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| **Section:** | BIOG.140.603 |  | **Due Date:** | 23-Apr-2025 |

**Data table.1:** **Step 1: Go to the AlphaFold Protein Structure Database.**

🌐 Link: <https://deepmind.google/technologies/alphafold/>

**Step 2: In the search bar, paste each UniProt ID from the table below (one at a time) to find the protein.**

**Step 3: Answer the data table below:**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| UniProt ID | Protein Name | Function | Sequence length | Picture of the protein |
| P01308 | Insulin | Regulates blood glucose levels by facilitating cellular glucose uptake; plays a key role in carbohydrate and lipid metabolism. | 110 amino acids |  |
| P69905 | Hemoglobin subunit alpha | Facilitates oxygen transport from the lungs to peripheral tissues by binding oxygen molecules. | 142 amino acids |  |
| P02452 | Collagen alpha-1(I) chain | Provides structural support in connective tissues; a major component of the extracellular matrix. | 1,464 amino acids |  |

**Data table.2:** **Step 1: Go to the using SnapGene Viewer.**

🌐Link: <https://www.snapgene.com/plasmids> .

**Step 2:**  **Search for one of the following plasmids: pUC19, pBR322, or pET28a**

**Step 3: Answer the data table below:**

|  |  |
| --- | --- |
| Question | Your Answer |
| What is the name of your chosen plasmid? | pUC19 |
| What antibiotic resistance gene does it have? | Ampicillin resistance gene (bla) |
| Is there a gene inserted? If yes, what gene? | No specific gene inserted; pUC19 contains a multiple cloning site (MCS) for gene insertion. |

1. **What are the advantages of using AI tools like AlphaFold to predict protein structures instead of only relying on experimental methods like X-ray crystallography or Cryo-EM?**

AI tools like AlphaFold can predict the 3D structure of a protein from its amino acid sequence in just a few minutes or hours, compared to experimental methods like X-ray crystallography or cryo-electron microscopy that take weeks or even months. These traditional methods are very precise but also expensive, time-consuming, and sometimes not possible if the protein is hard to crystallize or purify. AlphaFold allows researchers to skip some of those hurdles and get high-quality structural predictions faster, which means they can move on to analyzing protein function or drug interactions more quickly. It's like having a powerful shortcut to understand protein shape and behavior that can support or even guide future lab experiments.

1. **How could AlphaFold help scientists design new medicines or understand genetic diseases?**

AlphaFold has the potential to revolutionize drug discovery and our understanding of genetic diseases. By accurately predicting the 3D structure of proteins, scientists can identify how a protein functions and where potential drugs could bind. This structural information is essential for designing targeted treatments that interact with proteins in specific ways. Furthermore, AlphaFold helps researchers understand the effects of genetic mutations by showing how they change a protein's shape and possibly disrupt its function. This insight is especially useful for studying inherited diseases and for developing personalized medicine approaches based on an individual's genetic makeup.

1. **Do you think AI predictions are always accurate? What are some limitations or risks in using AI for scientific research?**

Although AI tools like AlphaFold are incredibly powerful, their predictions are not always 100% accurate. There are still limitations to consider. For example, proteins with flexible or disordered regions can be difficult to predict precisely, and AlphaFold’s accuracy may drop for proteins that don’t resemble those in its training data. Another risk is overreliance on AI without proper experimental validation, which can lead to incorrect conclusions. Additionally, the way AI reaches its predictions is sometimes difficult to interpret, which can be a problem when scientists need to understand the reasoning behind a result. Therefore, while AI is a valuable tool, it should be used in combination with experimental methods and scientific judgment.

1. **Why is it helpful to visualize DNA plasmids or gene maps using tools like SnapGene instead of reading the raw DNA sequence?**

Visualizing DNA plasmids or gene maps with tools like SnapGene is much more helpful than reading raw DNA sequences. Long sequences of A, T, C, and G are difficult to interpret, especially when looking for specific genetic features or planning cloning experiments. SnapGene allows users to see the structure of a plasmid, including genes, promoters, restriction sites, and other elements in a clear, visual format. This not only helps in understanding the design but also reduces the likelihood of errors during experiments. It makes genetic engineering more accessible and easier to communicate, especially for students or researchers working in teams.

1. **How do tools like AlphaFold and SnapGene change the way we learn biology and genetics in the classroom compared to 10 years ago?**

Tools like AlphaFold and SnapGene have dramatically changed how biology and genetics are taught in classrooms today compared to ten years ago. Instead of relying only on textbooks and static images, students now have access to interactive models and simulations that make learning more engaging and realistic. These tools allow learners to visualize complex structures and processes, making it easier to grasp challenging concepts. They also provide hands-on experience with the same types of software used in professional labs, which better prepares students for real-world research and careers in biotechnology. By making science more visual, accessible, and collaborative, these tools are transforming education in meaningful ways.