11 - Translation

Translation is the cellular process that converts the language of nucleic acids contained within the mRNA molecule (A, U, G, C) into the language of amino acids in a synthesized protein (methionine, alanine, histidine, etc.). This translation process relies on a **genetic code** that converts nucleic acid sequence into amino acid sequence. Note that the genetic code that is translated into protein functions within the mRNA molecule, not in the DNA.

The mRNA molecule is read by the **ribosome** during translation as a group of three consecutive nucleotides, a so called **triplet code**. Each combination of three nucleotides within the mRNA sequence is a **codon**. In addition to the codons, the mRNA contains several RNA sequence features that play roles in translation (**figure 11.1**). These sequence features are listed from 5′ to 3′ along the mRNA molecule below:

- **5′ untranslated region (5′-UTR)**. The 5′-UTR of the mRNA is not translated by the ribosome. Instead, the 5′-UTR allows the ribosome to bind to the mRNA and positions the ribosome to interact properly with the start codon (see below). In bacteria, the 5′-UTR of the mRNA contains a **Shine-Dalgarno sequence** that serves as the binding site for the ribosome. In eukaryotes, the 5′-UTR contains the **7-methylguanosine (7-mG)** cap added during RNA modification (see Part 10), which serves as the ribosome binding site. The 5'-UTR in eukaryotes also contains a **Kozak sequence**, which positions the ribosome to recognize the start codon.
- **Start codon**. The **start codon** in the mRNA codes for the first amino acid in the synthesized protein. The start codon is usually **5'-AUG-3'** and encodes the amino acid ***N*-formylmethionine (fmet)** in bacteria and **methionine (met)** in eukaryotes.
- **Sense codons.** After the start codon, the mRNA is read as consecutive three nucleotide-long **sense codons**. Each sense codon specifies an amino acid in the protein; the specific amino acid sequence of the protein depends on the sequence of sense codons. Note that since the start codon and the sense codons encode amino acids, the start and sense codons constitute the **coding region** of a gene.
- **Stop codon.** The stop codon in the mRNA serves as a signal to end translation. The possible stop codons within prokaryotic and eukaryotic mRNAs include **5′-UAG-3′**, **5′-UAA-3′**, or **5′-UGA-3′**; each mRNA uses one of these three stop codons. The stop codon does not encode an amino acid within the synthesized polypeptide.
- **3′ untranslated region (3′-UTR).** The 3′-UTR of the mRNA, located downstream of the stop codon, plays a role in transcription termination. In prokaryotes, the 3′-UTR contains the *rut*, stem-loop, and the uracil-rich sequences that function in rho (ρ)-dependent and rho (ρ)-independent transcriptional termination (see Part 9). In eukaryotes, the 3′-UTR contains the polyadenylation signal sequences recognized by the CPSF and CstF proteins during transcription termination (see Parts 9 and 10).

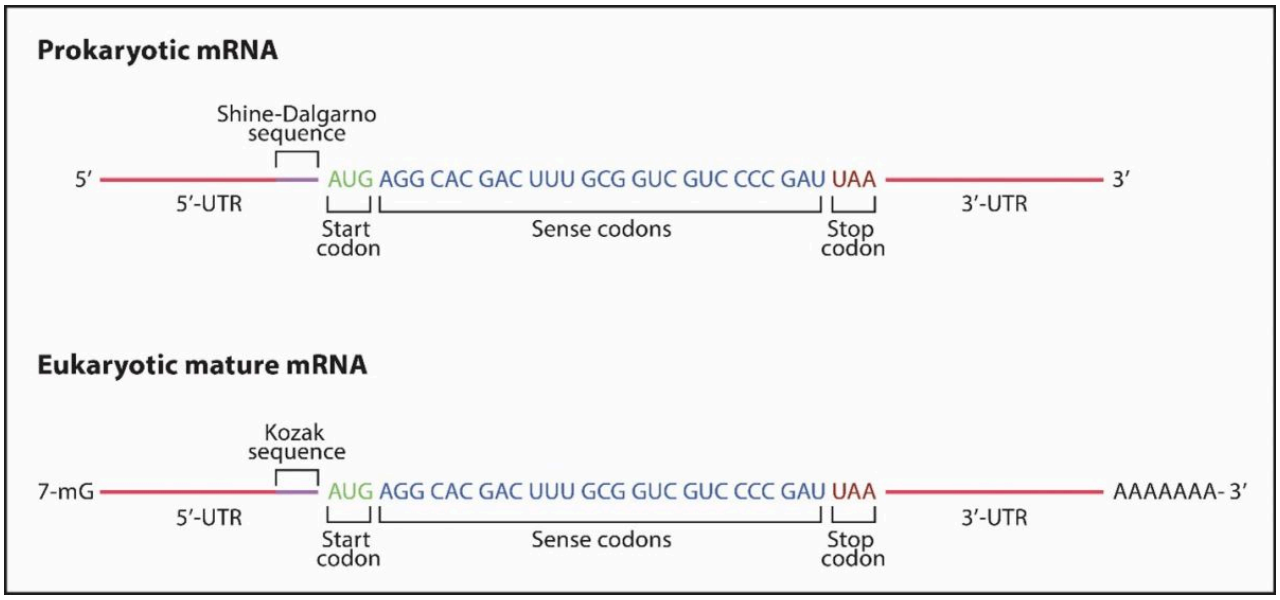

Figure 11.1 ***- Prokaryotic and eukaryotic mRNA features.*** *--- Image created by SL*

Key Questions

- Identify one important sequence feature found in the 5′-UTR of bacterial mRNAs.
- Identify two important sequence features found within the 5′-UTR of eukaryotic mRNAs.
- What amino acid is encoded by 5′-AUG-3′ in bacteria?
- What amino acid is encoded by 5′-AUG-3′ in eukaryotes?
- What is the function of the coding region?
- What is the function of the stop codon?
- Is the stop codon part of the coding region?
- What is the function of the 3′-UTR?

The Genetic Code

There are 20 different types of amino acids typically incorporated in proteins; however, there are 64 possible combinations of four nucleotides (A, U, G, and C) in a triplet codon RNA sequence. As a result, there are more codons than amino acid possibilities (see **figure 11.2**). Thus, the genetic code is **degenerate**, meaning that more than one codon encodes a particular amino acid type. For example, the amino acid valine (val) is encoded by four codons (5′-GUU-3′, 5′-GUC-3′, 5′-GUA-3′, and 5′-GUG-3′) that differ only in the 3′-most base (**wobble base**). These four codons are called **synonymous codons** because they all encode valine.

The genetic code is also **unambiguous**, meaning that a particular codon sequence only encodes one type of amino acid. For example, the codon 5′-AAA-3′ always encodes the amino acid lysine (lys). Further, the genetic code is **commaless**, meaning that codons are read by the ribosome consecutively one triplet sequence after another, with no spacer nucleotides between codons. The codons are also **nonoverlapping**, meaning each nucleotide in the coding region of the mRNA is a member of only one codon. Finally, the genetic code is **universal**, meaning that the same genetic code is used in all organisms.

