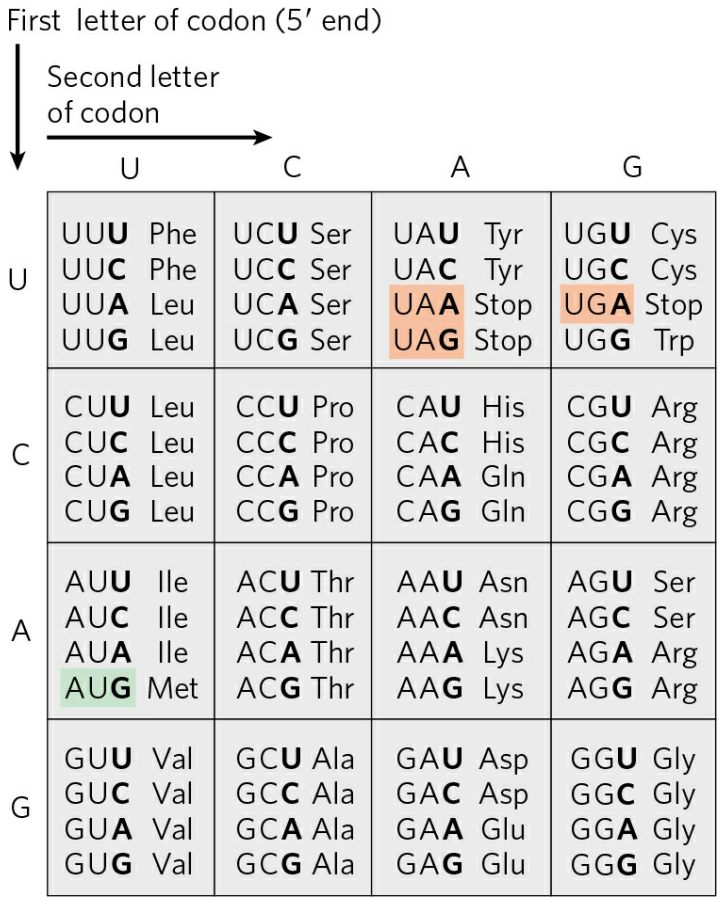


FIGURE 27-7 "Dictionary" of amino acid code words in mRNAs. The codons are written in the 5′→3′ direction. The third base of each codon (in bold type) plays a lesser role in specifying an amino acid than the first two. The three termination codons are shaded in light red, the initiation codon AUG in green. All the amino acids except methionine and tryptophan have more than one codon. In most cases, codons that specify the same amino acid differ only at the third base.

Codons are the key to the translation of genetic information, directing the synthesis of specific proteins. The reading frame is set when translation of an mRNA molecule begins, and it is maintained as the synthetic machinery reads sequentially from one triplet to the next. If the initial reading frame is off by one or two bases, or if translation somehow skips a nucleotide in the mRNA, all the subsequent codons will be out of register; the result is usually a "missense" protein with a garbled amino acid sequence.

Several codons serve special functions (Fig. 27-7). The **initiation codon** AUG is the most common signal for the beginning of a polypeptide in all cells, in addition to coding for Met residues in internal positions of polypeptides. The **termination codons** (UAA, UAG, and UGA), also called

stop codons or nonsense codons, normally signal the end of polypeptide synthesis and do not code for any known amino acids. Some deviations from these rules are discussed in Box 27-1.

As described in Section 27.2, initiation of protein synthesis in the cell is an elaborate process that relies on initiation codons and other signals in the mRNA. In retrospect, the experiments of Nirenberg, Khorana, and others to identify codon function should not have worked in the absence of initiation codons. Serendipitously, experimental conditions caused the normal initiation requirements for protein synthesis to be relaxed. Diligence combined with chance to produce a breakthrough—a common occurrence in the history of biochemistry.

In a random sequence of nucleotides, 1 in every 20 codons in each reading frame is, on average, a termination codon. In general, a reading frame without a termination codon among 50 or more consecutive codons is referred to as an **open reading frame (ORF)**. Long open reading frames usually correspond to genes that encode proteins. In the analysis of sequence databases, sophisticated programs are used to search for open reading frames in order to find genes among the often huge background of nongenic DNA. An uninterrupted gene coding for a typical protein with a molecular weight of 60,000 would require an open reading frame with 500 or more codons.

A striking feature of the genetic code is that an amino acid may be specified by more than one codon, so the code is described as **degenerate**. This does *not* suggest that the code is flawed: although an amino acid may have two or more codons, each codon specifies only one amino acid. The degeneracy of the code is not uniform. Whereas methionine and tryptophan have single codons, for example, three amino acids (Arg, Leu, Ser) have six codons, five amino acids have four, isoleucine has three, and nine amino acids have two (Table 27-3).

BOX 27-1 Exceptions That Prove the Rule: Natural Variations in the Genetic Code

In biochemistry, as in other disciplines, exceptions to general rules can be problematic for instructors and frustrating for students. At the same time,

though, they teach us that life is complex and inspire us to search for more surprises. Understanding the exceptions can even reinforce the original rule in unpredictable ways.

