

I. Open the PDB file of the myoglobin protein with PDB ID: 1PKN in the Pymol visualization software and answer the following questions.

1. The metal ions bound to this protein are
  - a. **Mn<sup>2+</sup> and K<sup>+</sup>**
  - b. Ca<sup>2+</sup> and K<sup>+</sup>
  - c. Na<sup>+</sup> and K<sup>+</sup>
  - d. Mn<sup>2+</sup> and Ca<sup>2+</sup>
2. The following statement for the sequence from Thr44 to Asn44 is correct
  - a. It is a super secondary structure: alpha – alpha – beta
  - b. **It is a super secondary structure: beta – alpha – beta**
  - c. It is a secondary structure: alpha
  - d. It is a secondary structure: beta
3. The total number of helix structures in this protein are:
  - a. 15
  - b. 16
  - c. **17**
  - d. 18
4. The following function is most likely correct for this protein
  - a. It generates Mn<sup>2+</sup>, Ca<sup>2+</sup> for the cells
  - b. It generates Ca<sup>2+</sup> for the cells
  - c. It reduces acetyl- CoA to pyruvate
  - d. **It converts pyruvate to phosphoenol pyruvate**

II. Open the PDB file of the myoglobin protein with PDB ID: 3FK8 in the Pymol visualization software and answer the following questions.

5. Which one of the following statements about the beta conformation is correct?
  - a. There are 2 beta sheets of size 7 and 6 amino acids
  - b. **There are 2 beta sheets of size 6 amino acids each**
  - c. There are 4 beta sheets arranged as beta-loop-beta motifs
  - d. There are 4 beta sheets arranged as the beta-loop-helix motifs
6. The helix structure which is the longest contains the following number of amino acids:
  - a. 16
  - b. 22
  - c. **24**
  - d. 25
7. Which of the following sequence of this protein is the longest unstructured loop?
  - a. **F43 – K50**
  - b. S92 – L104
  - c. L77 – P88
  - d. T95 – I99

III. Go to the KEGG data base and find the Carbon Metabolism pathway "01200" and within this consider "Glycolysis" pathways M00001 and M00002 and answer the following questions.

8. The total number of intermediates including the starting and ending compounds are:

- a. 9
- b. 10
- c. **11**
- d. 12

9. The intermediate Fructose-1,6-P<sub>2</sub> is important because

- a. It produces two six carbon molecules leading to pyruvate
- b. **It produces two 3-carbon molecules leading to pyruvate**
- c. It produces sedoheptulose-1,7-P<sub>2</sub>
- d. It produces ribose-5-P

10. The specific activity of the enzyme converting phosphoenol pyruvate to pyruvate in the liver of *Homo sapiens* is possibly (go to BRENDA)

- a. 280  $\mu\text{mol/min/mg}$
- b. 300  $\mu\text{mol/min/mg}$
- c. 320  $\mu\text{mol/min/mg}$
- d. **420  $\mu\text{mol/min/mg}$**

11. Part of a sequence of a protein is given below

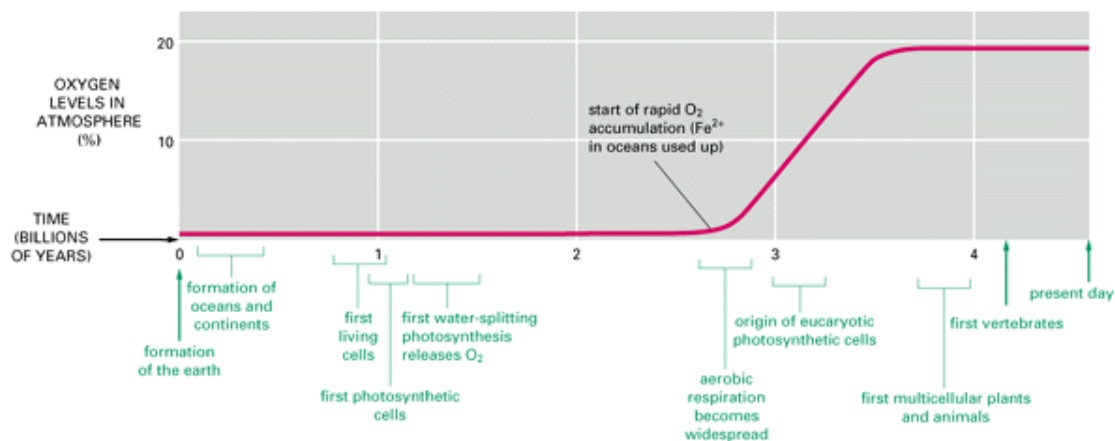
-Pro-Trp-Asp-Glu-Tyr-Leu-Leu-Ser-Thr-Phe-Pro-Arg-Arg-Asp-Val-Thr-Gln-Ser-Asp-

The segment that is most likely to form a beta turn is following:

- a. Ser-Thr-Phe-Pro
- b. **Thr-Phe-Pro-Arg**
- c. Phe-Pro-Arg-Arg
- d. Pro-Arg-Arg-Asp

12. A protein has a sequence of 365 amino acids. It has 10 cysteine residues that make 5 di-sulphide bonds to stabilize the protein. This protein is denatured by heat treatment to the point where it just loses all its secondary structure. This protein is then re-natured to bring it back to its native conformation. Theoretically, the total number of ways this protein could form di-sulphide bonds is:

- a. 45
- b. 105
- c. 120
- d. **945**



13. The creation of an oxygen-rich atmosphere on planet earth occurred between 2.5 – 3.5 billion years. It converted the then existing anaerobic atmosphere to the oxygen rich atmosphere as we find it today. One of the most probable reasons driving this change is:
- Prokaryotic cells evolved into eukaryotic cells
  - Utilization of the simplest carbon molecule glucose for energy
  - Selective advantage gained by organisms able to utilize carbon and nitrogen atoms directly from the atmosphere**
  - Predator-prey relations that led to endo-symbiosis
14. The Ramachandran plot is the representation of the phi-psi angles of proteins. The following application of the Ramachandran plot is correct.
- Predicting the region for glycine phi-psi angles
  - Predicting the region of the zero angles of new peptides
  - Validation the super-secondary structures of proteins
  - Validation of protein structures**
15. The codon of the genetic code consists of triplets of RNA bases that codes for a specific amino acid. The triplet code is non-overlapping. On this basis following statement regarding mutations is correct.
- An insertion of a base in the coding region alters the entire protein sequence**
  - A change in the base occurring in the coding region alters the entire protein sequence
  - An insertion followed by a subsequent deletion in the coding region alters the entire protein sequence
  - An insertion of a base in the coding region is auto-corrected and does not affect the protein sequence