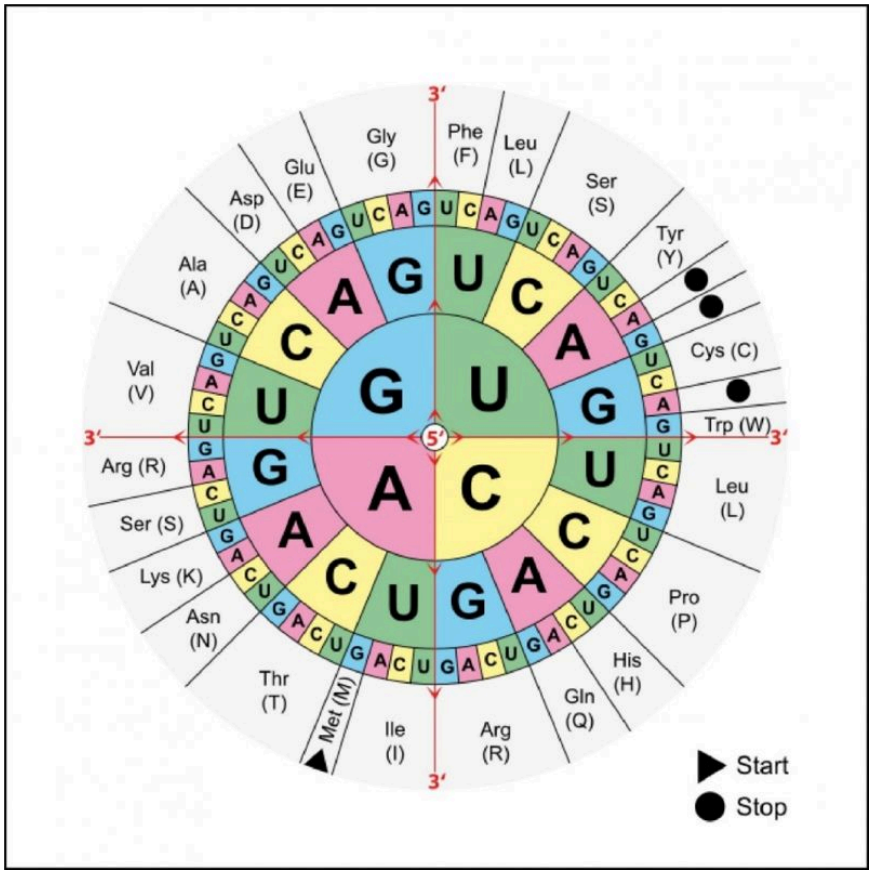

Figure 11.2 ***The genetic code.*** *This representation of the genetic code is read from the center of the circle (the 5'-most base in the codon) to the periphery of the circle (the 3'- most base in the codon). The encoded amino acids are indicated on the outside of the circle. Aminoacids Table was created by Mouagip and is used under CC0*

Key Questions

- How do the words degenerate, unambiguous, commaless, nonoverlapping, and universal apply to the codons in a mRNA sequence?

Directionality of Polypeptide Chains

The polypeptide chains synthesized during translation have directionality (polarity); however, since the language of proteins is different than the language of nucleic acids, the labels 5' and 3' do not apply to the polarity of polypeptide chains. Instead, the amino acid encoded by the start codon (closer to the 5' end of the mRNA) contains a free amino (NH_3^+) chemical group and thus is said to be the **amino** or **N-terminus** of the polypeptide chain**.** As the polypeptide chain is synthesized, **peptide bonds** are formed between the carboxyl group (COO^-) of the growing amino acid chain and the amino groups of incoming amino acids (see **figure 11.3**). Peptide bond formation involves a condensation reaction that releases water as a product. The final amino acid added to a polypeptide contains a free carboxyl chemical group and is called the **carboxyl terminal** or C-terminal end of the polypeptide chain. The C-terminal end of the polypeptide corresponds to the codon immediately before the stop codon (closer to the 3' end of the mRNA).

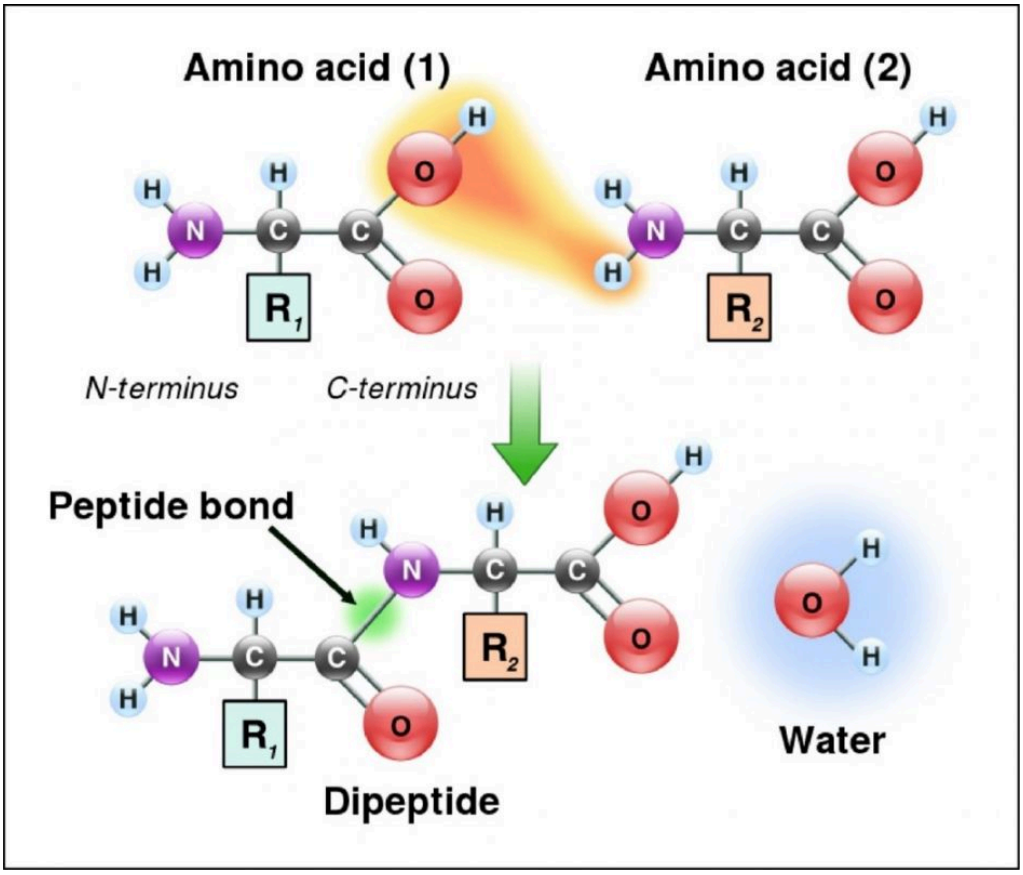

Figure 11.3 ***Peptide bond formation*** *--- Image Peptide Bond Formation was created by Yassine Mrabet and used under CC0*

Key Questions

- How do the N- and C-terminal ends of a protein compare to the 5' and 3' ends of an mRNA molecule?

tRNAs are Adaptor Molecules

Transfer RNA molecules **(tRNAs)** act as **adaptor molecules** in translation. tRNAs function to:

- **Recognize the codon nucleotide sequence within the mRNA.** This recognition process involves hydrogen bonding between the mRNA codon and an **anticodon** nucleotide sequence within the tRNA.
- **Carry a specific amino acid.** tRNA molecules carry amino acids to the ribosome. The carried amino acid is then incorporated into the growing polypeptide chain. The particular amino acid transported to the ribosome is specified by the anticodon sequence in the tRNA.

There are many different types of tRNA molecules in a cell. Each tRNA type is encoded by a different gene in the genome and has a unique anticodon sequence. tRNA types are also distinguished by the amino acid carried. For example, $tRNA^{val}$ carries the amino acid valine, while $tRNA^{phe}$ carries the amino acid phenylalanine. tRNA molecules are example **noncoding RNAs (ncRNAs)**, meaning that tRNA molecules themselves are untranslated; however, tRNAs function directly in the cell.

Key Questions

- What are the two functions of a tRNA molecule?

