10.4 Translation

Learning objectives

By the end of this section, you will be able to:

- *Describe the different steps involved in translation*
- *Discuss the role of rRNA, mRNA, and tRNA in protein synthesis*
- *Describe the genetic code and how the nucleotide sequence determines the amino acid sequence of a protein*
- *Be able to take an mRNA sequence and transcribe and translate the corresponding protein*
- *Be prepared to define and explain all bolded terms*

Proteins perform a wide variety of functions in a cell and are necessary to maintain homeostasis. Protein synthesis is one of a cell's most energy-consuming metabolic processes. The process of **translation**, or protein synthesis, involves "decoding" a mRNA molecule with the purpose of forming a polypeptide chain. Amino acids are linked together through covalent bonds to form polypeptide chains that range in lengths from approximately 50 amino acids to more than 1,000.

The Protein Synthesis Machinery

In addition to the mature mRNA, many other molecules contribute to the process of translation. Translation requires not only mRNA, but also ribosomes, tRNAs, and various other enzymes (Figure 10.29). Although each of these components is necessary, their composition may vary across species. For instance, ribosomes may consist of different **ribosomal RNA**s (rRNA) and enzymes depending on the organism. Prokaryotic and eukaryotic cells have distinctly different ribosomes that vary in size. Although living cells may have slight differences, the general structures and functions of the protein synthesis machinery are comparable (Figure 10.29).

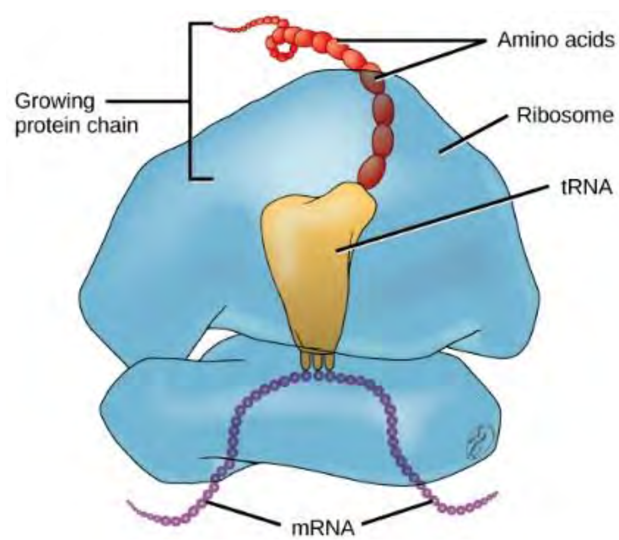

Figure 10.29 The protein synthesis machinery includes the large and small subunits of the ribosome, mRNA, and tRNA. (credit: modification of work by NIGMS, NIH / [Concepts of Biology OpenStax](#))

Ribosomes

A ribosome is a complex macromolecule composed of structural and catalytic **rRNA**s. Ribosomes also consist of many distinct proteins, some of which have enzymatic properties. In eukaryotes, the nucleolus, a region found in the nucleus, is completely specialized for the synthesis and assembly of rRNAs.

Ribosomes are located in the cytoplasm in both prokaryotic and eukaryotic cells. In eukaryotes, ribosomes are also found attached to the rough endoplasmic reticulum. Ribosomes are made up of a large and small subunit that come together for translation. The small subunit is responsible for binding directly to the mRNA, whereas the large subunit sequentially binds transfer RNAs (Figure 10.30). **Transfer RNA (tRNA)** is a type of RNA molecule that brings amino acids to the growing polypeptide chain. Each mRNA is simultaneously translated by many ribosomes, all synthesizing the polypeptide chain in the same direction. Once the polypeptide chain is synthesized it must fold into its three-dimensional shape before it is functional. Once folded, the polypeptide chain is considered a protein.

