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NBG-003-006402 Seat No. _____

B. Sc. (Bioinformatics) (Sem. IV) (CBCS) Examination

April / May - 2017

BI - 402 : Structural Bioinformatics

(Old Course)

Faculty Code : 003

Subject Code : 006402

Time : **2½** Hours] [Total Marks : **70**

Instructions : (1) All questions are compulsory.

(2) The right side figure indicates total marks of the question.

SECTION – I

1 Answer the short answer questions : **20**

(1) _____ first summarize a supposed relationship between chemical structures and biological activity in a data-set of chemicals

(2) All amino acid residues in protein are remarkably in _____ configuration.

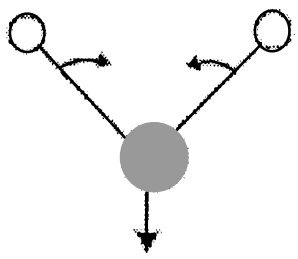
(3) _____ amino acid is responsible for the formation of disulfide bridge.

(4) Which bond is rigid and planner in protein?

(5) An "oil drop with a polar coat" is a metaphor referring to the three-dimensional structure of _____,

(6) X-rays provides the best resolution because Wavelength of X-rays is about the same length of _____ bond

(7) Identify the vibrational mode in the following molecule



(8) Globplot is a tool used for _____ prediction

(9) Which method is used for protein-protein interaction study?

(10) CAPRI is related to _____ interaction study

(11) _____ represents a distinct protein sequence and its natural or artificial variants in SCOP

(12) In distance matrix, each matrix position represents distance between _____

(13) Which tool can be used for both structure visualization and superposition?

(14) PSIPRED work based on _____ based method

(15) What is the window length generally taken by secondary structure predictors?

(16) What are the general assumptions in *ab initio* methods?

(17) Which tool is considered as the most comprehensive tool for mitochondrial protein localization prediction?

(18) Which method is used for protein domain analysis?

(19) 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 _____

(20) Gel Retardation assay is used for _____ interaction

SECTION – II

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) Vibrational modes in IR Spectroscopy

(2) SPDBV

(3) CATH

(4) Quaternary structure of Protein

(5) Super secondary structures

(6) Forces responsible for protein folding

(c) Attempt any **Two** : **10**

(1) Distance matrix method for structure alignment

(2) Fold recognition

(3) X-Ray Crystallography

(4) Protein Secondary Structure Prediction

(5) How can you predict pockets and Post translational Modifications?

3 (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) Post translational modification prediction

(2) Modification interference

(3) Protein-protein docking

(4) Protein localization prediction

(5) Phylogenetic profile method for protein-protein interaction

(6) What are the problems in experimental determination of protein structure

(c) Attempt any **Two** : **10**

(1) IR Spectroscopy

(2) Protein ligand docking

(3) Yeast two hybrid approach

(4) Homology modeling

(5) QSAR