Features of tRNAs

Even though different tRNA types ($tRNA^{val}$ RNA^{phe}) have unique anticodons and carry unique amino acids, all tRNA molecules share similar structural features (**figure 11.4**):

- **tRNA molecules are small**. Each tRNA type is 75–90 nucleotides in length.
- **tRNA molecules are shaped like a cloverleaf**. Three stem-loop structures are formed by hydrogen bonding within the tRNA molecule. The anticodon RNA sequence is located within one of these stem-loop structures (i.e., the **anticodon loop**).
- **tRNA molecules contain a 3′ single-stranded region called an acceptor stem**. The acceptor stem region is covalently linked to the amino acid.
- **tRNA molecules contain variable regions**. The tRNA variable regions differ between tRNA types (e.g., $tRNA^{val}$ compared to $tRNA^{his}$) in the number of nucleotides and the specific nucleotide sequence that they contain. Variability in these regions can make the stem loops of different tRNA types larger or smaller.
- **tRNA molecules contain unusual nitrogenous bases**. Many tRNA types have unusual nitrogenous bases, such as inosine (I), methylinosine (mI), and dimethylguanine (m_2G). These unusual nitrogenous bases are created from the four conventional RNA nitrogenous bases (A, U, G, C) after transcription of the tRNA molecule has occurred.

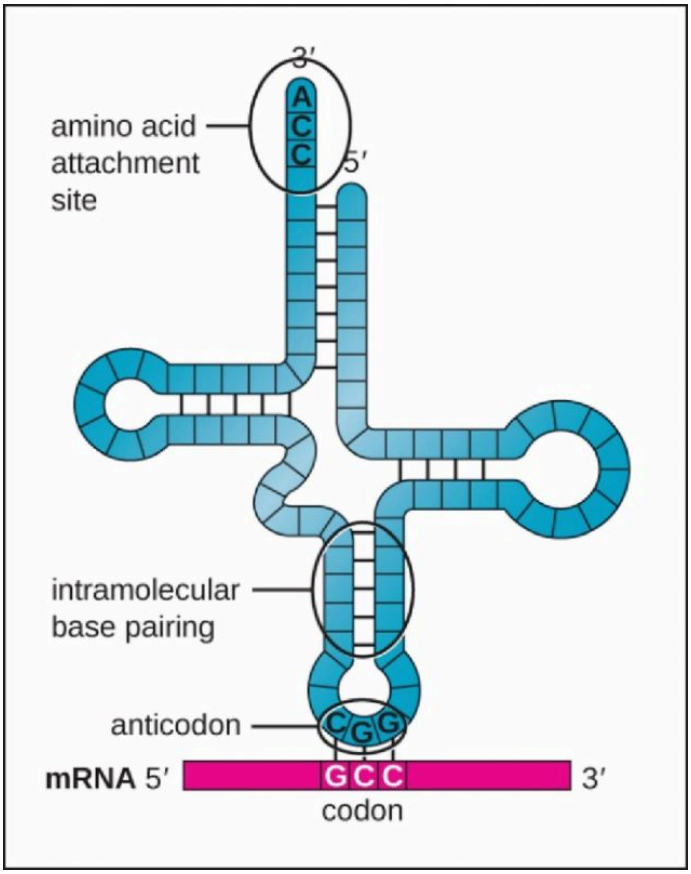

Figure 11.4 ***tRNA Structure.*** *tRNA molecules have three stem loop structures and an acceptor stem. --- Image used from OpenStax (access for free at* https://openstax.org/books/biology-2e/pages/1-introduction*)*

Key Questions

- Where is the anticodon in a tRNA molecule?
- Where is the amino acid attached to a tRNA molecule?

Charging tRNAs

The process of attaching an amino acid to the 3' end of a tRNA molecule is called **charging**. Charging tRNAs involves enzymes called **aminoacyl-tRNA synthetases**. Aminoacyl-tRNA synthetases have the following features:

- There are twenty different pools of aminoacyl-tRNA synthetases per cell, one pool for each of the twenty amino acid types.
- Aminoacyl-tRNA synthetases are named for the amino acid that is attached to the tRNA. For example, alanyl-tRNA synthetases attach the amino acid alanine (ala) to a tRNA molecule, while prolyl-tRNA synthetases attach the amino acid proline (pro) to a tRNA molecule.
- Aminoacyl-tRNA synthetases attach the incorrect amino acid to a tRNA rarely. In fact, it is estimated that aminoacyl-tRNA synthetases attach the wrong amino acid only one time per 100,000 tRNA molecules charged.

The mechanism used by an aminoacyl-tRNA synthetase to charge a tRNA molecule has the following steps (see **figure 11.5**):

1. The aminoacyl-tRNA synthetase binds to its preferred amino acid type and ATP. For example, the alanyl-tRNA synthetases bind to the amino acid alanine and ATP.
2. The ATP molecule is cleaved, PP_i (pyrophosphate) is released, and the remaining AMP is covalently linked to the amino acid. When AMP is linked to the amino acid, the aminoacyl-tRNA synthetase changes its conformation (shape) to produce the active form of the enzyme. This active enzyme conformation allows the aminoacyl-tRNA synthetase to bind to a tRNA molecule.
3. The aminoacyl-tRNA synthetase binds to a tRNA molecule that contains an anticodon sequence specific for the amino acid carried by the aminoacyl-tRNA synthetase. For example, an alanly-tRNA synthetase would only bind to tRNA molecules that have anticodons that would form hydrogen bonds with alanine codons in the mRNA. If the anticodon on the incoming tRNA is incorrect, the tRNA is released from the aminoacyl-tRNA synthetase and a new tRNA binds instead.
4. The aminoacyl-tRNA synthetase attaches the amino acid to the acceptor stem (3' single-stranded region) of the tRNA.
5. AMP is released.
6. The **charged tRNA** (i.e., tRNA covalently linked to the correct amino acid) is released from the aminoacyl-tRNA synthetase. This charged tRNA can then be delivered to the ribosome.

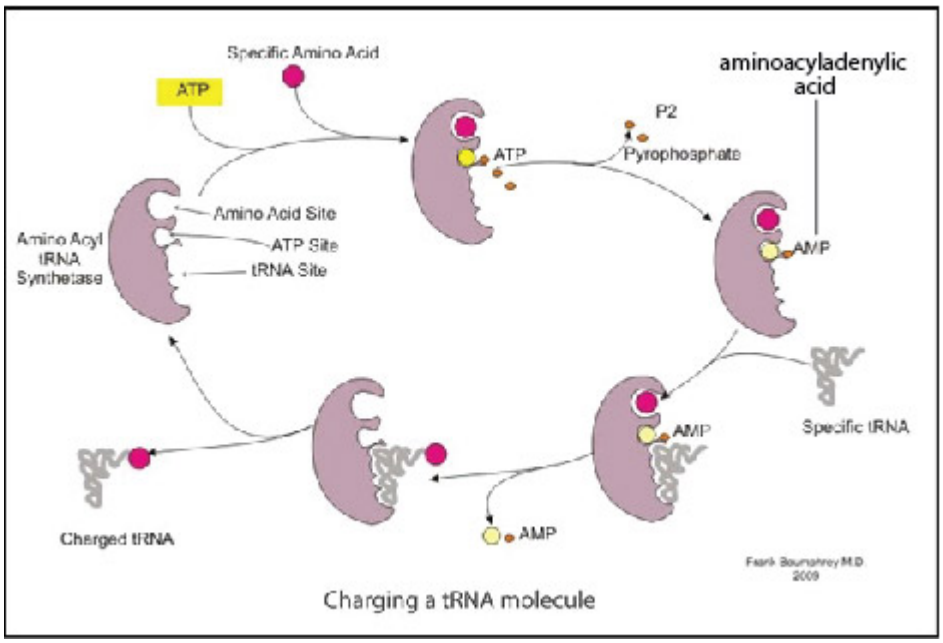

Figure 11.5 ***Charging a tRNA Molecule ---*** *Image by Dr. Frank Boumphrey used under license CC BY-SA 3.0*

Key Questions

- Which molecule provides the energy for the tRNA charging reaction?
- Explain the major events that occur during tRNA charging.

