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Anatomy & Physiology 12
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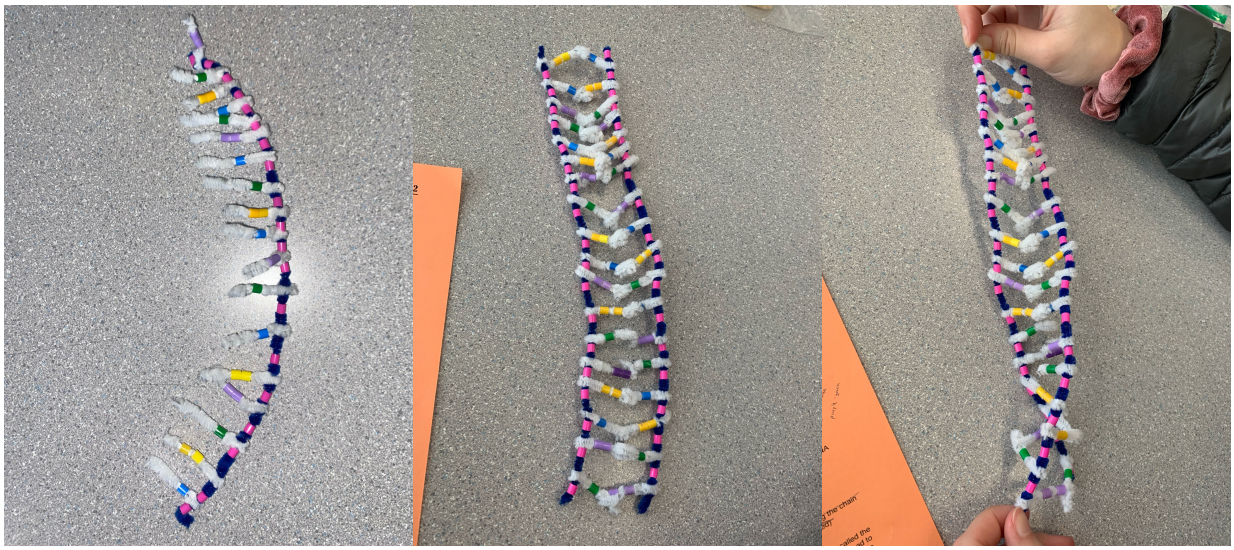
DNA and Protein Synthesis

DNA Model



1. The structure of Deoxyribose Nucleic Acid, commonly known as DNA, is made out of sugars called deoxyribose, phosphates, and nitrogen bases. It is a double helix shape that had twisted due to forces. The structure of DNA is that it is a large polymer made of nucleotide monomers. In the picture, it has two "backbones" which are formed by bonded sugar-phosphate portions of adjacent nucleotides in which the nucleotide bases face in towards the ladder. The bases always bond with the same partner- a purine and a pyrimidine. The pairs would be adenine (yellow) and thymine (blue), then guanine (purple) with cytosine (green). The two strands in DNA are described as antiparallel and complementary. Antiparallel strands are when the strands are "read" in opposite directions. Complementary base pairing is when the strands can give the same message- meaning that a purine must pair with a pyrimidine and vice versa.

2. This activity helped model the structure of DNA because it gave us a chance to physically build the 3D model of the DNA. Through this, we were able to visualize how the DNA would look like and how the bonds are paired since in real life, it would only be possible to view it under technology. It helped create an understanding of the more specific structures such as the backbones consisted of sugar and phosphate as well as the complementary bases. The coloured beads used to indicate the purines and pyrimidines as well as double or single ringed bases helped the understanding of the DNA molecule. Some changes that could be made to improve the accuracy of this model is for the white pipe cleaners to be more accurate in length in order for the double helix to be represented more clearly.

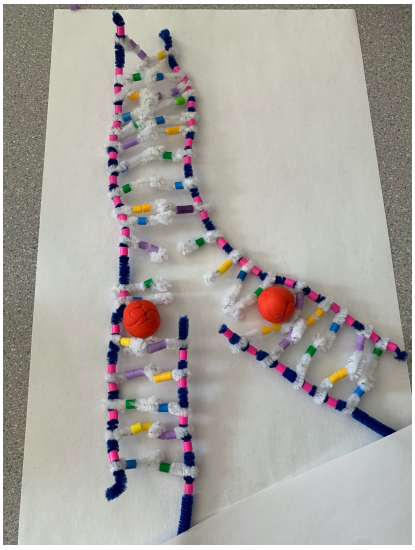
DNA Replication Model


1. DNA replication occurs when a DNA strand duplicates itself. It occurs prior to cell division and is a semi-conservative process, which is when each daughter DNA molecule contains one parent strand and one new strand; because each new DNA molecule contains one backbone from the original DNA strand.

2. The 3 Steps Involved in DNA Replication:
   *Note: For the images below, we realized that we had paired the purines and pyrimidines wrong

   a. Unwinding & Unzipping
      - In this step, the helix unwinds and the H-bonds between the base-pairs "break." This is due to an enzyme called the "DNA Helicase" that plays the role of a zipper and breaks the hydrogen bonds, causing the helix to unwind.

b. Complementary Base Pairing
   - After the helix has been unzipped by the DNA Helicase, the “DNA Polymerase” facilitates this step by starting to reconnect the nucleotides to their complementary base pair. In this step, the nucleotides are always present in the nucleus. Therefore, the nucleotides move into place and for H-bonds with their “partner” on the strand.



c. Joining
   - This step is when the nucleotides on the new strand form covalent bonds. The leading strand is continuous as the DNA “unzips.” However, the lagging strands are when fragments form as DNA “unzips” and DNA Ligase glues fragments.

3. We were able to model the complementary base pairing through nucleotides bonding with their complementary base. The H-bonds were shown by using white pipe cleaners, but we were unable to demonstrate the covalently bonded nucleotides. We used green playdough to show the DNA Helicase, used red playdough for the DNA Polymerase when modelling the complementary base pairing, and used blue playdough for the DNA Ligase when modelling the joining of adjacent nucleotides steps of DNA replication. This activity was well suited to showing this process in ways that it had given me the opportunity to see how the processes of DNA replication worked on a bigger scale. It was helpful because it gave us the opportunity to physically break and attach the bond ourselves- which gave us a better understanding of the roles of the different parts in the DNA since we were able to visualize the model better. In some ways, it was inaccurate due to small mistakes that we made in the beginning due to confusion but once a mistake is caught, it helped us learn more in depth about the structure since we had to figure out where we went wrong. As seen in the pictures above, the structures are very unstable and not straight- especially when we were trying to represent the helix models and tried to straighten the ladder after. Even though these were not an error, it would be good to find solutions to this for experiments after.