Review Questions
Translation (protein synthesis)

1. What is the genetic code?

   The genetic code consists of a sequence of three letter "words" (called 'codons'), written one after another along the length of the DNA strand.

   Each codon is a unique combination of three letters (like the ones shown above and below) that will eventually be interpreted as a single amino acid in a polypeptide chain. There are 64 code words possible from an 'alphabet' of four letters.
One of these code words, several are know as “signal codons”. The “start codon” begins all the sequences that code for amino acid chains. The start codon also codes for the amino acid methionine (MET). Three of these signal codons act as “stop codons” that tell the translating machinery that the message is over. All the other codons code for specific amino acids.

Some amino acids are only coded for by a single codon (like tryptophan), while some others are coded for by up to six codons (like leucine). The redundancy of the genetic code is due to the fact that it is a triplet code. If the code worked as one base specifies one amino acid. Since there are only four bases, there could only be a code for four amino acids. But we have twenty! If a sequence of two bases coded for one amino acid, that could only be a code for 16 amino acids. Still not enough. But with a sequence of three bases coding for one amino acid, we have 64 combinations; more than enough to code all 20 amino acids.
2. Explain the central dogma.

The central dogma represents the flow of information from the gene in DNA to the final assemblage of the sequence of amino acids in a polypeptide. Since DNA is physically separated from the protein-making machinery, the information in a gene is first transcribed into a mRNA molecule. The mRNA travels to the ribosomes (organelles that build proteins) where the recipe is "translated" into a chain of amino acids. (see figure on next page and last page)

![Diagram of the Central Dogma](image)

**The Central Dogma of Molecular Biology**

Replication → DNA → Transcription → RNA → Translation → Protein

- **Transcription** is carried out by RNA polymerase
- **Translation** is performed on ribosomes
- **Replication** is carried out by DNA polymerase

3. Describe the players in translation.

The three players in translation are mRNA, tRNA, and a ribosome. The function of "Transfer RNA (tRNA)" is to bring amino acids to the ribosome to build a polypeptide. Transfer RNA binds to mRNA at the
ribosome. A tRNA molecule has two important spots on it: the amino acid attachment site and the anticodon (see figures below). The anticodon is a sequence of three bases that are complementary to a mRNA codon and will bind to it. There are 64 different kinds of tRNA molecules in a cell. Each type of tRNA has a specific anticodon that is complementary to one codon of the genetic code. For example, if you have the codon for phenylalanine on the mRNA (UUU), the tRNA that carries phenylalanine will have the anticodon (AAA), the complement of UUU (see figure below).

The function of the ribosome is to cradle the mRNA, assist the bonding the mRNA codons with their corresponding tRNA anticodons, form peptide bonds between the amino acids brought by the tRNA’s and detach the tRNA’s from the amino acids. Ribosomes are an abundant organelle found in all cells. Bacteria have them. Plants, animals, fungi, and protists all have them. A ribosome is the site of protein synthesis in a cell. A ribosome has two parts called subunits. When not translating, the small subunit is unattached to the large subunit. During translation, the small subunit will bond to the mRNA and the large subunit bonds to the small subunit cradling the mRNA between them. Each subunit is made of proteins and an RNA called ribosomal RNA (rRNA). The small subunit is smaller because it is built of a single rRNA whereas large subunit is built of two. (see figure below)

4. Describe the process of translation.
**Initiation**

In the cytoplasm, the small subunit of the ribosome binds to mRNA and the larger subunit binds to the small subunit. The large subunit has three tRNA binding site on it; E site, P site, and A site. (see figure below)

**Elongation**

A tRNA with the complementary anticodon enters the P site and binds to the start codon on the mRNA. (see figure below)

A second tRNA with a complementary anticodon enters the A site and binds to the second codon on the mRNA strand. (see figure on next page)

The two amino acids form a peptide bond. (see figure on next page)

Next, the first tRNA breaks off and moves to the E site leaving its amino acid attached to the second amino acid. (see figure below)

The second tRNA moves from the A site to the P site and the ribosome moves down one codon. (see figure below)

A third tRNA moves into the vacated A site and binds to the third codon in the sequence. (see figure below)

The second and third amino acids now bind together with a peptide bond. (see figure below)

The first tRNA leaves the E site and then out of the ribosome, the second tRNA detaches from the amino acids it was carrying and moves to the E site, the third tRNA moves to P site, the ribosome moves down one codon, and then the fourth tRNA enters the A site and binds to the fourth codon. (see figure below)

The process repeats itself each time growing the polypeptide one amino acid at a time. (see figure below)
Termimnation

When the ribosome gets to the stop codon, the last tRNA enters the A site. (see figure below)

Stop codons do not code for amino acids but code for a molecule called a release factor. The tRNA’s that correspond to these stop codons carry the release factor.

The amino acid from the tRNA in the P site cannot bond to the release factor. So when the tRNA in the P site detaches its amino acid bound to the polypeptide chain, the polypeptide has nothing to hold it and breaks free. (see figure below)

We have just translated the mRNA and made a polypeptide.

Lastly, the remaining tRNA’s leave the E and P binding sites and the subunits disengage from mRNA and each other. (see figure above)

Electron micrographs show that a whole train of ribosomes will descend onto a mRNA and translate it one after another. In bacteria, translation begins even before transcription has finished. (see figure below)
5. **Describe the process of mRNA editing. What is the purpose of Alternative RNA Splicing?**

In bacteria, you can sequence a raw polypeptide and then working backwards through the central dogma determine the gene in the DNA. However, in eukaryotic cells (animals, plants, fungi, protists), the raw polypeptides are often much shorter than the genes that coded for them. In fact, whole sections of a gene may not be translated at all. Eukaryotic cells have mRNA editing. Immediately after a gene is transcribed and before the mRNA leaves the nucleus, sections of the transcript are cut out (called introns) and the remaining sections (called exons) are spliced together and then moved to the ribosomes in the cytoplasm.

This unusual editing (also known as alternative RNA splicing) helps explain why we can make so many proteins (~100,000) with so few genes (~20,000). A single gene is edited differently each time it is transcribed can produce dozens of different proteins. (see figures below)

![Diagram of mRNA processing](image)