One would expect little room for variation in the genetic code. Even a single amino acid substitution can have profoundly deleterious effects on the structure of a protein. Nevertheless, variations in the code do occur in some organisms, and they are both interesting and instructive. The types of variation and their rarity provide powerful evidence for a common evolutionary origin of all living things.

To alter the code, changes must occur in the gene(s) encoding one or more tRNAs, with the obvious target for alteration being the anticodon. Such a change would lead to the systematic insertion of an amino acid at a codon that, according to the standard code (see Fig. 27-7), does not specify that amino acid. The genetic code, in effect, is defined by two elements: (1) the anticodons on tRNAs, which determine where an amino acid is placed in a growing polypeptide, and (2) the specificity of the enzymes—the aminoacyl-tRNA synthetases—that charge the tRNAs, which determines the identity of the amino acid attached to a given tRNA.

Most sudden changes in the code would have catastrophic effects on cellular proteins, so code alterations are more likely to persist where relatively few proteins would be affected—such as in small genomes encoding only a few proteins. The biological consequences of a code change could also be limited by restricting changes to the three termination codons, which do not generally occur *within* genes (see Box 27-3 for exceptions to *this* rule). This pattern is, in fact, observed.

Of the very few variations in the genetic code that we know of, most occur in mitochondrial DNA (mtDNA), which encodes only 10 to 20 proteins. Mitochondria have their own tRNAs, so their code variations do not affect the much larger cellular genome. The most common changes in mitochondria involve termination codons. These changes affect termination in the products of only a subset of genes, and sometimes the effects are minor, because the genes have multiple (redundant) termination codons.

Vertebrate mtDNAs have genes that encode 13 proteins, 2 rRNAs, and 22 tRNAs (see Fig. 19-40). Given the small number of codon reassignments, along with an unusual set of wobble rules (p. 1084), the 22 tRNAs are sufficient to decode the protein-coding genes, as opposed to the

32 tRNAs required for the standard code. In mitochondria, these changes can be viewed as a kind of genomic streamlining, as a smaller genome confers a replication advantage on the organelle. Four codon families (in which the amino acid is determined entirely by the first two nucleotides) are decoded by a single tRNA with a U residue in the first (or wobble) position in the anticodon. Either the U pairs somehow with any of the four possible bases in the third position of the codon or a "two out of three" mechanism is used—that is, no base pairing is needed at the third position. Other tRNAs recognize codons with either A or G in the third position, and yet others recognize U or C, so that virtually all the tRNAs recognize either two or four codons.

In the standard code, only two amino acids are specified by single codons: methionine and tryptophan (see Table 27-3). If all mitochondrial tRNAs recognize two codons, we would expect additional Met and Trp codons in mitochondria. And we find that the single most common code variation is UGA, usually a termination codon, specifying tryptophan. The $tRNA^{Trp}$ recognizes and inserts a Trp residue at either UGA or the usual Trp codon, UGG. The second most common variation is conversion of AUA from an Ile codon to a Met codon; the usual Met codon is AUG, and a single tRNA recognizes both codons. The known coding variations in mitochondria are summarized in Table 1.

Turning to the much rarer changes in the codes for cellular (as distinct from mitochondrial) genomes, we find that the only known variation in a bacterium is again the use of UGA to encode Trp residues, occurring in the simplest free-living cell, *Mycoplasma capricolum*. Among eukaryotes, rare extramitochondrial coding changes occur in a few species of ciliated protists, in which both termination codons UAA and UAG can specify glutamine. There are also rare but interesting cases in which stop codons have been adapted to encode amino acids that are not among the standard 20, as detailed in Box 27-2.

Changes in the code need not be absolute; a codon might not always encode the same amino acid. For example, in many bacteria—including *E. coli*—GUG (Val) is sometimes used as an initiation codon that specifies Met. This occurs only for those genes in which the GUG is properly located relative to particular mRNA sequences that affect the initiation of translation (as discussed in Section 27.2).

TABLE 1 Known Variant Codon Assignments in Mitochondria

	Codons[a]				
	UGA	**AUA**	**AGA AGG**	**CUN**	**CGG**
Normal (cellular) code assignment	Stop	Ile	Arg	Leu	Arg
Animals					
Vertebrates	Trp	Met	Stop	+	+
Drosophila	Trp	Met	Ser	+	+
Yeasts					
Saccharomyces cerevisiae	Trp	Met	+	Thr	+
Torulopsis glabrata	Trp	Met	+	Thr	?
Schizosaccharomyces pombe	Trp	+	+	+	+
Filamentous fungi	Trp	+	+	+	+
Trypanosomes	Trp	+	+	+	+
Higher plants	+	+	+	+	Trp
Chlamydomonas reinhardtii	?	+	+	+	?

[a]N indicates any nucleotide; +, codon has the same meaning as in the cellular code; ?, codon not observed in this mitochondrial genome.

