Enrolment no..... *Roll no*.....

Date: .....

Examination: B.Sc. (Toxicology), - Semester V semester (2023)
Paper: Computational Toxicology, Code: BTX-CC-07(P)

Time: **30 min** MM: 20

This Q paper contains 2 questions, each of 10 marks.

Q1. Choose the correct answer of the following questions **[1×10= 10]**

i. STRING is a _____
   a) software b) computer language c) database d) statistical tool

ii. Protein-protein interaction network contain nodes representing
   a) DNA b) RNA c) Protein d) none of these

iii. Functional enrichment in STRING network **does not** include the following
   a) Biological process b) Reactome pathways c) Molecular functions d) Proteomic profile

iv. In molecular docking, better protein structure from PDB should have _____ number of amino acids residues?
   a) minimum b) maximum c) optimum d) any

v. How should be the resolution of protein structure used in molecular docking?
   a) minimum b) maximum c) optimum d) any

vi. During the process of protein preparation in molecular docking, water molecule are _____.
   a) added b) removed c) arranged in order d) not disturbed.

vii. Instadock is a _____.
   a) software b) computer language c) database d) statistical tool RMSD

viii. What is the purpose of molecular docking?
   a) To check the fate of test molecule in the body
   b) To check the interaction of test molecule with protein
   c) To check the bond strength of test molecule
   d) To check the reactions of test molecules with the protein

ix. What is the application of molecular docking in toxicology?
   a) To find the toxic effect of xenobiotics
   b) To find out the potential target of xenobiotics

c) To find out the pathogenesis of toxic effect of xenobiotics
d) None of these

Q2. Write a short note on any 5. **[2×5= 10]**

i. STRING
ii. PDB
iii. Steps of protein preparation for molecular docking
iv. Molecular docking
v. PubChem
vi. Selection of best protein structure from PDB