Wobble

Most synonymous codons (codons that encode the same amino acid) have identical bases at the first two nucleotide positions (the 5'-most base and the middle base of the codon). These first two bases obey the AU/GC base pairing rules when forming hydrogen bonds with the tRNA anticodon. Degeneracy in the genetic code typically occurs at the 3'-most base within the codon; the 3'-most base in the codon does not have to form conventional base pairing interactions with the 5'-most base of the anticodon, leading to "wobble." The rules that govern codon-anticodon at this wobble position

interactions are called the **wobble rules** (see **Table 11.1**). For example, a U base in the wobble position of the codon (3'-most base) can form hydrogen bonds with A, G, or I in the wobble position of the anticodon (5'-most base). Similarly, a U in the wobble position of the anticodon (5'-most base) can form hydrogen bonds with either A or G in the wobble position of the codon (3'-most base).

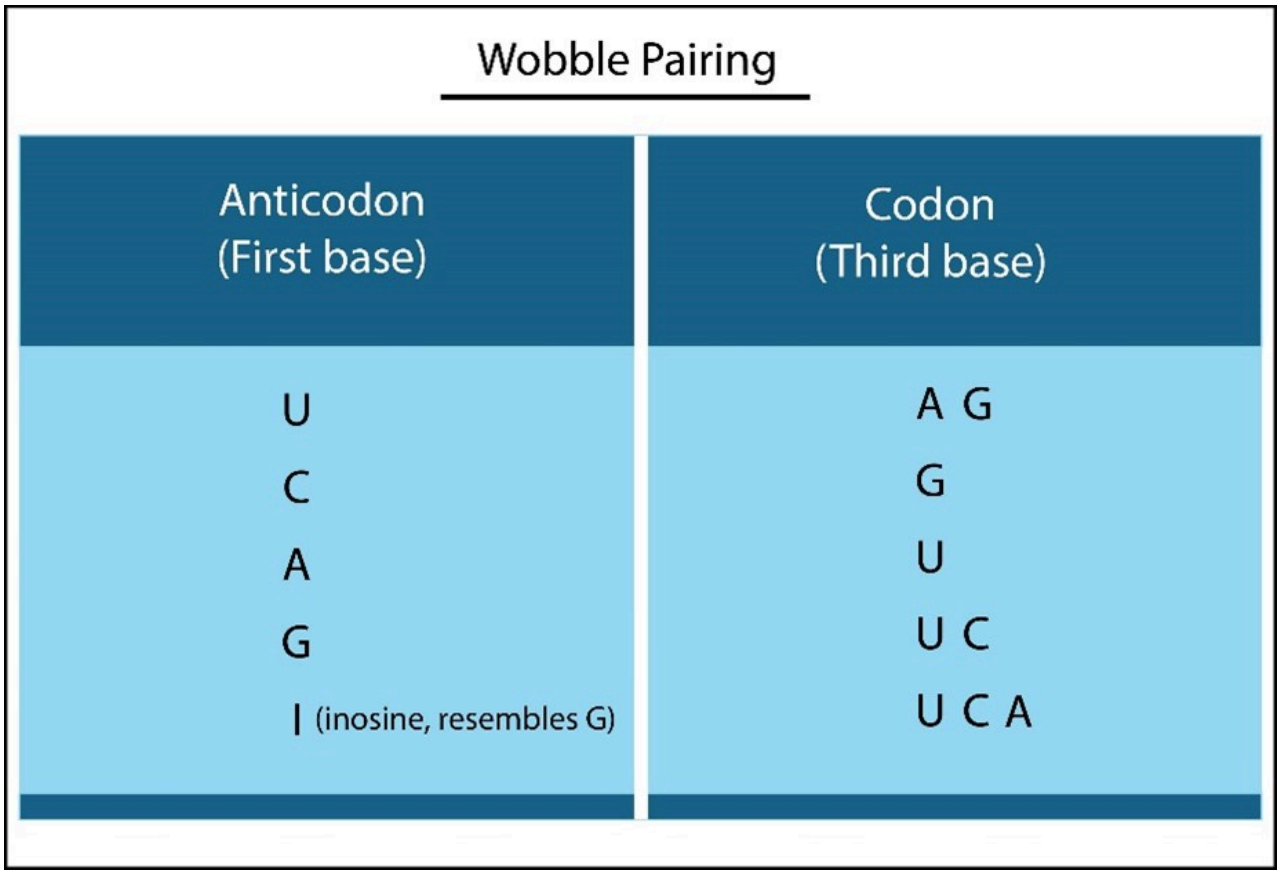

Table 11.1 ***Wobble Rules Table.***

A group of tRNA types, with slightly different anticodon sequences, which recognize the same mRNA codon sequence are called **isoacceptor tRNAs**. For example, suppose we have the codon 5'-UUU-3' in the mRNA. tRNA molecules containing either 3'-AAA-5', 3'-AAG-5', or 3'-AAI-5' anticodons can recognize this mRNA codon, according to the wobble rules (see Table 11.1). Note that these isoacceptor tRNAs are charged by the same aminoacyl-tRNA synthetase and therefore, bear the same amino acid (phenylalanine). Alternatively, a tRNA with the 3'-GGU-5' anticodon can recognize two codons: 5'-CCA-3'and 5'-CCG-3' according to the wobble rules. Both codons encode proline.

Why is this wobble phenomenon advantageous to cells? Wobble gives the cell tremendous flexibility in codon:anticodon interactions. A single mRNA codon can be recognized by more than one tRNA anticodon, and a single tRNA anticodon can bind to more than one mRNA codon. This flexibility allows translation to occur at a reasonable rate and allows a cell to save energy in the synthesis of tRNA molecules. Instead of assembling 61 different types of tRNA molecules (one type for each possible sense codon, minus the three stop codons), a cell can get away with synthesizing only 30-40 types of tRNA molecules, with some tRNAs recognizing multiple mRNA codon sequences.

Key Questions

- What is meant by wobble?
- What are isoacceptor tRNAs?
- What are the two advantages of wobble?

Prokaryotic Ribosomes

The multisubunit **ribosome** is the central figure in the translation process. The ribosome binds to the mRNA, serves as a site for mRNA codon:tRNA anticodon recognition, breaks the covalent bond between the 3' end of the tRNA and the amino acid, and synthesizes peptide bonds between amino acids.

A single bacterial cell is thought to contain approximately 10,000 ribosomes; these bacterial ribosomes are called **70S ribosomes**. Note that the "S" designation of ribosomes correlates roughly with the overall three-dimensional shape of the ribosome component; the larger the molecule, the larger the "S" value. The 70S ribosome consists of the following subunits (see **figure 11.6**):

- **Small subunit (30S subunit).** The small subunit of the ribosome is composed of several different ribosomal proteins and a **16S ribosomal RNA (rRNA)** molecule. The 16S rRNA molecule helps the ribosome bind to the bacterial mRNA molecule (see below).
- **Large subunit (50S subunit)**. The large subunit of the ribosome is composed of many ribosomal proteins, a 5S rRNA, and a **23S rRNA** molecule. The 23S rRNA molecule is the catalytic core of the ribosome; the 23S rRNA is the RNA enzyme (ribozyme) that forms peptide bonds between amino acids during prokaryotic translation (see below).