The most surprising alteration in the genetic code occurs in some fungal species of the genus *Candida*, as originally discovered for *Candida albicans*. *C. albicans* is an organism of high genomic complexity, yet its genetic code has undergone a dramatic change: the CUG codon, which usually encodes Leu residues, encodes Ser instead. The natural selection pressure for this change is completely unknown. Furthermore, Ser and Leu

are quite different in chemical structure. However, even this change can be understood based on the properties of a universal code. When several codons encode the same amino acid and use multiple tRNAs, not all of the codons are used with equal frequency. In a phenomenon called **codon bias**, some codons for a particular amino acid are used more frequently (sometimes much more frequently) than others. The tRNAs for the frequently used codons are often present at much higher concentrations than the tRNAs required for the rarely used codons. Code degeneracy leads to the presence of six codons for Leu. In bacteria, CUG often encodes Leu. However, in fungi of genera that are very closely related to *Candida* but do not have the coding change, CUG only rarely encodes Leu and is often entirely absent in highly expressed proteins. A change in the coding sense of CUG would thus have a much smaller effect on fungal cell metabolism than might be expected if all codons were used equally. The coding change may have occurred by a gradual loss of CUG codons in genes and of the tRNA that recognizes CUG as a Leu codon, followed by a capture event—a mutation in the anticodon of a $tRNA^{Ser}$ that allowed it to recognize CUG. Alternatively, there may have been an intermediate stage in which CUG was recognized as encoding both Leu and Ser, perhaps with contextual signals in the mRNAs that helped one tRNA or another recognize specific CUG codons (see Box 27-2). Phylogenetic analysis indicates that the reassignment of CUG as a Ser codon occurred in *Candida* ancestors about 150 to 170 million years ago.

These variations tell us that the code is not quite as universal as once believed, but that its flexibility is severely constrained. The variations are obviously derivatives of the cellular code, and no example of a completely different code has been found. The limited scope of code variants strengthens the principle that all life on this planet evolved on the basis of a single (slightly flexible) genetic code.

The genetic code is nearly universal. With the intriguing exception of a few minor variations in mitochondria, some bacteria, and some single-celled eukaryotes (Box 27-1), amino acid codons are identical in all species examined so far. Human beings, *E. coli*, tobacco plants, amphibians, and viruses share the same genetic code. This suggests that all life-forms have a common evolutionary ancestor, whose genetic code has been preserved throughout biological evolution. Even the variations reinforce this theme.

TABLE 27-3 Degeneracy of the Genetic Code

Amino acid	Number of codons
Met	1
Trp	1
Asn	2
Asp	2
Cys	2
Gln	2
Glu	2
His	2
Lys	2
Phe	2
Tyr	2
Ile	3
Ala	4
Gly	4
Pro	4
Thr	4
Val	4
Arg	6
Leu	6
Ser	6

Wobble Allows Some tRNAs to Recognize More than One Codon

When several different codons specify one amino acid, the difference between them usually lies at the third base position (at the 3′ end). For example, alanine is encoded by the triplets GCU, GCC, GCA, and GCG. The codons for most amino acids can be symbolized by $\mathbf{XY}\begin{matrix}\mathbf{U}\\\mathbf{C}\end{matrix}$ or $\mathbf{XY}\begin{matrix}\mathbf{A}\\\mathbf{G}\end{matrix}$. The first two letters of each codon are the primary determinants of specificity, a feature that has some interesting consequences.

Transfer RNAs base-pair with mRNA codons at a three-base sequence on the tRNA called the **anticodon**. The first base of the codon in mRNA (read in the 5′→3′ direction) pairs with the third base of the anticodon **(Fig. 27-8a)**. If the anticodon triplet of a tRNA recognized only one codon triplet through Watson-Crick base pairing at all three positions, cells would have a different tRNA for each amino acid codon. This is not the case, however, because the anticodons in some tRNAs include the nucleotide inosinate (designated I), which contains the uncommon base hypoxanthine (see Fig. 8-5b). Inosinate can form hydrogen bonds with three different nucleotides (U, C, and A; Fig. 27-8b), although these pairings are much weaker than the hydrogen bonds of Watson-Crick base pairs G≡C and A═U. In yeast, one $tRNA^{Arg}$ has the anticodon (5′)ICG, which recognizes three arginine codons: (5′)CGA, (5′)CGU, and (5′)CGC. The first two bases are identical (CG) and form strong Watson-Crick base pairs with the corresponding bases of the anticodon, but the third base (A, U, or C) forms rather weak hydrogen bonds with the I residue at the first position of the anticodon.

Examination of these and other codon-anticodon pairings led Crick to conclude that the third base of most codons pairs rather loosely with the corresponding base of its anticodon; to use his picturesque word, the third base of such codons (and the first base of their corresponding anticodons) “wobbles.” Crick proposed a set of four relationships called the **wobble hypothesis**:

