



DK-003-006402

Seat No. _____

**Second Year B. Sc. (Bio. Info.) (CBCS) (Sem. IV)
Examination**

April / May – 2015

BI-402 : Structural Bioinformatics

Faculty Code : 003

Subject Code : 006402

Time : $2\frac{1}{2}$ Hours]

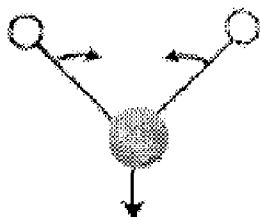
[Total Marks : 70

PART-A

Attempt MCQ:

20

1 Identify the vibrational mode.



- (a) Rocking (b) Twisting
(c) Wagging (d) Scissoring

2 _____ represents a distinct protein sequence and its natural or artificial variants in SCOP.

- (a) Protein (b) Species
(c) Class (d) Domain

3 In distance matrix, each matrix position represents distance between

- (a) Corresponding Ca atoms in sequence
(b) Corresponding Ca atoms in 3D structure
(c) Bond angles of nearby atoms
(d) R groups of nearby amino acids

- 4 Which tool should I use for structure superposition?
- (a) Rasmol
 - (b) Chime
 - (c) Jmol
 - (d) Swiss-PDB Viewer
- 5 PSIPRED is based on
- (a) Chou Fasman method
 - (b) GOR method
 - (c) Neural Network based method
 - (d) Nearest neighborhood method
- 6 What is the window length generally taken by secondary structure predictors?
- (a) 8-10
 - (b) 10-15
 - (c) 13-17
 - (d) 20-26
- 7 The general assumptions in ab initio methods are that:
- (a) The tertiary structure of a protein is uniquely determined by its amino acid sequence.
 - (b) The native ensemble of protein conformations will fall around a global free-energy minimum for that sequence.
 - (c) Both
 - (d) None of above

- 8 Which tool is considered as the most comprehensive tool for mitochondrial protein localization prediction?
- (a) TMHMM
 - (b) PSORTb
 - (c) MitoProt
 - (d) TargetP
- 9 Which method is used for protein domain analysis?
- (a) Multiple sequence alignment
 - (b) HMM
 - (c) Neural Network
 - (d) All of above
- 10 If the bond angles, bond lengths and torsion angles of the components are not modified at any stage of complex generation, it is known as _____.
- (a) Rigid body docking
 - (b) Flexible docking
 - (c) Hybrid docking
 - (d) Cooperative docking
- 11 Gel Retardation assay is used for
- (a) Protein protein interaction
 - (b) Protein nucleic acid interaction
 - (c) Protein docking
 - (d) ligand docking
- 12 GlobPlot is a tool used for
- (a) Protein stability prediction
 - (b) Protein localization
 - (c) Pocket prediction
 - (d) Protein globularity prediction

- 13 Which method is used for protein-protein interaction study?
- (a) Yeast two hybrid
 - (b) Chromatography and MS
 - (c) Gene fusion and Phylogeny
 - (d) All of above
- 14 CAPRI is related to
- (a) structure prediction
 - (b) protein-protein interaction study
 - (c) localization prediction
 - (d) QSAR
- 15 _____ first summarize a supposed relationship between chemical structures and biological activity in a data-set of chemicals.
- (a) DOCK
 - (b) AMBER
 - (c) QSAR
 - (d) Rosetta
- 16 All amino acid residues in protein are remarkably in
- (a) L-configuration
 - (b) D-configuration
 - (c) Both
 - (d) None
- 17 _____ is responsible for the formation of disulfide bridge.
- (a) Methionine
 - (b) Cystein
 - (c) Tryptophan
 - (d) Alanine

- 18 Which bond is rigid and planner in protein?
- (a) Peptide bond
 - (b) Psi bond
 - (c) Phi bond
 - (d) All of above
- 19 An "oil drop with a polar coat" is a metaphor referring to the three dimensional structure of:
- (a) fibrous proteins
 - (b) collagen
 - (c) globular proteins
 - (d) silk protein
- 20 X-rays provides the best resolution because
- (a) X-rays are easily produced
 - (b) Wavelength of X-rays is much more
 - (c) Wavelength of X-rays is about the same length of covalent bond
 - (d) Energy is lower than infrared

PART-B

- 1 (a) Explain any Three : **6**
- (1) Protein domain
 - (2) Flexible docking
 - (3) Gel retardation assay
 - (4) Gene fusion
 - (5) Ab initio method
 - (6) Combinatorial Chemistry

- (b) Explain any Three **9**
- (1) Protein localization prediction
 - (2) Phylogenetic profile method for protein-protein interaction
 - (3) Post translational modification prediction
 - (4) Modification interference
 - (5) Protein-protein docking
 - (6) What are the problems in experimental determination of protein structure
- (c) Attempt any Two **10**
- (1) Protein ligand docking
 - (2) Yeast two hybrid approach
 - (3) Homology modeling
 - (4) QSAR
 - (5) IR Spectroscopy
- 2** (a) Explain any Three **6**
- (1) Protein folding
 - (2) Turn or loops
 - (3) Architecture of protein
 - (4) SCOP
 - (5) Double Dynamic Programming
 - (6) Rational Drug designing
- (b) Explain any Three **9**
- (1) Super secondary structures
 - (2) Forces responsible for protein folding
 - (3) Vibrational modes in IR Spectroscopy
 - (4) SPDBV
 - (5) CATH
 - (6) Quaternary structure of Protein

(c) Attempt any Two

10

- (1) Distance matrix method for structure alignment
 - (2) Fold recognition
 - (3) X-Ray cryallography
 - (4) Protein Secondary Structure Prediction
 - (5) How can you predict pockets and Post translational Modifications.
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