1. **Explain the structure of DNA**
   DNA is built from 2 sugar-phosphate backbones that are bonded with nucleotides. The backbones are antiparallel strands, which means that if the left strand starts with a phosphate (pink beads), the right strand will start with a sugar (blue pipe cleaner) and end with a phosphate. There are two groups of nucleotides: purines and pyrimidines. The purines are double-ringed structures and are named adenine (yellow beads) and guanine (purple beads). These should be modeled by 2 beads together to show the double ringed structure, but we forgot to do that part. The pyrimidines are single ring structures and are called thymine (blue beads) and cytosine (green beads). The nucleotides bond together in specific ways: adenine hydrogen bonds (white pipe cleaner) to thymine only and cytosine hydrogen bonds only with guanine. This is called complimentary based pairing. The hydrogen bonds between

2. **How does this activity help model the structure of DNA? What changes could we make to improve the accuracy of this model? Be detailed and constructive.**

This model gives us a hands-on way of seeing how DNA is structured and it shows us the technicality of it all. It helps us see the complimentary bases and the antiparallel lines clearly. To improve the accuracy of this model, the purines should have been modeled by 2 beads instead of 1, but that was a mistake made by our group. I think that we also could have used a more consistent material as the white pipe-cleaners were different sizes which makes it hard to create an easy double helix, so it would be better to use a material that is easy to twist. I also think that we should have made it a bit longer so the we can really the double helix shape, but that could also come from an easier twisting material.

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3. **When does DNA replication occur?**
   The replication of DNA occurs before the division of a cell. DNA replication needs to happen so that, when the cell splits, both cells have a copy of the same DNA.

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4. **Name and describe the 3 steps involved in DNA replication. Why does the process occur differently on the "leading" and "lagging" strands.**

The first step is called unwinding. During this phase, the DNA helicase enzyme (green play dough) causes the double helix shape of the DNA to unwind, then it "unzips," meaning that the hydrogen bonds between nucleotides break. The next step is complimentary base pairing. This is where nucleotides on the new strand come into place with their "partner" on the old strand: adenine always bonds with thymine and guanine always bonds with cytosine. This step is assisted by DNA Polymerase (orange play dough). The final step is joining. This is where the nucleotides form covalent bonds. The polymerase starts at the end of the strand that has the carbon three at the bottom and works its way up to the carbon five. On the leading strand, the polymerase starts at the carbon three at the end of the strand and keeps going continuously. Due to their anti-parallel strands, the other strand is "lagging," which means that it ends in a carbon five, so the polymerase has to work backwards. It will join a section, and then because there is more DNA unwinding, it has to jump forward and work its way back again. The result of this is two DNA molecules that have one new strand and one strand of the

old/parent DNA molecule and they are identical to each other and the parent DNA.

5. **The model today wasn't a great fit for the process we were exploring. What did you do to model the *complimentary base pairing* and *joining of adjacent nucleotides* steps of DNA replication? In what ways was this activity well suited to showing this process? In what ways was it inaccurate?**

This activity let us show complimentary base pairing fairly well by letting us use the different colour beads for each nucleotide. We knew and showed that blue always went with yellow and green always with purple, though when we were copying the copying the sequence of the nucleotides onto the new strand, we started at the top of the strand with the complimentary colours, but we really should have started near the end where we were starting with the joining aspect fof the replication. This could be more accurately shown, especially for the lagging strand, by having the blue backbone cut up so we could see how the polymerase has to work backwards and how it has to jump forward to the next area to join the bases. We were also able to show the hydrogen bonds between the nucleotides with the white pipe cleaners, though because the purines always bonds with pyrimidines to keep the same width throughout the DNA molecule, but in our model, the white pipe cleaner weren't all the same size, so we weren't able to o show that the DNA is the same width throughout. Using the play dough made it easy to see where the DNA helicase, ligase, and polymerase were and what they do.