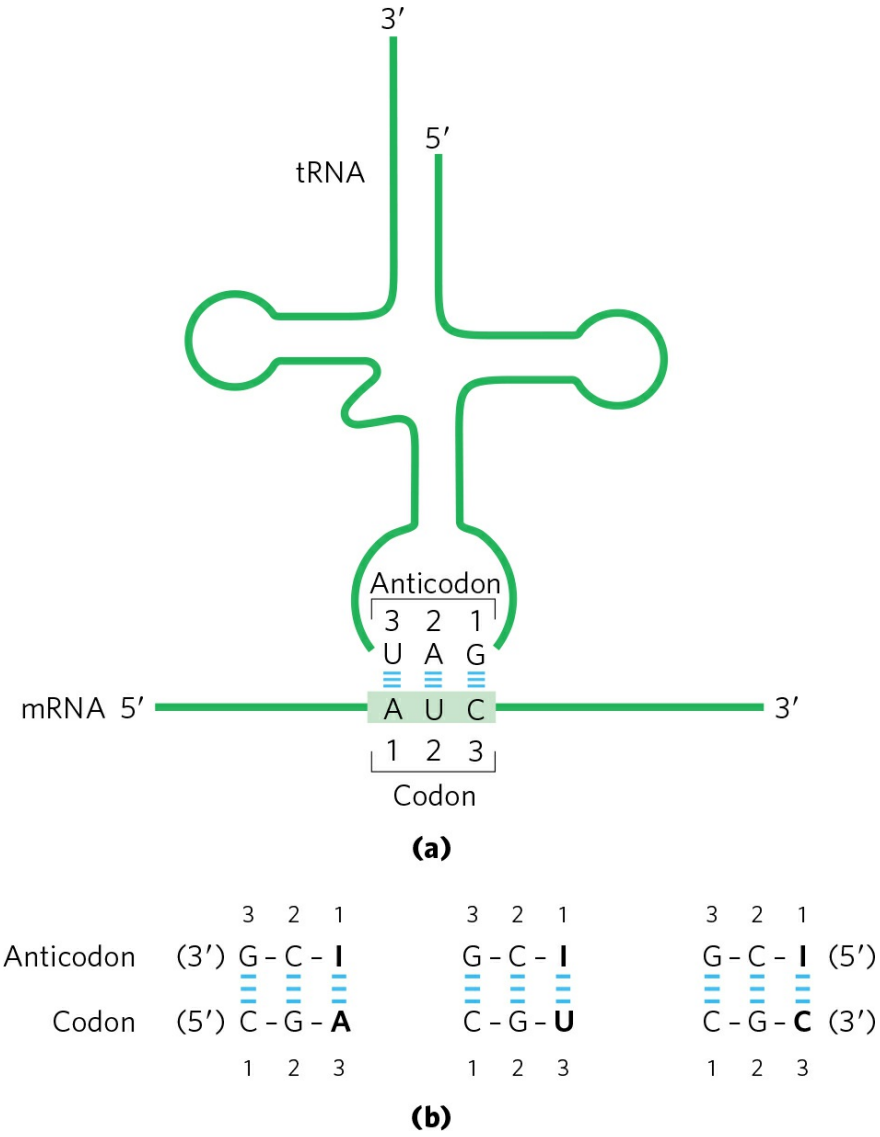


FIGURE 27-8 Pairing relationship of codon and anticodon. (a) Alignment of the two RNAs is antiparallel. The tRNA is shown in the traditional cloverleaf configuration. **(b)** Three different codon pairing relationships are possible when the tRNA anticodon contains inosinate.

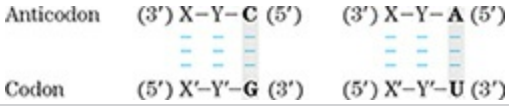
1. The first two bases of an mRNA codon always form strong Watson-Crick base pairs with the corresponding bases of the tRNA anticodon and confer most of the coding specificity.
2. The first base of the anticodon (reading in the 5′→3′ direction; this pairs with the third base of the codon) determines the number of codons recognized by the tRNA. When the first base of the anticodon is C or A, base pairing is specific and only one codon is recognized by that tRNA. When the first base is U or G, binding is less specific and two different

codons may be read. When inosine (I) is the first (wobble) nucleotide of an anticodon, three different codons can be recognized—the maximum number for any tRNA. These relationships are summarized in Table 27-4.

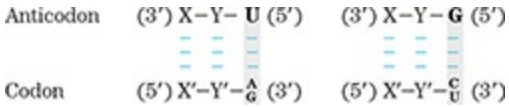
3. When an amino acid is specified by several different codons, the codons that differ in either of the first two bases require different tRNAs.
4. A minimum of 32 tRNAs are required to translate all 61 codons (31 to encode the amino acids, 1 for initiation).

TABLE 27-4 How the Wobble Base of the Anticodon Determines the Number of Codons a tRNA Can Recognize

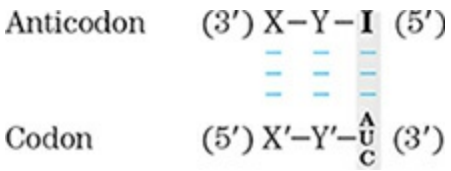
1. One codon recognized:



2. Two codons recognized:



3. Three codons recognized:



Note: X and Y denote bases complementary to and capable of strong Watson-Crick base pairing with X′ and Y′, respectively. Wobble bases–in the 3′ position of codons and 5′ position of anticodons—are shaded in white.

The wobble (or third) base of the codon contributes to specificity, but because it pairs only loosely with its corresponding base in the anticodon, it permits rapid dissociation of the tRNA from its codon during protein synthesis. If all three bases of a codon engaged in strong Watson-Crick pairing with the three bases of the anticodon, tRNAs would dissociate too slowly and this would limit the rate of protein synthesis. Codon-anticodon interactions balance the requirements for accuracy and speed.

