Protein synthesis- transcription


Figure 1

- mRNA is different from DNA in a few different ways. Firstly, when DNA uses deoxyribose as its sugar to form the backbone of the DNA strand, mRNA uses ribose instead. Secondly, DNA's alphabet of nucleotides includes adenine, cytosine, thymine, and guanine (A,C,G,T). mRNA's is the same except for it uses uracil in place of thymine, which makes its alphabet consist of A, C, G, and U.


Figure 2

- Transcription is a bit like a simplified version of DNA replication. It starts with the unwinding and unzipping of a DNA double helix, but instead of using the enzyme it did in replication its using RNA polymerase. This enzyme only unzips the section that it needs to read, and is shown in fig. 1. The next step in transcription (in fig. 2) is complementary base pairing of the nucleotides along the "sense strand" (only one side of the unzipped DNA carries the actual instructions on building proteins, so only the information from one side is important in this process). Once this is complete, the nucleotides that just lined themselves up create the mRNA's ribose backbone, shown in red pipe cleaner in fig. 3 and 4. This is done by the same RNA polymerase enzyme, represented by the fuzzy peach candy in all the photos. After the backbone is created and the nucleotides are covalently bonded to it, this RNA structure breaks apart from the original DNA sense strand (fig. 5) and is edited before it is ready to move onto the next step in the process of protein synthesis. The original DNA reforms its shape and is unaffected by this process (fig. 6)


Figure 3


Figure 4


Figure 5


Figure 6

- The model we made in class provided a very good medium for visualizing the process of transcription, especially when representing how the RNA joins and splits off from the DNA strand and seeing how the enzyme RNA polymerase makes its way through to unzip and carry out its other functions. What I think could have been improved in this model was how we showed the RNA leaving the nucleus. We weren't able to show how it was edited to remove any introns because of the materials we worked with, but overall, I found the model very helpful in my understanding of transcription.

Translation

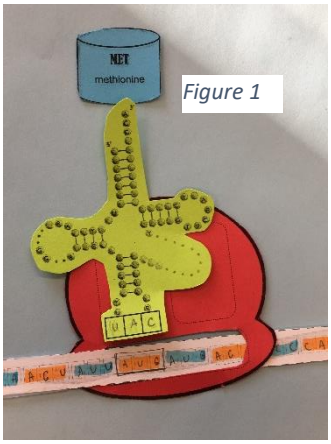

Figure 1

- Initiation- Translation begins when the small ribosome unit attaches to the mRNA strand reads the codon AUG. A tRNA carrying the anticodon for AUG (UAC) will go into place in the P site. The larger portion of the ribosome attaches on top of the smaller unit to complete the ribosome. In figure one the tRNA is carrying the amino acid methionine to start the chain that will eventually become a protein.

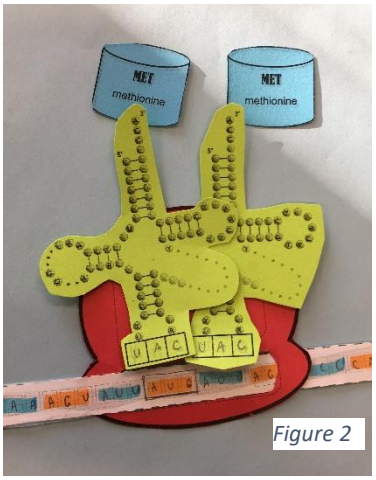

Figure 2

- Elongation- The codon aligned in the A site of the ribosome has a corresponding tRNA that carries a corresponding amino acid. This second tRNA comes into place to occupy the A site, as pictured in fig. 2. Now that both spots are filled, the tRNA in the P site can be released and floats away (fig. 3), and the amino acid it was carrying transfers over to the A site. Now, the RNA strand, the tRNA, and the start of the amino acid chain all shift over to the P position, to make room for a new codon and its corresponding tRNA to repeat this process many times over (fig. 4). The process is pictured here with only one ribosome, but on real sets of mRNA multiple ribosomes can work at the same time.

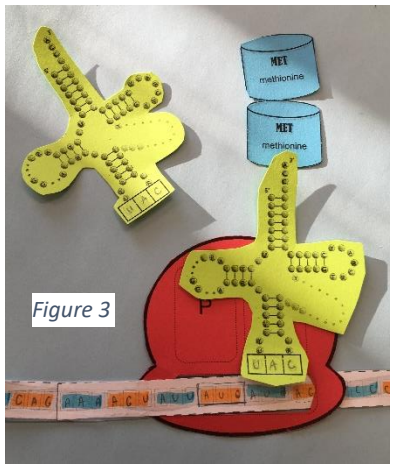

Figure 3

- Termination- The process of elongation continues until it encounters a codon that has no corresponding anticodon, also known as stop codons (UAG, UAA, and UGA are the three stop codons). When it encounters a stop codon, a release factor is put in place of a tRNA and releases the bond holding the last tRNA in the P site. Everything is released and floats away, and the chain of amino acids can now either start its function in its current state or become a full protein to do its job. In our model, our RNA strand didn't have a stop codon, so we were unable to fully demonstrate termination.
- The model helped me better understand how translation works, and in particular, the step of elongation. The hands-on use of pieces of paper made the movement of the mRNA strand on the ribosome, and the placement of the tRNA units clearer. What we weren't able to show with the medium we used was the 3D aspect, and one thing in particular I didn't understand with the model is where the anticodons and tRNA came from. (Were they formed specifically when the ribosome reads the codon or are they all floating around waiting to be called on?). But overall, using the paper model helped a lot in understanding and preparing for tests/ quizzes

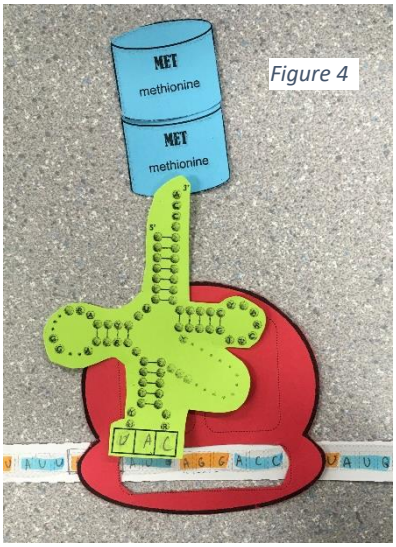

Figure 4