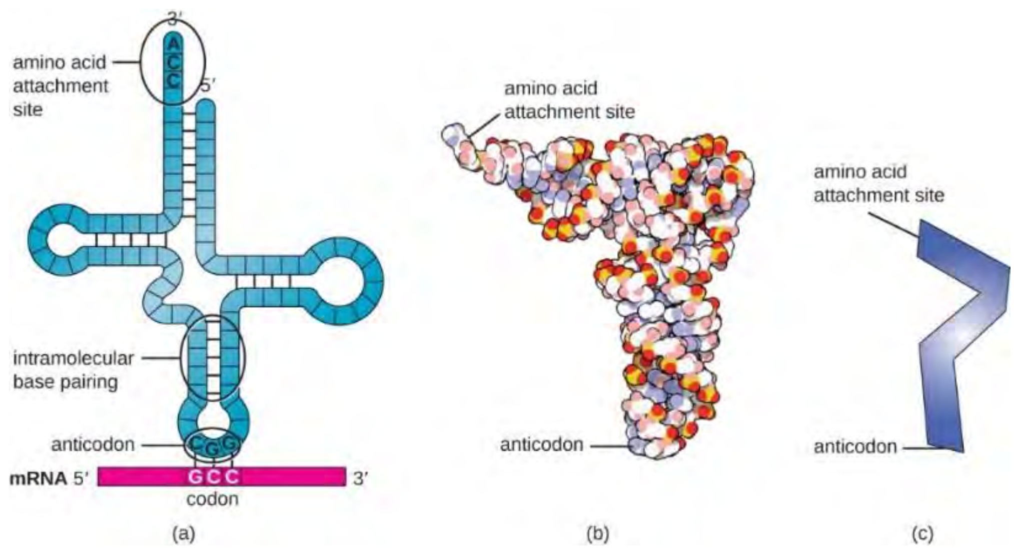

Figure 10.30 (a) After folding caused by intramolecular base pairing, a tRNA molecule has one end that contains the anticodon, which interacts with the mRNA codon, and the CCA amino acid binding end. (b) A space-filling model is helpful for visualizing the three-dimensional shape of tRNA. (c) Simplified models are useful when drawing complex processes such as protein synthesis. (credit: Parker et al. / Microbiology OpenStax)

Depending on the species, 40 to 60 types of tRNA exist in the cytoplasm. tRNA carrying a specific amino acid binds to sequences on the mRNA template and adds the corresponding amino acid to the polypeptide chain. Therefore, tRNAs are the molecules that actually “translate” the language of RNA into the language of proteins.

How is it that tRNA translates the mRNA nucleotide sequence into protein? To answer this question, we must first understand the **genetic code**, the relationship between the nucleotide sequence and the different amino acids that make up a protein.

The Genetic Code

To summarize what we know to this point, transcription generates messenger RNA from the DNA housed in the nucleus of eukaryotic cells. The mRNA is a mobile complement of one or more genes. mRNA is generated using the nitrogenous bases adenine, cytosine, guanine, and uracil.

During translation the mRNA nucleotide sequence is used to generate a protein. Proteins can be made up of as many as 20 different amino acids. Each amino acid is defined by a three-nucleotide sequence called the triplet **codon**. The relationship between a nucleotide codon and its corresponding amino acid is called the genetic code. The three-nucleotide codon means that there is a total of 64 possible combinations (4^3), with four different nucleotides possible at each of the three different positions within the codon. This number is greater than the number of amino acids used to generate proteins. This means that some amino acids are encoded by more than one codon (Figure 10.31). This redundancy in the genetic code is called degeneracy. Typically, whereas the first two positions in a codon are important for determining which amino acid will be incorporated into a growing polypeptide, the third position, called the wobble position, is less critical. In many cases, if the nucleotide in the third position is changed, the same amino acid is still incorporated.

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

Figure 10.31 This figure shows the genetic code for translating each nucleotide triplet, or codon, in mRNA into an amino acid or a termination signal in a nascent protein. (credit: modification of work by NIH / Concepts of Biology OpenStax)

The codon AUG specifies the amino acid methionine and has a special function. AUG serves as the only **start codon.** The start codon is where a ribosome begins translation on that mRNA. Three of the 64 codons terminate protein synthesis and release the polypeptide chain from the ribosome. These triplets are called **stop codons;** they do not code for an amino acid. Once the stop codon is reached, no additional amino acids will be added to the polypeptide chain.

The genetic code is nearly universal. With a few exceptions, virtually all species use the same genetic code for protein synthesis. This is powerful evidence that all existing life on earth shares a common origin. However, there are some unusual amino acids such as pyrrolysine that have currently only been observed in archaea and bacteria. Research is being done to understand the relevance of this discovery.