The Genetic Code Is Mutation-Resistant

The genetic code plays an interesting role in safeguarding the genomic integrity of every living organism. Evolution did not produce a code in which codon assignments appeared at random. Instead, the code is strikingly resistant to the deleterious effects of the most common kinds of mutations —**missense mutations**, in which a single new base pair replaces another. In the third, or wobble, position of the codon, single base substitutions produce a change in the encoded amino acid only about 25% of the time. Most such changes are thus **silent mutations**, in which the nucleotide is different but the encoded amino acid remains the same.

Due to the types of spontaneous DNA damage that affect genomes (see Chapter 8), the most frequent missense mutation is a **transition mutation**, in which a purine is replaced by a purine, or a pyrimidine by a pyrimidine (for example, G≡C changed to A=T). All three codon positions have evolved so that there is some resistance to transition mutations. A mutation in the first position of the codon will usually produce an amino acid coding change, but the change often results in an amino acid with similar chemical properties. This is especially true for the hydrophobic amino acids that dominate the first column of the code shown in Figure 27-7. Consider the Val codon GUU. A change to AUU would substitute Ile for Val. A change to CUU would replace Val with Leu. The resulting changes in the structure and/or function of the protein encoded by that gene would often (but not always) be small.

Computational studies have shown that alternative genetic codes, delineated at random, are almost always less resistant to mutation than the existing code. The results indicate that the code underwent considerable streamlining before the appearance of LUCA, the ancestral cell.

The genetic code tells us how protein sequence information is stored in nucleic acids and provides some clues about how that information is

27.2 Protein Synthesis

As we have seen for DNA and RNA (Chapters 25 and 26), the synthesis of polymeric biomolecules can be considered in terms of initiation, elongation, and termination stages. These fundamental processes are typically bracketed by two additional stages: activation of precursors before synthesis and postsynthetic processing of the completed polymer. Protein synthesis follows the same pattern. The activation of amino acids before their incorporation into polypeptides and the posttranslational processing of the completed polypeptide play particularly important roles in ensuring both the fidelity of synthesis and the proper function of the protein product. The process is outlined in **Figure 27-13**. The cellular components involved in the five stages of protein synthesis in *E. coli* and other bacteria are listed in Table 27-5; the requirements in eukaryotic cells are similar, although the components are usually more numerous. An initial overview of the stages of protein synthesis provides a useful outline for the discussion that follows.

Protein Biosynthesis Takes Place in Five Stages

Stage 1: Activation of Amino Acids For the synthesis of a polypeptide with a defined sequence, two fundamental chemical requirements must be met: (1) the carboxyl group of each amino acid must be activated to facilitate formation of a peptide bond, and (2) a link must be established between each new amino acid and the information in the mRNA that encodes it. Both these requirements are met by attaching the amino acid to a tRNA in the first stage of protein synthesis. Attaching the right amino acid to the right tRNA is critical. This reaction takes place in the cytosol, not on the ribosome. Each of the 20 amino acids is covalently attached to a specific tRNA at the expense of ATP energy, through the action of Mg^{2+}-dependent activating enzymes known as aminoacyl-tRNA synthetases. When attached to their amino acid (aminoacylated), the tRNAs are said to be "charged."

