PARUL INSTITUTE OF APPLIED SCIENCES
MID SEMESTER INTERNAL EXAMINATION, March 2020

B.Sc. Biotechnology   **Semester IV**

Paper Name: Bioinformatics - I   **Date: 03/03/2020**

Paper Code: 11102255   **Time: 1hr 30min**

Max. Marks: 40

Instructions:

1. All questions are compulsory and options are given in first and second question only.
2. Numbers to the right of question indicate the marks of respective question.

Q. 1	Attempt any one question of the following. (i) Describe history of Bioinformatics (ii) Decipher Genbank and its data mining to public domain	**(08)**
Q. 2	Attempt any three questions of the following. (i) NCBI and its access to public domain. (ii) PDB and its different domains. (iii) EMBL and its different operational sites in European country. (iv) Different file formats in Bioinformatics (v) PAM matrix with example	**(12)**
Q. 3	Do as directed. Attempt all five questions. (i) DDBJ & PIR (ii) Ig BLAST & Vect BLAST (iii) Pairwise alignment (iv) Mutations and its types (v) ftp site	**(05)**
Q. 4	Write correct option in your answer sheet for following 15 multiple choice questions.	**(15)**

MCQ 1	dbEST is a part of			
	(A)	NCBI	(B)	ENA
	(C)	DDBJ	(D)	None
MCQ 2	The headquarter of EMBL in----------------------			
	(A)	Hinxton	(B)	Heidelberg
	(C)	Rome	(D)	Grenoble
MCQ 3	MIPS related to			
	(A)	DNA	(B)	Protein
	(C)	RNA	(D)	None
MCQ 4	NCBI is maintained by			
	(A)	INSD	(B)	DDBJ
	(C)	NIH	(D)	None
MCQ 5	NCBI is -----------------database			
	(A)	Primary	(B)	Composite
	(C)	Secondary	(D)	All
MCQ 6	Homologous database is			
	(A)	TAIR	(B)	PlasmoDB
	(C)	Hovergen	(D)	GeneDB

MCQ 7	Indels are			
	(A)	Mutations	(B)	Substitutions
	(C)	Inversion	(D)	None
MCQ 8	Needleman-Wunsch algorithm use ------------------alignment			
	(A)	Local	(B)	Both
	(C)	Global	(D)	None
MCQ 9	MSA software			
	(A)	EMBOSS	(B)	Clustal Omega
	(C)	MUSCLE	(D)	All
MCQ 10	Cross-diagonal represents			
	(A)	Similar sequences	(B)	Inversion sequences
	(C)	Connecting sequences	(D)	Palindromic sequences
MCQ 11	BESTFIT program used for			
	(A)	Local alignment	(B)	Dot matrix
	(C)	Homologous sequences	(D)	None
MCQ 12	Match, Mis-match and Gap includes in			
	(A)	Needleman-Wunsch algo.	(B)	Smith – Waterman algo.
	(C)	Both	(D)	None
MCQ 13	Most used PAM is			
	(A)	1	(B)	150
	(C)	250	(D)	100
MCQ 14	BLOSUM used for			
	(A)	Homologous sequences	(B)	Heterologous sequences
	(C)	Distantly related	(D)	All
MCQ 15	Lethal mutations are			
	(A)	Natural	(B)	Continuous
	(C)	Artificial	(D)	None

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