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| **Section:** | 60L1 |  | **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 | Insulin lowers blood sugar level and is used by the body to balance blood sugar levels. | 110 |  |
| P69905 | Hemoglobin subunit alpha | It is a protein in red blood cells that carries oxygen to cells and tissues throughout the body. | 142 |  |
| P02452 | Collagen alpha-1(I) chain | It is utilized as a structural component of cartilages and has an effect on joint laxity. | 1464 |  |

**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? | First-generation E. coli vector for DNA cloning. This plasmid has a low copy number (~20 copies per cell) due to the rop gene. |
| What antibiotic resistance gene does it have? | Contains two antibiotic resistance genes, ampicillin (Amp) and tetracycline (Tet) |
| Is there a gene inserted? If yes, what gene? | Yes, the gene bla encoding the ampicillin resistance (AmpR) protein, and the gene tetA encoding the tetracycline resistance (TetR) protein. |

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?

Ans. Advantages:

* Much faster than X-ray or Cryo-EM.
* Cheaper and doesn't need lab equipment.
* Can predict structures for many proteins, even hard-to-study ones.
* Helps fill in missing structure data.

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

Ans. AlphaFold can be useful in many fields. Knowing a protein's 3D shape helps researchers design molecules that fit and bind to it, like a key in a lock in drug design. AlphaFold shows how genetic mutations affect protein shape and function, which is essential for understanding genetic diseases in understanding mutations. It also helps identify potential drug targets on pathogens like viruses and bacteria in target identification.

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

Ans. AI predictions are powerful but not as perfect as we expect. Limitations include:

* Not always perfect, especially in flexible regions.
* Still needs experimental confirmation.
* Can be affected by data bias.
* Risk of over-relying on AI results.

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

Ans. It’s much easier to understand gene organization, plasmid structure, and insertions visually than by reading long DNA sequences. SnapGene shows antibiotic resistance genes, promoters and restriction sites clearly for identifying features. Scientists can simulate cloning, PCR and restriction digests, helping plan and troubleshoot experiments.

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

Ans. Tools like AlphaFold and SnapGene have made biology learning much more interactive and hands-on. Instead of just reading about genes or protein structures, students can now visualize and explore them using real scientific tools. This makes learning more engaging, realistic and easier to understand. It also prepares students for actual research work by exposing them to technologies used by professionals in the field.