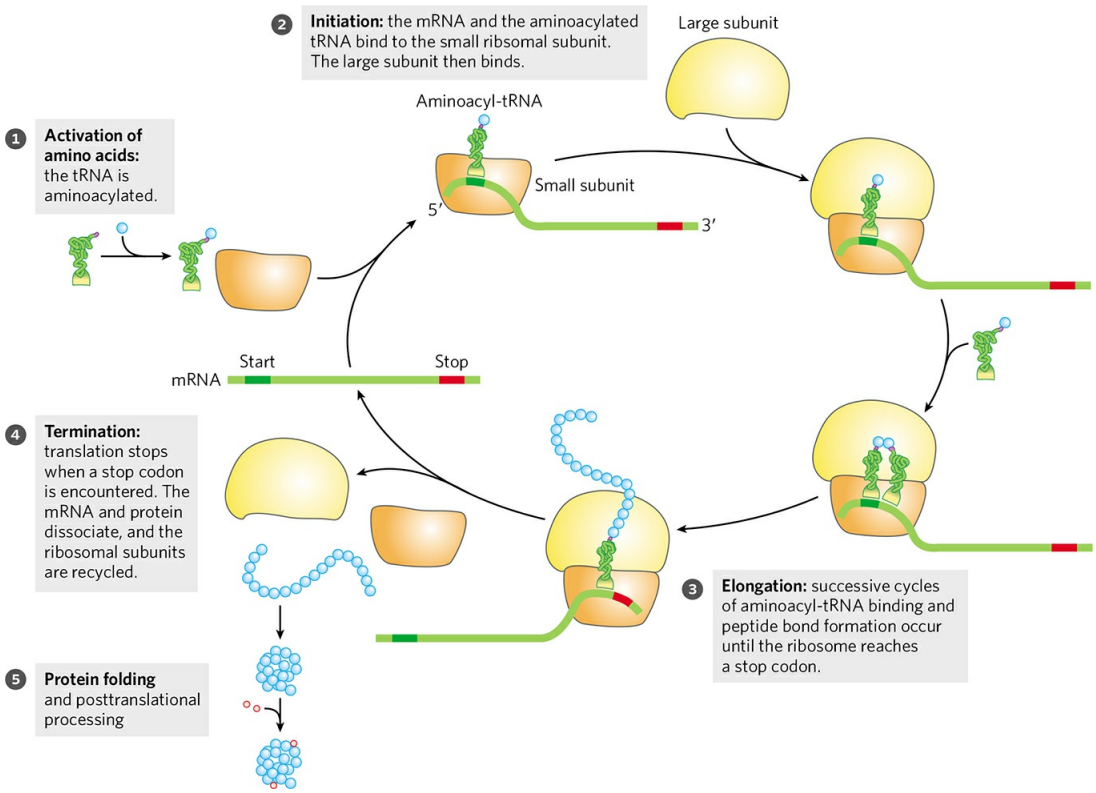


FIGURE 27-13 An overview of the five stages of protein synthesis. 1 The tRNAs are aminoacylated. 2 Translation is initiated when an mRNA and an aminoacylated tRNA are bound to the ribosome. 3 In elongation, the ribosome moves along the mRNA, matching tRNAs to each codon and catalyzing peptide bond formation. 4 Translation is terminated at a stop codon, and the ribosomal subunits are released and recycled for another round of protein synthesis. 5 Following synthesis, the protein must fold into its active conformation and ribosome components are recycled. Most proteins are processed after synthesis. Some amino acids may be removed; others can undergo any of hundreds of known chemical modifications.

TABLE 27-5 Components Required for the Five Major Stages of Protein Synthesis in *E. Coli*

Stage	Essential components
1. Activation of amino acids	20 amino acids 20 aminoacyl-tRNA syntheses 32 or more tRNAs ATP

	Mg^{2+}
2. Initiation	mRNA *N*-Formylmethionyl-$tRNA^{fMet}$ Initiation codon in mRNA (AUG) 30S ribosomal subunit 50S ribosomal subunit Initiation factors (IF1, IF2, IF3) GTP Mg^{2+}
3. Elongation	Functional 70S ribosomes (initiation complex) Aminoacyl-tRNAs specified by codons Elongation factors (EF-Tu, EF-Ts, EF-G) GTP Mg^{2+}
4. Termination and ribosome recycling	Termination codon in mRNA Release factors (RF1, RF2, RF3, RRF) EF-G IF3
5. Folding and posttranslational processing	Chaperones and folding enzymes (PPI, PDI); specific enzymes, cofactors, and other components for removal of initiating residues and signal sequences, additional proteolytic processing, modification of terminal residues, and attachment of acetyl, phosporyl, methyl, carboxyl, carbohydrate, or prosthetic groups

Stage 2: Initiation The mRNA bearing the code for the polypeptide to be synthesized binds to the smaller of two ribosomal subunits and to the initiating aminoacyl-tRNA. The large ribosomal subunit then binds to form an initiation complex. The initiating aminoacyl-tRNA base-pairs with the mRNA codon AUG that signals the beginning of the polypeptide. This process, which requires GTP, is promoted by cytosolic proteins called initiation factors.

Stage 3: Elongation The nascent polypeptide is lengthened by covalent attachment of successive amino acid units, each carried to the ribosome and correctly positioned by its tRNA, which base-pairs to its corresponding codon in the mRNA. Elongation requires cytosolic proteins known as elongation factors. The binding of each incoming aminoacyl-tRNA and the movement of the ribosome along the mRNA are facilitated by the hydrolysis of GTP as each residue is added to the growing polypeptide.

Stage 4: Termination and Ribosome Recycling Completion of the polypeptide chain is signaled by a termination codon in the mRNA. The new polypeptide is released from the ribosome, aided by proteins called release factors, and the ribosome is recycled for another round of synthesis.

Stage 5: Folding and Posttranslational Processing To achieve its biologically active form, the new polypeptide must fold into its proper three-dimensional conformation. Before or after folding, the new polypeptide may undergo enzymatic processing, including removal of one or more amino acids (usually from the amino terminus); addition of acetyl, phosphoryl, methyl, carboxyl, or other groups to certain amino acid residues; proteolytic cleavage; and/or attachment of oligosaccharides or prosthetic groups.

Before looking at these five stages in detail, we must examine two key components of protein biosynthesis: the ribosome and tRNAs.