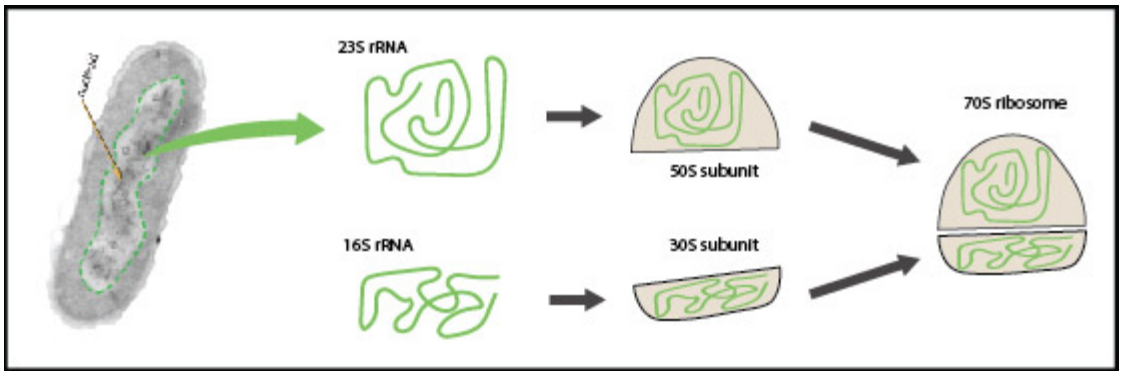

Figure 11.6 ***Prokaryotic Ribosomes*** *--- Prokaryotic cell (Left) used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction).Image created by SL*

Eukaryotic Ribosomes

Eukaryotic cells have cytosolic ribosomes called **80S ribosomes**. Mitochondrial and chloroplast ribosomes resemble prokaryotic 70S ribosomes. The 80S ribosomes in the cytosol synthesize most cellular proteins and consist of the following subunits (see **figure 11.7**):

- **Small subunit (40S).** The 40S subunit is composed of many proteins and an 18S rRNA molecule.
- **Large subunit (60S).** The 60S subunit is composed of a collection of proteins, 5S, 5.8S, and **28S rRNA** molecules. The 28S rRNA molecule is the RNA enzyme (ribozyme) that forms peptide bonds between amino acids during eukaryotic translation (see below).

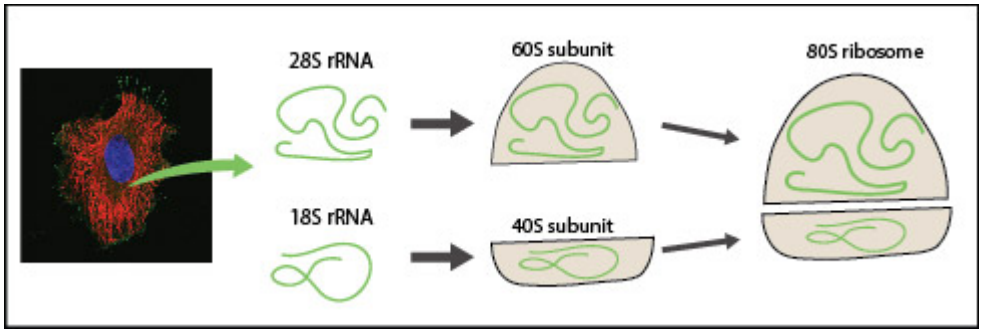

Figure 11.7 ***Eukaryotic ribosomes*** *--- Image created by SL*

Key Questions

- Compare and contrast the structural features of prokaryotic vs. eukaryotic ribosomes.
- What is the name of the enzyme that forms peptide bonds within the 70S ribosome?
- What is the name of the enzyme that forms peptide bonds within the 80S ribosome?

Overview of Translation

Translation in prokaryotes and eukaryotes occurs in three stages (see **figure 11.8**):

1. During **initiation**, the large and small ribosomal subunits assemble near the mRNA start codon with an **initiator tRNA** molecule that has an anticodon sequence specific for the start codon mRNA sequence. Once all translation components have assembled correctly, the initiator tRNA is located at the P site (see below) within the ribosome.
2. During **elongation**, the ribosome **translocates** (moves) along the mRNA in the 5' to 3' direction, reading triplet codons within the mRNA, converting the codon sequences into a chain of amino acids. During elongation, three tRNA binding sites within the ribosome are used. These tRNA binding sites are the:
   - **Aminoacyl site (A site).** Charged tRNAs enter the ribosome at the A site.
   - **Peptidyl site (P site).** During a translation elongation cycle (see below), the polypeptide chain attached to the tRNA molecule in the P site is transferred to the tRNA in the A site as a peptide bonds is formed.
   - **Exit site (E site)**. The E site allows uncharged tRNA molecules to exit the ribosome.
3. When the ribosome reaches a stop codon, translation **terminates**. The mRNA and the polypeptide chain are released from the ribosome, and the large and small subunits of the ribosome dissociate from each other. The ribosome subunits and the mRNA can be recycled to synthesize another copy of the protein.

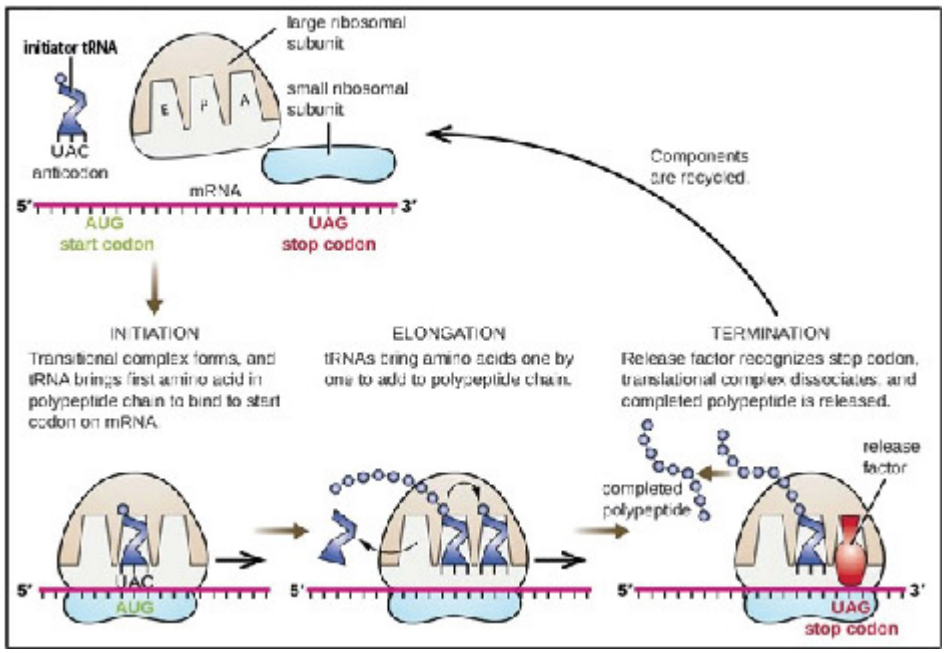

Figure 11.8 ***Overview of Translation ---*** *image used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction), modified by SL*

Key Questions

- What major events are occurring during the initiation, elongation, and termination stages of translation?
- What are the functions of the A, P, and E sites?

Shine-Dalgarno Sequence

The **5'-untranslated region (5'-UTR)** of prokaryotic mRNAs plays a critical role in translation initiation, as the 5'-UTR contains the ribosome-binding site. Specifically, the 5'-UTR contains a recognition sequence (5'-AGGAGGU-3') called the **Shine-Dalgarno sequence** that forms hydrogen bonds with a complementary sequence within the **16S rRNA** of the small ribosomal subunit (30S) (see **figure 11.9**). Hydrogen bond formation between the Shine-Dalgarno sequence and the 16S rRNA promotes ribosome assembly. Additionally, the Shine-Dalgarno sequence positions the P site of the ribosome properly at the start codon to initiate polypeptide synthesis.

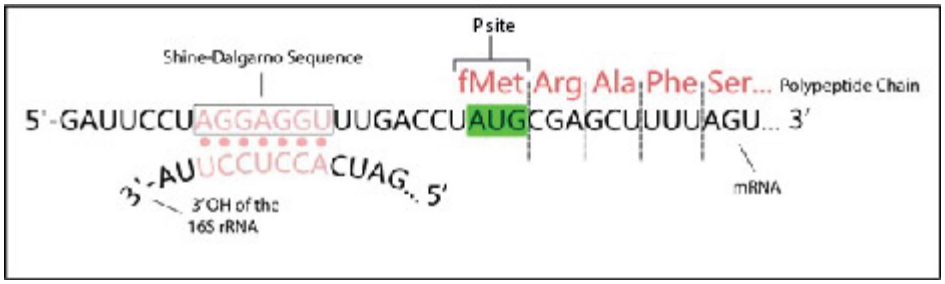

Figure 11.9 ***The Shine-Dalgarno Sequence ---*** *image created by Alejandro Porto and modified by SL. Used under license CC BY-SA 3.0*

Key Questions

- What is the function of the Shine-Dalgarno sequence?

