

COMPUTATIONAL BIOLOGY
(BIOT 4221)

Time Allotted : 2½ hrs

Full Marks : 60

Figures out of the right margin indicate full marks.

*Candidates are required to answer Group A and
any 4 (four) from Group B to E, taking one from each group.*

Candidates are required to give answer in their own words as far as practicable.

Group – A

1. Answer any twelve:

12 × 1 = 12

Choose the correct alternative for the following

- (i) Examples of non polar amino acids are
 - (a) Glutamic acid and Aspartic acid
 - (b) Glycine and Leucine
 - (c) Histidine and Lysine
 - (d) Methionine and Lysine
- (ii) The repeating unit of protein is
 - (a) Glucose
 - (b) fatty acid
 - (c) Amino acid
 - (d) Glycerol
- (iii) The Henderson-Hasselbalch Equation is represented as
 - (a) $pK_a = pH + \log_{10}([HA]/[A^-])$
 - (b) $pH = pK_a + \log_{10}([HA]/[A^-])$
 - (c) $pH = pK_a + \log_{10}([A^-]/[HA])$
 - (d) $pK_a = pH + \log_{10}([A^-]/[HA])$
- (iv) A comprehensive database for the study of human genetics and molecular biology is
 - (a) PDB
 - (b) STAG
 - (c) OMIM
 - (d) PSD.
- (v) Which one of the following is not a primary protein database?
 - (a) GenBank
 - (b) PDB
 - (c) PIRT
 - (d) TREMBL
- (vi) Find the odd one out for -Philosophy of development of LINUX is to
 - (a) Ready to run programs
 - (b) It is free and open-source, accessible to everyone.
 - (c) This promotes global collaboration and innovation.
 - (d) It offers efficient performance and strong security.
- (vii) Which variable can give the concrete form to the representation of the transition model?
 - (a) Single variable
 - (b) Discrete state variable
 - (c) Random variable
 - (d) Both Single and Discrete state variable.

- (viii) In the design of the OpenMM the API must support
 - (a) efficient implementations on a variety of architectures
 - (b) non implementations on a variety of architectures
 - (c) formation of a variety of architectures
 - (d) Efficient implementations on a variety of variables.
- (ix) Which condition is correct according to the growth of cells in beginning?
 - (a) Cells are in small amount
 - (b) Cells are negligible in amount
 - (c) Cells are in medium amount
 - (d) Cells are in large amount
- (x) Which of the following method used for virtual screening
 - (a) ADMET analyses
 - (b) QSAR modeling
 - (c) Pharmacophore modelling
 - (d) All of the above

Fill in the blanks with the correct word

- (xi) In a DNA, the nucleotides are joined by _____ linkages.
- (xii) _____ is a repository for the 3-dimensional structure data for large biomolecules.
- (xiii) Python supports the creation of anonymous functions at runtime, using a construct called _____.
- (xiv) Template based protein modeling techniques is called as _____.
- (xv) Energy minimization of a modeled protein can be done using _____.

Group - B

- 2. (a) State the Link reaction. [[CO2](Analyse/IOCQ)]
 (b) Enumerate the characteristics of Codons. [[CO2](Remember/IOCQ)]
 (c) Enumerate the structure and function of steroids. [[CO1](Apply/IOCQ)]
4 + 4 + 4 = 12
- 3. (a) Enumerate the Okazaki fragments? [[CO2](Remember/LOCQ)]
 (b) Explain the statement –“Amino acids exist as zwitterions in physiological condition”. [[CO1](Analyse/IOCQ)]
 (c) Explain the statement –“Antiparallel β-sheets are more stable as compared to Parallel β-sheets”. [[CO1](Analyse/IOCQ)]
4 + 4 + 4 = 12

Group - C

- 4. Write the short notes on the following databases: Swissprot, PIR, PDB. [[CO3](Remember-understand/LOCQ)]
(4 × 3) = 12
- 5. (a) Define motif. Name 2 databases which contains this type of data. [[CO3](Remember-understand/LOCQ)]

- (b) Mention two secondary databases that can classify protein according to their structure and describe about them. [[CO4](Remember-understand/LOCQ)]
- (c) Analyse the significance of PRINT and PROSITE databases. [[CO4](Remember-understand/IOCQ)]
- (2 + 2) + (2 + 4) + 2 = 12**

Group - D

6. (a) Write short notes on steepest descent method and conjugate gradient method. [[CO5](Remember/IOCQ)]
- (b) Mention the steps followed in comparative modeling for the prediction of 3D structure of target proteins. [[CO5](Remember/LOCQ)]
- (c) Name any one software which are followed for this case. [[CO5](Apply/IOCQ)]
- (4 + 4) + 3 + 1 = 12**
7. (a) Define pattern. [[CO6](Remember/LOCQ)]
- (b) Classify pattern and analyse the areas briefly where pattern recognition technique is used. [[CO6](Remember-analysis/HOCQ)]
- (c) Mention two tools which are based on this pattern analysis [[CO6](Remember-analysis/IOCQ)]
- 2 + (4 + 4) + 2 = 12**

Group - E

8. (a) What is metabolic engineering? Mention the fundamental requirements for metabolic engineering. [[CO4](Remember/LOCQ)]
- (b) Different approaches can be used to study metabolic engineering - Discuss these approaches with examples. [[CO4](Remember/HOCQ)]
- (2 + 4) + 6 = 12**
9. (a) Write in short the basic steps of drug discovery. [[CO6](Describe/IOCQ)]
- (b) Justify the reasons of trials in drug discovery process. [[CO6](Examine/HOCQ)]
- (c) State the application of drug discovery. [[CO6](Analyse/IOCQ)]
- 5 + 3 + 4 = 12**

Cognition Level	LOCQ	IOCQ	HOCQ
Percentage distribution	29.17	53.12	17.71

