Registration No : | | | | | | | | | | |

Total Number of Pages : 02 **B.Tech.**
PBT6I102

6th Semester Regular Examination 2017-18
BIOINFORMATICS
BRANCH : BIOTECH
Time : 3 Hours
Max Marks : 100
Q.CODE : C204

Answer Part-A which is compulsory and any four from Part-B.
The figures in the right hand margin indicate marks.

Part – A (Answer all the questions)

Q1. **Answer the following questions : *multiple type or dash fill up type :*** **(2 x 10)**

a) PAM matrix is formulated by _____.

b) DDBJ is _____.

c) Swissprot is a _____ database.

d) OMIM is _____.

e) MCQ: Promoter is required for
i) Transcription ii) Translation
iii) Replication iv) Signal Transduction

f) NCBI is funded by _____.

g) MCQ: If you want to BLAST the non-redundant nucleotide database using a new protein sequence as query, which is the BEST search program to use?
i) blastp, ii) blastn,
iii) tblastx, iv) blastx,
v) blastq

h) A multiple sequence alignment of related genes can identify amino acids required for protein function (True/False)

i) The method most suitable for finding conserved region in sequences.
i) Pairwise alignment ii) multiple alignment
iii) local alignment iv) Global alignment

j) _____ is a protein tertiary structure predicting software.

Q2. **Answer the following questions : *Short answer type :*** **(2 x 10)**

a) Define ORF.

b) What is local alignment?

c) What are Log-odd values?

d) What is KEGG?

e) What is the significance of R value in a PDB file?

f) What is protein threading?

g) What do you mean by force field?

h) What is phylogenetic tree?

i) Explain Pharmacophore.

j) What is the significance of gap extension penalty?

Part – B (Answer any four questions)

Q3.	**a)**	Explain different primary sequence databases along with the tools.	**(10)**
	b)	Describe PIR.	**(5)**
Q4.	**a)**	Explain different types of dynamic programming methods for sequence alignment.	**(10)**
	b)	Explain PDB file.	**(5)**
Q5.	**a)**	Explain the methods of insilico gene prediction	**(10)**
	b)	Explain HMM in sequence analysis.	**(5)**
Q6.	**a)**	Describe the process of homology modeling.	**(10)**
	b)	Differentiate between CATH and SCOP.	**(5)**
Q7.	**a)**	Explain docking with its application.	**(10)**
	b)	Differentiate between 2D and 3D QSAR.	**(5)**
Q8.	**a)**	Define substitution matrix. Describe different typesof substitution matrix.	**(10)**
	b)	Explain CSD and its limitations.	**(5)**
Q9.	**a)**	Explain MD simulation with suitable flow chart explaining the process.	**(10)**
	b)	What do you mean by molecular descriptor?	**(5)**