Translation Initiation in Bacteria

Translation initiation in the bacterium *E. coli* includes the following steps (see **figure 11.10**):

1. **The mRNA binds to the small ribosomal subunit (30S) via the Shine-Dalgarno sequence.** An initiation factor protein called **IF3** promotes the formation of hydrogen bonds between the 16S rRNA (ribosome) and the Shine-Dalgarno sequence (mRNA).
2. **The initiator tRNA (tRNA^{fmet}) recognizes the start codon within the P site of the ribosome.** The initiator tRNA anticodon forms hydrogen bonds with the mRNA start codon in the P site. In bacteria, this initiator tRNA is covalently attached to a modified form of methionine called ***N*-formylmethionine (fmet)**. Thus, the N-terminal amino acid in all newly synthesized prokaryotic proteins is fmet. Binding of the tRNA^{fmet} to the start codon requires the initiation factor protein **IF2.** IF2 cleaves GTP to load the tRNA^{fmet} into the ribosome P site. The complex of the 30S subunit, the mRNA, IF3, and IF2 is called the **initiation complex**.
3. **The 50S subunit of the ribosome is added to the initiation complex.** The addition of the 50S ribosome subunit requires the release of IF2 and IF3.

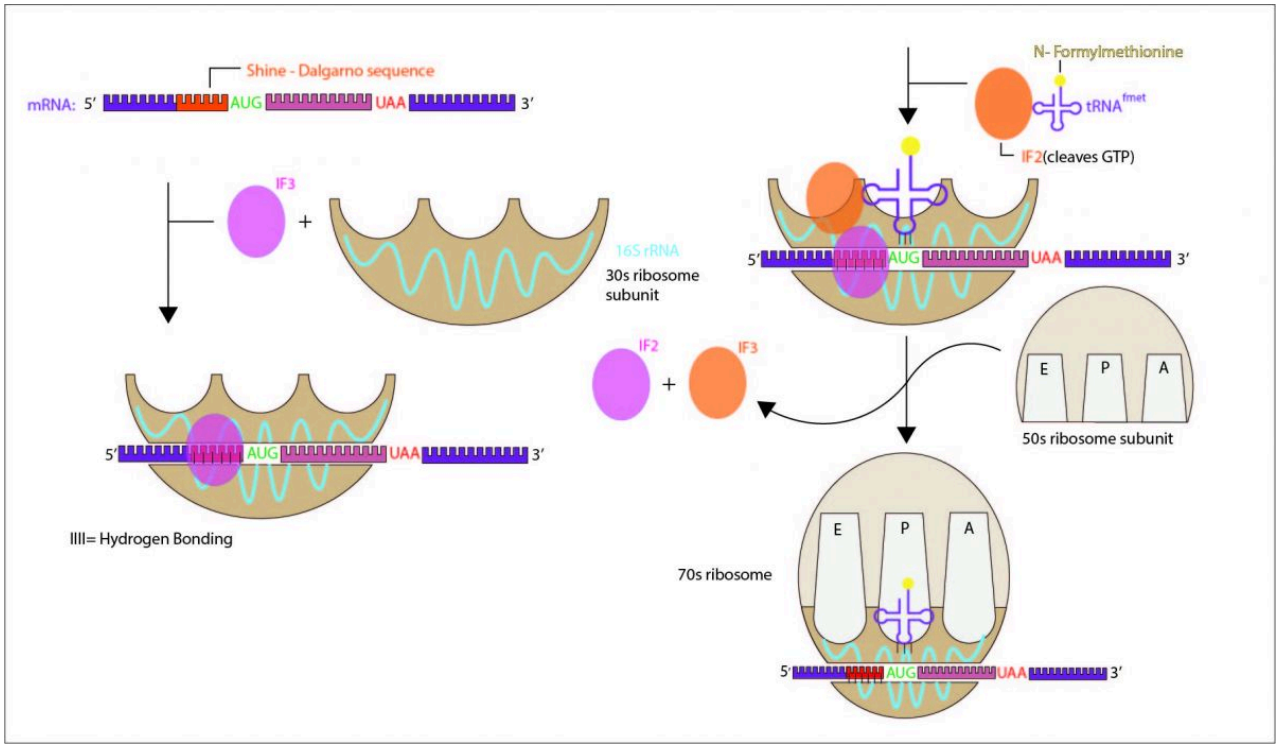

Figure 11.10 ***Translation initiation in bacteria*** *--- Image created by JET*

Key Questions

- How do IF2 and IF3 function in translation initiation in bacteria?
- What molecule provides the energy for translation initiation in bacteria?

Translation Initiation in Eukaryotes

Translation initiation is more complex in eukaryotes than in prokaryotes. Key differences between eukaryotic and prokaryotic translation initiation include (see **figure 11.11**):

- More initiation factor proteins are involved in eukaryotes. These initiation factor proteins are called **eukaryotic initiation factors (eIFs)**.
- The initiator tRNA in eukaryotes is **$tRNA^{met}$**. This initiator tRNA is charged with the amino acid **methionine (met)**.
- There is no Shine-Dalgarno sequence in the eukaryotic mature mRNA. Instead, the 5' UTRs of eukaryotic mature mRNAs contain a **7-methylguanosine (7-mG)** cap and a **Kozak sequence**.

The process of translation initiation in eukaryotes is as follows:

1. **The eIF2 protein brings $tRNA^{met}$ to the 40S ribosomal subunit**. eIF2 cleaves GTP to deliver $tRNA^{met}$ to the 40S ribosomal subunit.
2. **Assembly of a multiprotein initiation complex on the 7-methylguanosine (7-mG) cap on the mature mRNA.** This initiation complex includes:
   - the 40S ribosome subunit.
   - an **eIF4** protein.
   - a complex composed of eIF2 and $tRNA^{met}$
   - **cap-binding protein 1 (CBP1)**. CBP1 is the protein responsible for recognizing the 7-mG structure on eukaryotic mature mRNAs.
3. **Identification of the start codon**. The 40S ribosomal subunit and associated proteins move from the 7-mG cap 5’ to 3’ along the mRNA looking for a start codon. This scanning process requires the cleavage of ATP. Not all possible start codons (5’-AUG-3’) are chosen to initiate translation. The 5’-AUG-3’ that is chosen is within the **Kozak sequence:** 5’-GCC(A or G)CC**AUG**G-3’. When the $tRNA^{met}$ forms hydrogen bonds with the start codon, $tRNA^{met}$ is in the P site of the ribosome.
4. **Addition of the 60S ribosomal subunit to form the active 80S ribosome**. When the 60S ribosome subunit is added, eIF2, eIF4, and CBP1 are released.

