

(A-29)

No. of Printed Pages: 02

Sardar Patel University
M Sc IV Semester Biochemistry
PS04EBIC00 Bioinformatics
External Theory Examination

Date : 21st April, 2015
Time: 10:30 am to 1:30 pm

Max Marks : 70

Q. 1 Choose the correct answer

(08)

1. Find the odd one out

a) DDBJ	b) GenBank
c) REBASE	d) EMBL

2. GRAIL is used for

a) pairwise sequence alignment	b) Gene prediction
c) Structure prediction	d) structure alignment

3. Which of these is a structure alignment tool

a) Dot plot	b) VAST
c) BRENDA	d) PSI BLAST

4. The study of whole set of DNA molecules is called as

a) Genomics	b) Proteomics
c) Transcriptomics	d) Glycomics

5. Which of these is a repository for experimentally determined macromolecular structures

a) UniProt	b) SPDBV
c) Protein data bank	d) Entrez

6. Which of these is a tool for viewing protein structures

a) SPDBV	b) FindMod
c) VAST	d) ProtParam

7. SPDBV is used for

a) Sequence alignment	b) comparing structures
c) Phylogenetic analysis	d) none of these

8. Which of these is a secondary database

a) REBASE	b) SCOP
c) MEROPS	d) All of these

- Q. 2 Explain the terms in brief: **(any seven)** (14)
- a) Super secondary structures
 - b) Composite databases
 - c) e value
 - d) RMSD
 - e) H E and O
 - f) Heuristic
 - g) ProtParam
 - h) Threading
 - i) BLASTx
- Q. 3 A) List various databases and discuss any two in detail. (06)
B) Write a note (Any one) (06)
- a) BLAST
 - b) Scoring Matrices
- Q. 4 A) Explain Gene prediction (06)
B) Discuss RNA secondary structure prediction (06)
- OR**
- B) Write a note on: Comparative Genomics (06)
- Q. 5 A) Discuss CATHSOLID (06)
B) Write a note on: (any one) (06)
- a) SPDBV
 - b) Comparative modeling
- Q. 6 A) Explain Proteomics (06)
B) Write a note on (any one) (06)
- i) Molecular basis of evolution
 - ii) Bioinformatics tools

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