TABLE 27-6 RNA and Protein Components of the *E. Coli* Ribosome

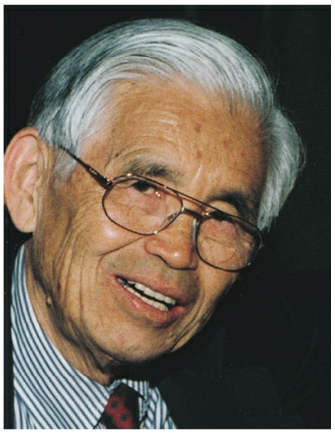
Subunit	Number of different proteins	Total number of proteins	Protein designations	Number and type of rRNAs
30S	21	21	S1–S21	1 (16S rRNA)
50S	33	36	L1–L36[a]	2 (5S and 23S rRNAs)

[a]The L1 to L36 protein designations do not correspond to 36 different proteins. The protein originally designated L7 is a modified form of L12, and L8 is a complex of three other proteins. Also, L26 proved to be the same protein as S20 (and not part of the 50S subunit). This gives 33 different proteins in the large subunit. There are four copies of the L7/L12 protein, with the three extra copies bringing the total protein count to 36.

The Ribosome Is a Complex Supramolecular Machine

Each *E. coli* cell contains 15,000 or more ribosomes, which comprise nearly a quarter of the dry weight of the cell. Bacterial ribosomes contain about 65% rRNA and 35% protein; they have a diameter of about 18 nm and are composed of two unequal subunits with sedimentation coefficients of 30S and 50S and a combined sedimentation coefficient of 70S. Both subunits contain dozens of ribosomal proteins (r-proteins) and at least one large rRNA (Table 27-6).

Following Zamecnik's discovery that ribosomes are the complexes responsible for protein synthesis, and following elucidation of the genetic code, the study of ribosomes accelerated. In the late 1960s Masayasu Nomura and colleagues demonstrated that both ribosomal subunits can be broken down into their RNA and protein components, then reconstituted in vitro. Under appropriate experimental conditions, the RNA and protein spontaneously reassemble to form 30S or 50S subunits nearly identical in structure and activity to native subunits. This breakthrough fueled decades of research into the function and structure of ribosomal RNAs and proteins. At the same time, increasingly sophisticated structural methods revealed more and more details about ribosome structure.



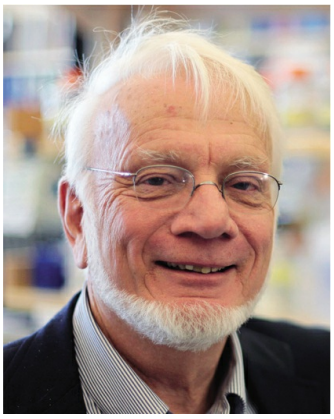
Masayasu Nomura, 1927–2011
[Source: Courtesy of Archives, University of Wisconsin–Madison.]

The dawn of a new millennium illuminated the first high-resolution structures of bacterial ribosomal subunits by Venki Ramakrishnan, Thomas Steitz, Ada Yonath, Harry Noller, and others. This work yielded a wealth of surprises **(Fig. 27-14a)**. First, a traditional focus on the protein components of ribosomes was shifted. The ribosomal subunits are huge RNA molecules. In the 50S subunit, the 5S and 23S rRNAs form the structural core. The proteins are secondary elements in the complex, decorating the surface. Second, and most important, there is no protein within 18 Å of the active site for peptide bond formation. The high-resolution structure thus confirms what Noller had predicted much earlier: the ribosome is a ribozyme. In addition to the insight that the detailed structures of the ribosome and its subunits provide into the mechanism of protein synthesis (as elaborated below), these findings have stimulated a new look at the evolution of life (Section 26.3). The ribosomes of eukaryotic cells have also yielded to structural analysis (Fig. 27-14b).

The bacterial ribosome is complex, with a combined molecular weight of ~2.7 million. The two irregularly shaped ribosomal subunits fit together to form a cleft through which the mRNA passes as the ribosome moves along it during translation (Fig. 27-14a). The 57 proteins in bacterial ribosomes vary enormously in size and structure. Molecular weights range from about 6,000 to 75,000. Most of the proteins have globular domains arranged on the ribosome surface. Some also have snakelike extensions that protrude into the rRNA core of the ribosome, stabilizing its structure. The functions of some of these proteins have not yet been elucidated in detail, although a structural role seems evident for many of them.

The sequences of the rRNAs of many organisms are now known. Each of the three single-stranded rRNAs of *E. coli* has a specific three-dimensional conformation with extensive intrachain base pairing. The folding patterns of the rRNAs are highly conserved in all organisms, particularly the regions implicated in key functions **(Fig. 27-15)**. The predicted secondary structure of the rRNAs has largely been confirmed by structural analysis, but fails to convey the extensive network of tertiary interactions apparent in the complete structure.

Venkatraman Ramakrishnan
[Source: © Alastair Grant/AP Photo.]



Thomas A. Steitz
[Source: © Lucas Jackson/ Reuters/Corbis.]

Ada E. Yonath
[Source: © Yin Bogu/Xinhua Press/Corbis.]

The ribosomes of eukaryotic cells (other than mitochondrial and chloroplast ribosomes) are larger and more complex than bacterial ribosomes

(Fig. 27-16; compare Fig. 27-14b), with a diameter of about 23 nm and a sedimentation coefficient of about 80S. They also have two subunits, which vary in size among species but on average are 60S and 40S. Altogether, eukaryotic ribosomes contain more than 80 different proteins. The ribosomes of mitochondria and chloroplasts are somewhat smaller and simpler than bacterial ribosomes. Nevertheless, ribosomal structure and function are strikingly similar in all organisms and organelles.