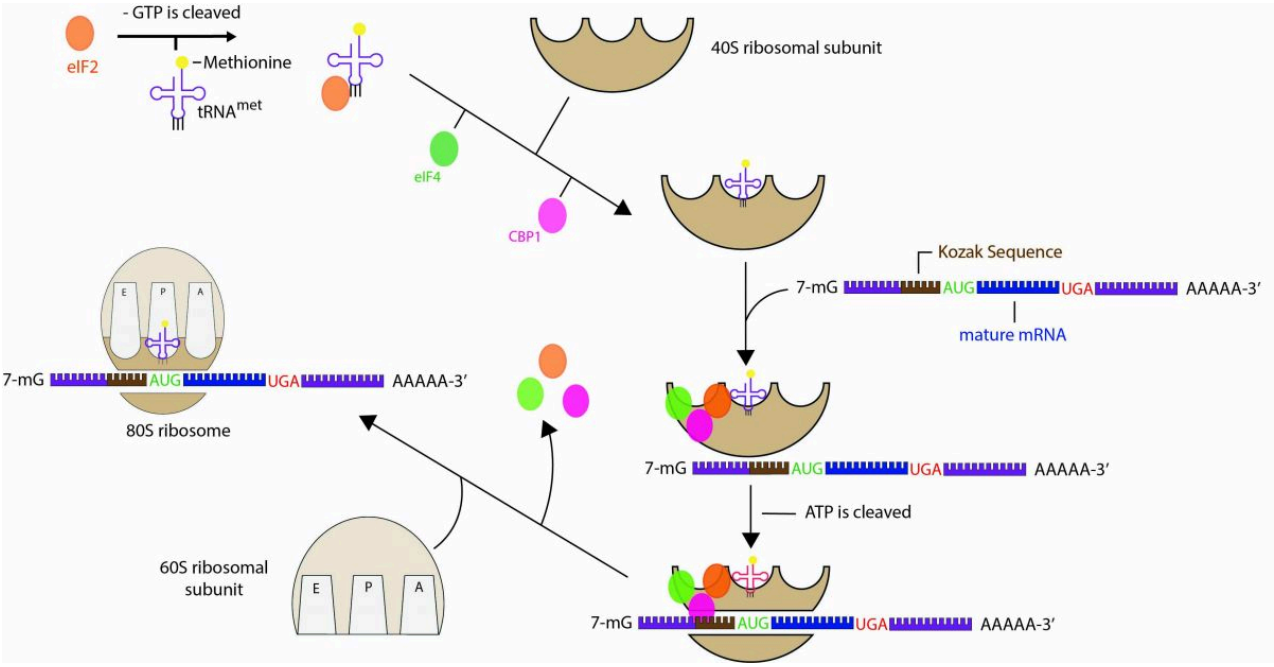

Figure 9.11 - Translation initiation in eukaryotes.

Key Questions

- How do eIF2 and CBP1 function in translation initiation in eukaryotes?
- What is the function of the Kozak sequence?
- Which two nucleotides provide the energy for translation initiation in eukaryotes?

Translation Elongation

Translation elongation in bacteria involves a series of cycles, one cycle per sense codon in the mRNA. At the beginning of each cycle, the tRNA molecule located within the P site of the ribosome is either attached to single amino acid (beginning of elongation cycle one) or a chain of amino acids (later elongation cycles; see **figure 11.12**). The A and E sites of the ribosome are empty. Each elongation cycle then proceeds as follows:

1. **A charged tRNA is delivered to the ribosome A site**. The prokaryotic **elongation factor** protein **EF-Tu** is responsible for loading a charged tRNA into the A site of the ribosome. This loading of a charged tRNA into the A site requires the cleavage of GTP.
2. **The codon:anticodon hydrogen bonds are checked**. Of course, the anticodon within the newly delivered tRNA must form complementary hydrogen bonds with the mRNA codon according to the wobble rules. An incorrect tRNA bound to the A site is recognized by the **16S rRNA**. When an incorrect anticodon is encountered, polypeptide synthesis is halted until the mismatched tRNA is released from the ribosome. This editing function of the 16S rRNA molecule allows for high fidelity in protein synthesis; it is estimated that only one mistake is made per 10,000 incorporated amino acids, or about one time in every 20 proteins synthesized by the ribosome.
3. **The formation of a peptide bond**. The amino acid or amino acid chain bound to the tRNA in the P site is transferred to the tRNA in the A site via the formation of a new peptide bond. This enzyme reaction is catalyzed by the **23S rRNA** component of the 50S ribosomal subunit; the 23S rRNA is an example of a ribozyme (RNA enzyme). The 23S rRNA ribozyme is also called **peptidyl transferase**.
4. **Ribosome translocation**. The ribosome **translocates** (moves) in the 5' to 3' direction one codon along the mRNA. The tRNA (with the attached polypeptide chain) that was in the A site moves to the P site. The uncharged tRNA that was in the P site moves to the E site and exits the ribosome. A bacterial elongation factor protein called **EF-G** cleaves GTP to translocate the ribosome to the next sense codon in the mRNA.
5. **Steps 1–4 are repeated for each sense codon in the mRNA**. The rate of protein synthesis is 15–18 cycles (i.e., 15-18 amino acids) per second in prokaryotes.

Translation elongation works similarly in eukaryotes; however, there are some minor differences:

- The 28S rRNA component of the 60S ribosomal subunit functions as the peptidyl transferase to synthesize peptide bonds between amino acids. The 28S rRNA is another example of a ribozyme (RNA enzyme).
- Eukaryotes have **eukaryotic elongation factor** proteins **(eEFs)** that function similarly to the EF-Tu and EF-G proteins from bacteria. The eukaryotic **eEF1** protein functions similarly to EF-Tu, delivering charged tRNA molecules to the A site of the ribosome. The eukaryotic **eEF2** protein functions similarly to EF-G in bacteria, translocating the ribosome to the next mRNA codon after peptide bond formation has taken place. Both eEF1 and eEF2 cleave GTP molecules.

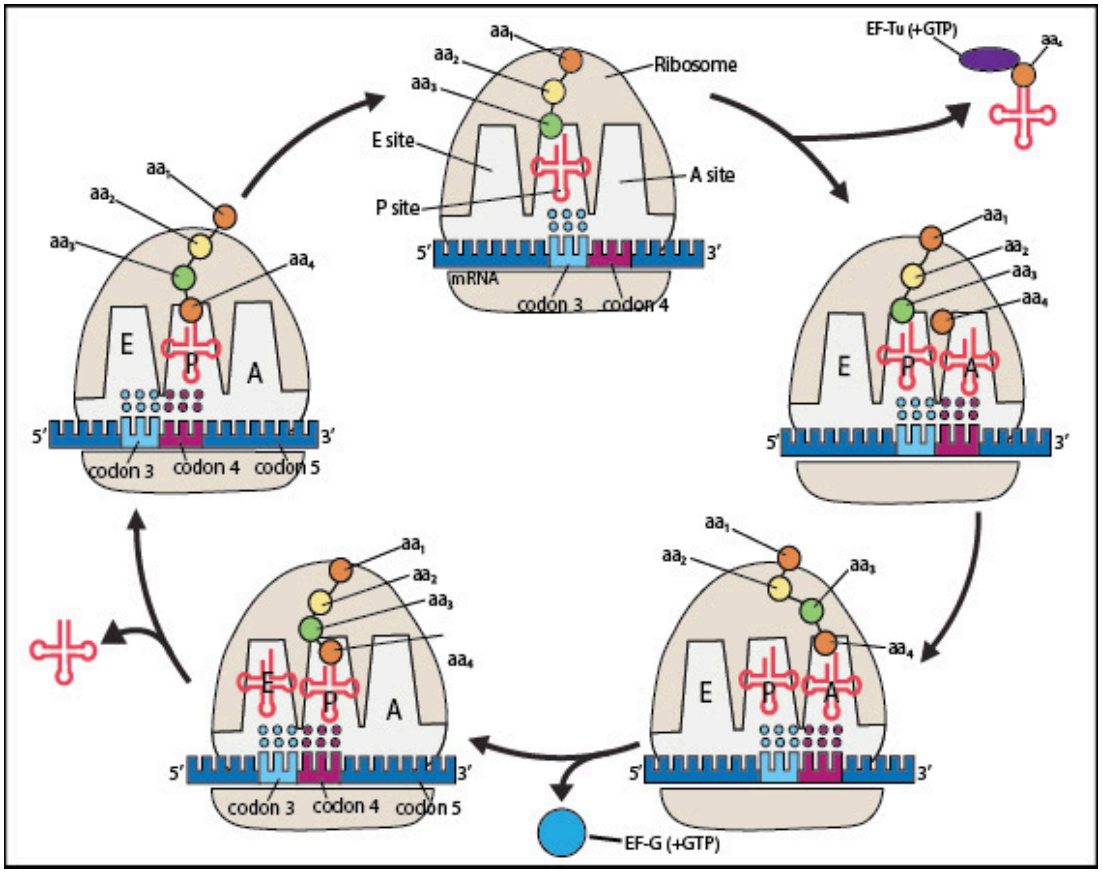

Figure 11.12 ***A translation elongation cycle in bacteria*** *-- The beginning of the translation cycle is shown at the top of the image. Image used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction), modified by SL*

Key Questions

- Describe the events involved in one translation elongation cycle.
- Explain when GTP is used during the elongation cycle.
- What is the eukaryotic equivalent of 23S rRNA, EF-Tu, and EF-G?

