# The genetic code

- A doublet code based on pairs of the four possible bases, A, C, G, and U, has $4^2$=16 , an insufficient number to encode the 20 amino acids.
- A triplet code of four bases has $4^3$ =64 possible code words, more than enough for the task.
- A group of three bases codes for one amino acid.
- The code is not overlapping
- The base sequence is read from a fixed starting point without punctuation.
- The genetic code is degenerate. With the exception of Met and Trp, every amino acid is coded by more than one codon. Several—Arg, Leu, and Ser—are represented by six different codons. Codons coding for the same amino acid are called synonymous codons.
- All the codons have meaning. Of the 64 codons, 61 specify particular amino acids. The remaining 3—UAA, UAG, and UGA—specify no amino acid and thus they are nonsense codons. Nonsense codons serve as termination codons; they are “stop” signals indicating that the end of the protein has been reached.

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- The genetic code is unambiguous. Each of the 61 “sense” codons encodes only one amino acid. .
- The genetic code is “universal.” Although certain minor exceptions in codon usage occur, the more striking feature of the code is its universality: Codon assignments are virtually the same throughout all organisms—archaea, bacteria, and eukaryotes. This conformity means that all extant organisms use the same genetic code, providing strong evidence that they all evolved from a common primordial ancestor.
- Codons representing the same amino acid or chemically similar amino acids tend to be similar in sequence. Often the third base in a codon is irrelevant, so, for example, all four codons in the GGX family specify Gly, and the UCX family specifies Ser . This feature is known as third-base degeneracy. Note also that codons with a pyrimidine as second base likely encode amino acids with hydrophobic side chains, and codons with a purine in the second-base position typically specify polar or charged amino acids. The two negatively charged amino acids, Asp and Glu, are encoded by GAX codons; GA–pyrimidine gives Asp and GA–purine specifies Glu. The consequence of these similarities is that mutations are less likely to be harmful because single base changes in a codon will result either in no change or in a substitution with an amino acid similar to the original amino acid

| First Position (5′-end) | Second Position | | | | Third Position (3′-end) |
|---|---|---|---|---|---|
| | U | C | A | G | |
| U | UUU Phe | UCU Ser | UAU Tyr | UGU Cys | U |
| | UUC Phe | UCC Ser | UAC Tyr | UGC Cys | C |
| | UUA Leu | UCA Ser | UAA Stop | UGA Stop | A |
| | UUG Leu | UCG Ser | UAG Stop | UGG Trp | G |
| C | CUU Leu | CCU Pro | CAU His | CGU Arg | U |
| | CUC Leu | CCC Pro | CAC His | CGC Arg | C |
| | CUA Leu | CCA Pro | CAA Gln | CGA Arg | A |
| | CUG Leu | CCG Pro | CAG Gln | CGG Arg | G |
| A | AUU Ile | ACU Thr | AAU Asn | AGU Ser | U |
| | AUC Ile | ACC Thr | AAC Asn | AGC Ser | C |
| | AUA Ile | ACA Thr | AAA Lys | AGA Arg | A |
| | AUG Met* | ACG Thr | AAG Lys | AGG Arg | G |
| G | GUU Val | GCU Ala | GAU Asp | GGU Gly | U |
| | GUC Val | GCC Ala | GAC Asp | GGC Gly | C |
| | GUA Val | GCA Ala | GAA Glu | GGA Gly | A |
| | GUG Val | GCG Ala | GAG Glu | GGG Gly | G |

Third-Base Degeneracy Is Color-Coded

| Third-Base Relationship | Third Bases with Same Meaning | Number of Codons |
|---|---|---|
| Third base irrelevant | U, C, A, G | 32 (8 families) |
| Purines | A or G | 12 (6 pairs) |
| Pyrimidines | U or C | 14 (7 pairs) |
| Three out of four | U, C, A | 3 (AUX = Ile) |
| Unique definitions | G only | 2 (AUG = Met) (UGG = Trp) |
| Unique definition | A only | 1 (UGA = Stop) |

