

- I. Open the PDB file of the myoglobin protein with PDB ID: 1MBN in the Pymol visualization software and answer the following questions.
- The heme group occupies the pocket between the following alpha helices
 - Alpha helices 1, 2, 3, 4
 - Alpha helices 2, 3, 4, 5**
 - Alpha helices 3, 4, 5, 6
 - Alpha helices 4, 5, 6, 1
 - Consider the 3 residues A90, Q91 and S92. The phi and psi angles measured about the C-alpha atom of Q91 are:
 - 77, -56.1
 - 178.1, -50.9
 - 77, -58.5
 - 58.5, -56.1**
 - The helix structure which is the longest contains the following number of amino acids:
 - 16
 - 21
 - 26**
 - 39
 - Which of the following sequence of this protein is the longest unstructured loop?
 - F43 – K50**
 - S92 – L104
 - L77 – P88
 - T95 – I99
- II. Go to the KEGG data base and find the Lysine biosynthesis pathway “00300” under amino acid metabolism and answer the following questions.
- Considering only the forward directions for the reactions (some are bi-directional, in which case, only take the forward direction), the total number of metabolic pathways leading to Lysine synthesis from L-aspartate are
 - 2
 - 3
 - 4**
 - 5
 - Starting from L-aspartate, the last enzyme responsible for the synthesis of lysine is
 - Diaminopimelate decarboxylase**
 - Aminopimelate carboxylase
 - Saccharopine dehydrogenase
 - Meso-2,6-diaminoheptanedioate
 - The specific activity of this enzyme in *E. coli* is possibly

- a. 0.008 $\mu\text{mol}/\text{min}/\text{mg}$
- b. 0.209 $\mu\text{mol}/\text{min}/\text{mg}$
- c. **7.5 $\mu\text{mol}/\text{min}/\text{mg}$**
- d. 28.3 $\mu\text{mol}/\text{min}/\text{mg}$