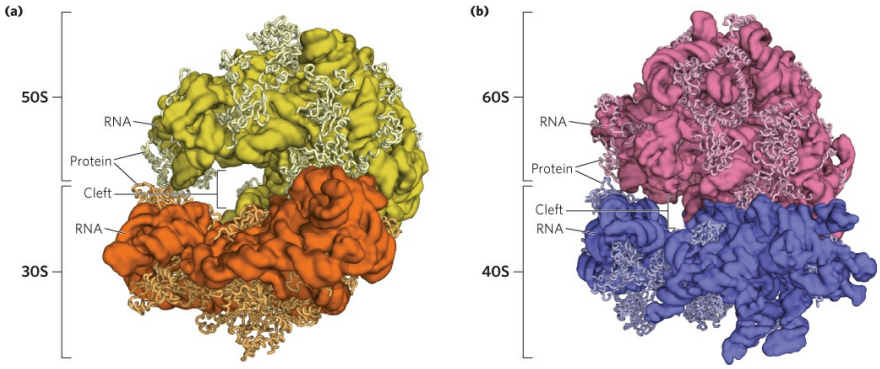


FIGURE 27-14 The structure of ribosomes. Our understanding of ribosome structure has been greatly enhanced by multiple high-resolution images of the ribosomes from bacteria and yeast. **(a)** The bacterial ribosome. The 50S and 30S subunits come together to form the 70S ribosome. The cleft between them is where protein synthesis occurs. **(b)** The yeast ribosome has a similar structure with somewhat increased complexity. [Sources: (a) Derived from PDB ID 4V4I, A. Korostelev et al., *Cell* 126:1065, 2006. (b) Derived from PDB ID 4V7R, A. Ben-Shem et al., *Science* 330:1203, 2010.]

In both bacteria and eukaryotes, ribosomes are assembled through a hierarchical incorporation of r-proteins as the rRNAs are synthesized. Much of the processing of pre-rRNAs (see Fig. 26-24) occurs within large ribonucleoprotein complexes. The composition of these complexes changes as new r-proteins are added, the rRNAs acquire their final form, and some proteins required for rRNA processing dissociate.

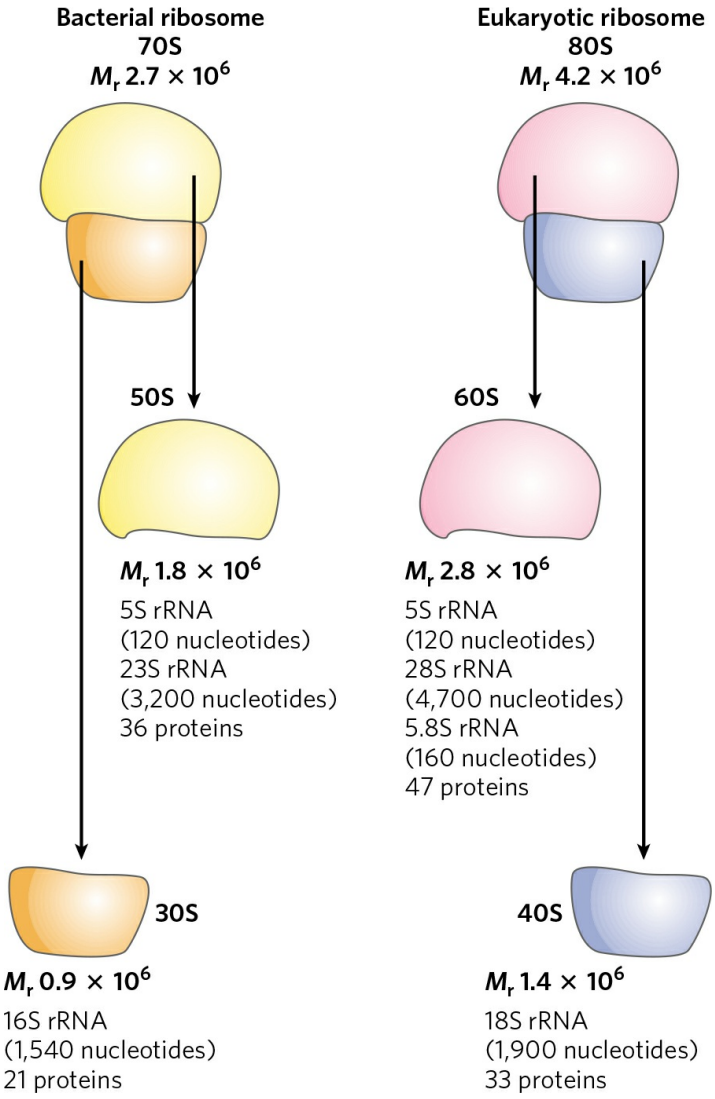


FIGURE 27-16 Summary of the composition and mass of ribosomes in bacteria and eukaryotes. Ribosomal subunits are identified by their S (Svedberg unit) values, sedimentation coefficients that refer to their rate of sedimentation in a centrifuge. The S values are not additive when subunits are combined, because S values are approximately proportional to the two-thirds power of molecular weight and are also slightly affected by shape.