2016

BIOTECHNOLOGY

BIT 402
COMPUTATIONAL BIOLOGY

Full Marks : 80
Time : 3 Hrs

Figures in the right hand margin indicate full marks for the question

1. Match the followings in column X with appropriate items in column Y: (any five)   5×1=5

Column X			Column Y
1.a	COBALT	A	protein families and domains resources
1.b	DIALIGN	B	Family and domain database search
1.c	InterProScan	C	Performs protein multiple sequence alignments
1.d	Jpred	D	Local multiple sequence aligment software
1.e	PANDITplus	E	Secondary Structure Prediction Server
1.f	PROF	F	protein physical and chemical parameters
1.g	ProtParam	G	Secondary Structure Prediction System

2. State whether the following statements are true or false (any five)   5×1=5

A. Zn-finger motif is ten to twenty amino acids long.
B. Domain consists of more than 40 residues and up to 700 residues.

1   **P.T.O.**

C. PRINTS is a amino acid sequence alignment tool.
D. SMART is a database.
E. Reverse PSI-BLAST is a protein structure analysis tool.
F. COG is a server.
G. The dihedral angle along the N–Cα bond in an amino acid is defined as phi (φ) angle.

3. Define (any five)-   2×5=10
A. Genome Sequencing
B. Genome Annotation
C. SAGE
D. DNA microarray
E. Protein Microarrays
F. Identification of Posttranslational Modifications in Proteomic Analysis
G. PROTEIN SORTING

4. Differentiate between (any three)-   3×5=15
A. SCOP and CATH
B. SAGE and DNA Microarrays
C. PSI-BLAST and PHI-BLAST
D. Homology modeling and Thread Recognition
E. Transcriptome and Metabolome

5. Answer the following questions (any three)   3×15=45
A. Describe the secondary structure prediction method for globular proteins. What are the applications of protein secondary structure prediction?   10+5=15
B. What are the two prediction methods used for Secondary Structure of RNA. Discuss any one of them.   2+13=15
C. Describe the methods of Computer Aided Drug Designing.   15
D. What are the techniques used to investigate Protein– Protein Interactions? Describe briefly.   15

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