Translation Termination

Translation termination in bacteria occurs as follows (see **figure 11.13**):

1. As the ribosome approaches the 3' end of the mRNA, a **stop codon (5'-UGA-3', 5'-UAG-3',** or **5'-UAA-3')** moves into the A site of the ribosome.
2. The stop codon is recognized by a **release factor** protein. The release factor protein mimics the three-dimensional structure of a tRNA molecule. In bacteria, the **release factor 1 (RF1)** protein recognizes the stop codons 5'-UAA-3' and 5'-UAG-3'. The **release factor 2 (RF2)** protein recognizes the 5'-UAA-3' and 5'-UGA-3' stop codons.
3. The release factor protein cleaves the covalent bond between the tRNA and the polypeptide chain in the ribosome P site. As a result, the tRNA and the polypeptide chain are released from the ribosome. The polypeptide chain folds to become the mature protein. This release step requires the release factor protein to cleave GTP.
4. The ribosomal subunits, mRNA, and release factor protein dissociate, terminating translation. The ribosome subunits and the mRNA can be recycled to begin translation again.

Translation termination works essentially the same way in eukaryotes. One minor diference is the use of a single **eukaryotic release factor (eRF)** protein that recognizes all three stop codons. eRF cleaves GTP to terminate translation in eukaryotes.

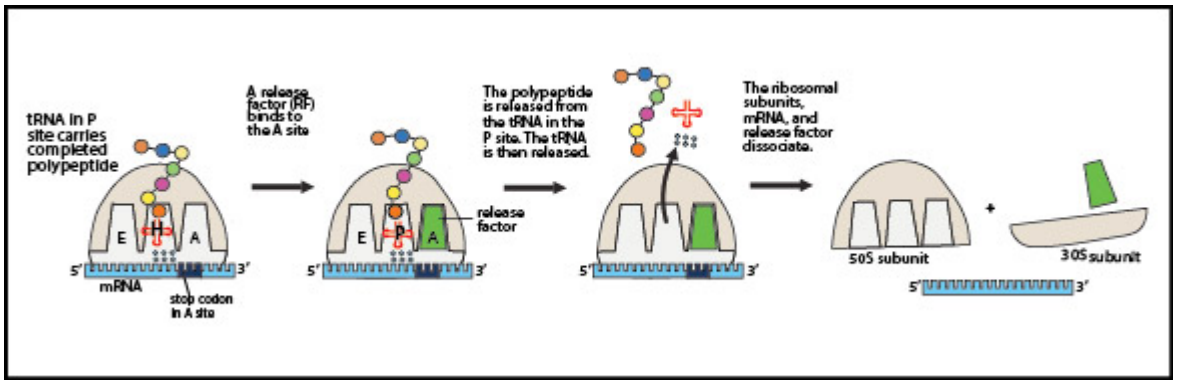

Figure 11.13 ***Translation termination*** *--- Image used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction), modified by SL*

Key Questions

- What is the difference between RF1 and RF2?
- What molecule provides the energy to terminate translation?
- Are some of the molecules involved in translation recycled? If so, which ones?

Polysomes and Coupled Transcription and Translation

In the electron microscope, multiple ribosomes (**polyribosomes** or **polysomes**) are often observed attached to a single mRNA transcript (see **figure 11.14**). Polysomes have been observed attached to both prokaryotic mRNA and eukaryotic mature mRNA transcripts.

Since prokaryotic cells lack nuclei, transcription and translation are **coupled**, meaning that translation can begin before transcription is completed. In eukaryotes, transcription and translation are uncoupled. Transcription and RNA modifications occur within the nucleus. Translation occurs later, after the mature mRNA has been transported from the nucleus to the cytoplasm.

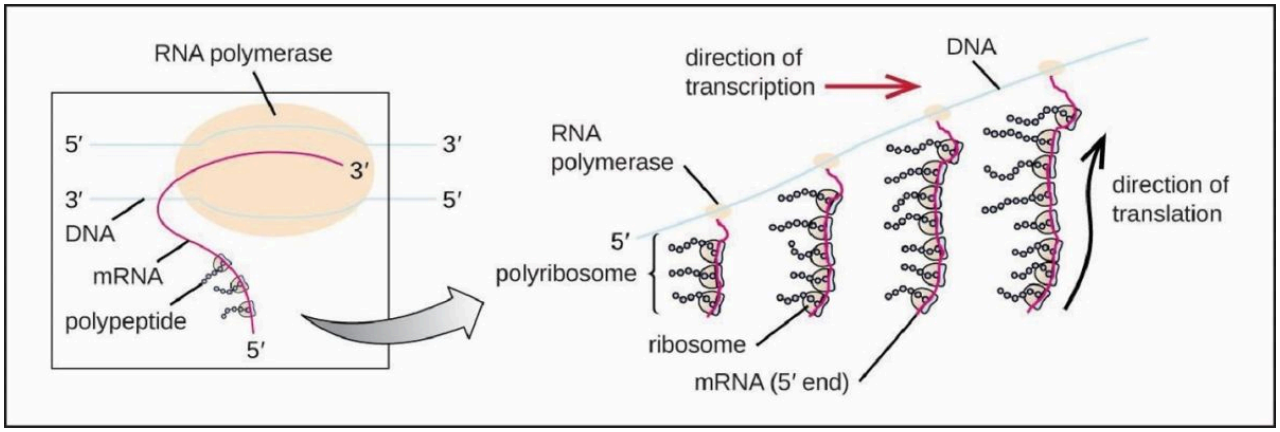

Figure 11.14 ***Polyribosomes and coupled transcription/translation in bacteria --- Image used from OpenStax (access for free at https://openstax.org/books/biology-2e/pages/1-introduction)***

Key Questions

- Why is it advantageous to have multiple ribosomes translating a mRNA molecule simultaneously?
- Why is prokaryotic transcription and translation coupled?
- Why is eukaryotic transcription and translation uncoupled?

Review Questions

Fill in the blanks:

1. The _____ portion of a eukaryotic mature mRNA contains the polyadenylation signal sequences.
2. The genetic code is said to be _____, which means that each codon only specifies one type of amino acid. (For example, 5'-UUU-3' always encodes phenylalanine)
3. The cloverleaf structure of the tRNA is such that the _____ is a stem-loop that forms hydrogen bonds with the mRNA codon, and the _____ is the single-stranded region where an amino acid is attached.
4. _____ is an enzyme that links the amino acid alanine to a tRNA molecule.
5. The 30S and 50S ribosomal subunits in a prokaryotic cell combine to form a final size of _____ while in eukaryotes the _____ and _____ ribosomal subunits combine to form a final size of _____.
6. The initiator tRNA binds to the _____ site of the ribosome, whereas the remaining charged tRNAs bind to the _____ site of the ribosome.
7. An *E. coli* protein called _____ delivers charged tRNAs to the ribosome during translation elongation.
8. The ribosome moves along the mRNA in the _____to _____ direction.
9. _____ is a eukaryotic translation factor protein that delivers charged tRNAs to the ribosome during elongation.
10. _____ is a eukaryotic translation factor that helps the ribosome move one codon in the 3' direction along the mRNA. The equivalent bacterial protein is called _____.
11. The _____ protein in bacteria mimics the structure of a tRNA and recognizes 5'-UGA-3' in the A site of the ribosome.
12. An *E. coli* protein called _____ delivers $tRNA^{fmet}$ to the ribosome during translation.