# Amino acid match with t-RNA

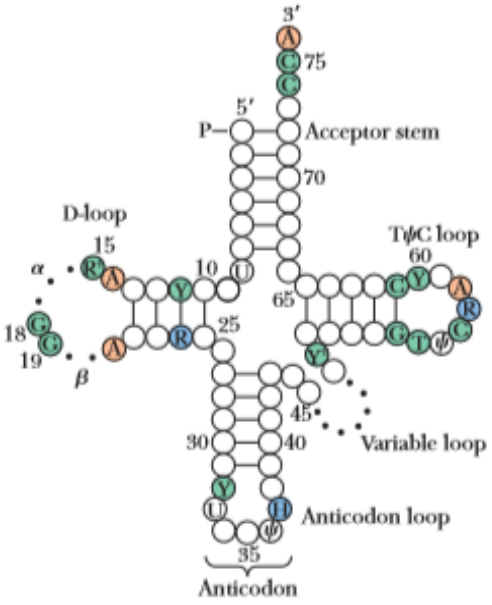
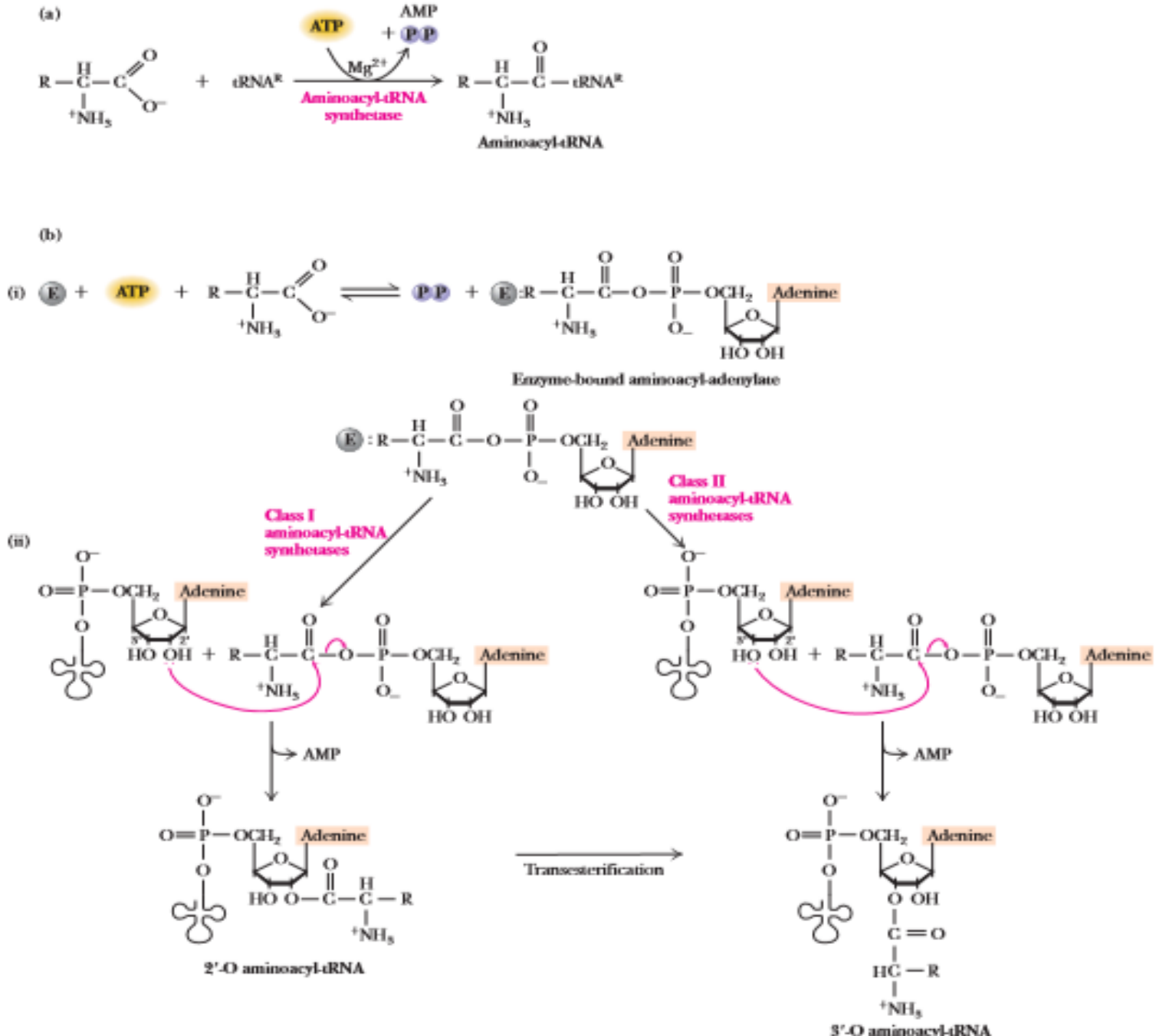
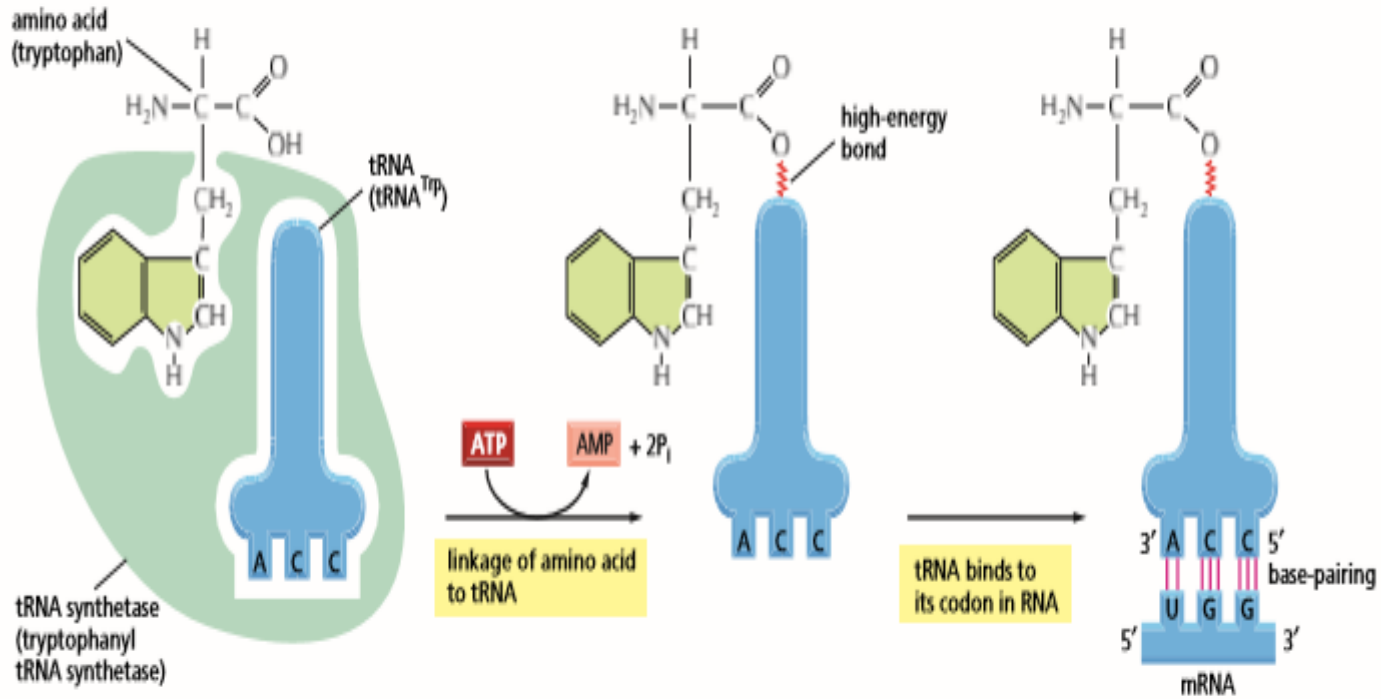



