Name:
Date:

WP3 – PyMOL Worksheet

Using the features available in PyMOL, answer the following questions about these proteins:

Human obesity protein, leptin
2m6z
1grj
1ubq

1. What is the PDBe code for the 'human obesity protein leptin'?
   1ax8

2. Looking at the secondary structure for this protein, how many α-helices are there?
   5

3. What is the main form of non-covalent bonding which gives the protein its overall structure?
   Hydrogen bonds hold the α-helices in place.

4. What would happen to the shape and structure of the protein if this bonding wasn't present?
   The protein would **lose its secondary structure**. The polypeptide chain would not stay in its current shape and would be **less rigid**. The chain itself **would not have as clear a defined shape**.

5. What would happen to the effectiveness of the protein to perform its function if this bonding wasn't present?
   The protein would **lose its shape**, and therefore it **wouldn't be able to effectively function** as it usually does. It would **lose any specificity** with other ligands and **wouldn't be able to effectively bind** to other molecules.

6. Looking at 2m6z, how many polypeptide chains are present?
   4

7. Does this protein have a quaternary structure?
   Yes, as it has **multiple polypeptide** tertiary structures which form the overall protein shape.

8. By using different types of representations, predict where ligands may bind to this structure. The two most useful representations to do this would probably be the cartoon and surface/mesh view, whilst colouring by chain.
   There appears to be a large site available in the centre of the protein, between the 4 polypeptide chains, and it would be easy to assume that a ligand could bind there. However, for this protein it is not the case. This is a hemoglobin structure, and binds **four heme units**, one to each polypeptide chain. If you look carefully at the surface view of the protein, then

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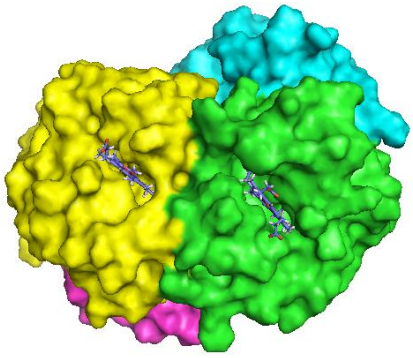
you will see a **small groove on the surface of each chain**, which is where the heme ligand binds. If a heme ligand tried to bind in the centre of the structure, then the site wouldn't be specific enough, it is essentially too big. A key idea to take from this is that the binding site depends very much on the ligand, it must have a complementary shape, with complementary interactions to hold it in place.



9. How many separate α-helices and β-strands are in the protein 1grj? – Be careful, it might help to colour by secondary structure!
   7 α-helices, 6 β-strands

10. Which two other secondary structural features are present?
    β-sheets and β-loops

11. For 1ubq, write a short description of the protein. Include what you know about its secondary structure, the number of each type of secondary structure, and the effect of hydrogen bonding on it. What would happen to this protein's structure without hydrogen bonding? Does this protein have a quaternary structure? What is its name on the PDBe website?
    1ubq is a **relatively small protein**. It has a primary structure of **76 amino acids**. Its secondary structures include **2 α-helices**, and **5 β-strands** arranged into **2 anti-parallel β-sheets**, as well as some **β-loops** which help the β-strands reverse their direction. These **secondary structures** are held together by **hydrogen bonds** which force the α-helices into coils, and align the β-strands into β-sheets. This arrangement of **secondary structures folds**, again with the help of hydrogen bonds, to form a **specific tertiary structure**. Without the hydrogen bonding in the protein, the polypeptide chains would lose their rigidity, and the protein wouldn't have its specific tertiary structure, which is key for its biochemical functions. This protein, ubiquitin, **doesn't have a quaternary structure**, as it is just **one long polypeptide chain**. A quaternary structure occurs when there are multiple polypeptide chains which form a macromolecular structure.

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