**FIGURE 30.1** Generalized secondary structure of tRNA molecules. Circles represent nucleotides in the tRNA sequence. The numbers given indicate the standardized numbering system for tRNAs (which differ in total number of nucleotides). Dots indicate places where the number of nucleotides may vary in different tRNA species. All tRNAs have the invariant 3-base sequence

- Codon recognition is achieved by aminoacyl-tRNAs. In order for accurate translation to occur, the appropriate aminoacyl-tRNA must “read” the codon through base pairing via its anticodon loop . The amino acid is passively chauffeured by its tRNA and becomes inserted into a growing peptide chain following codon–anticodon recognition between the mRNA and tRNA.
- An aminoacyl-tRNA synthetase must discriminate between the 20 amino acids and the many tRNAs and uniquely picks out its proper substrates—one specific amino acid and the tRNA(s) .
- The appropriate tRNAs are those having anticodons that can base-pair with the codons specifying the particular amino acid.
- Cells have 20 different aminoacyl-tRNA synthetases, one for each amino acid. Each of these enzymes catalyzes ATP-dependent attachment of its specific amino acid to the 3-end of its cognate tRNA molecules .
- The aminoacyl-tRNA synthetase reaction serves two purposes:
- 1. It activates the amino acid so that it will readily react to form a peptide bond.
- 2. It bridges the information gap between amino acids and codons.
- aminoacyl-tRNA synthetase can discriminate between two t-RNA.


(a)
ATP
AMP
+ PP
Mg2+
Aminoacyl-tRNA synthetase
tRNAR
Aminoacyl-tRNA
(b)
(i)
E
ATP
PP
Adenine
Enzyme-bound aminoacyl-adenylate
(ii)
Class I aminoacyl-tRNA synthetases
Class II aminoacyl-tRNA synthetases
AMP
2′-O aminoacyl-tRNA
Transesterification
3′-O aminoacyl-tRNA


amino acid
(tryptophan)
tRNA
(tRNA^Trp)
tRNA synthetase
(tryptophanyl
tRNA synthetase)
A C C
ATP
AMP + 2P_i
linkage of amino acid
to tRNA
high-energy
bond
A C C
tRNA binds to
its codon in RNA
3′ A C C 5′
base-pairing
5′ U G G 3′
mRNA

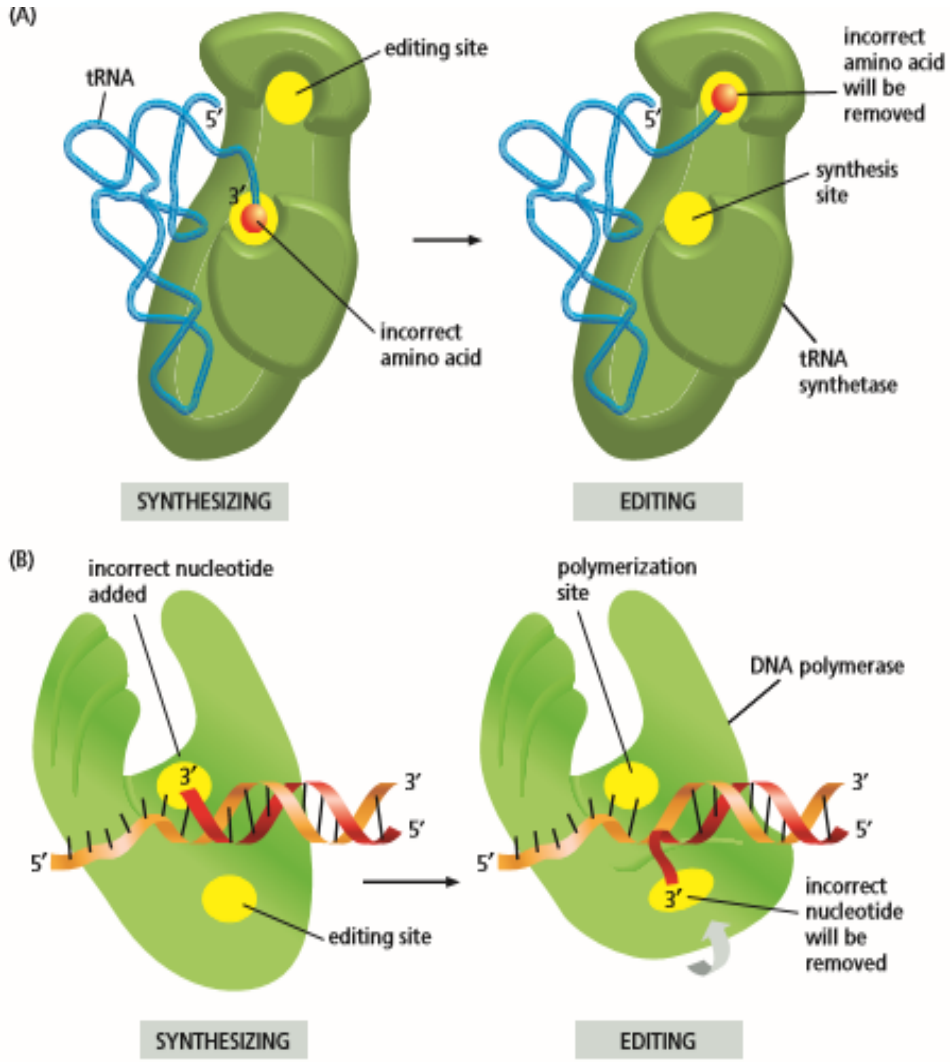



**Figure 6–59 Hydrolytic editing.** (A) tRNA synthetases remove their own coupling errors through hydrolytic editing of incorrectly attached amino acids. As described in the text, the correct amino acid is rejected by the editing site. (B) The error-correction process performed by DNA polymerase shows some similarities; however, it differs in so far as the removal process depends strongly on a mispairing with the template (see Figure 5–8).