M. SC. (MEDICAL BIOTECHNOLOGY) SEM-III (CHOICE BASED CREDIT SYSTEM) : SUMMER - 2018

SUBJECT: GENOMICS & PROTEOMICS

Day: **Thursday**
Date: **05/04/2018**

Time: **02.00 PM TO 05.00 PM**
Max. Marks: 60

S-2018-1172

N.B.:

1) **Q. No. 1** and **Q. No. 5** are **COMPULSORY**. Out of the remaining questions solve any **TWO** from each section.
2) Figures to the right indicate **FULL** marks.
3) Answers to both the sections should be written in **SEPARATE** answer book.

SECTION-I

Q.1 Define: **(10)**

i) High resolution map
ii) Line
iii) ENTREZ
iv) GDB
v) OMIM

Q.2 Differentiate between: (Any **TWO**) **(10)**

a) Genetic mapping and physical mapping
b) Mouse genome and expression database
c) Linkage map and radiation hybrid map.

Q.3 Write short notes on: (Any **FOUR**) **(10)**

a) SNP
b) Polymorphic markers
c) HUGO
d) STS
e) UCSC Browser

Q.4 Answer the following: (Any **TWO**) **(10)**

a) Describe the silent features of HGP.
b) Explain with neat labeled diagram of Eukaryotic gene structure.
c) Explain the Pseudo genes Theory.

SECTION-II

Q.5 Give two examples of : **(10)**

a) Literature databases
b) Transposable elements
c) EST
d) Phylogenetic comparison tools
e) 3D structure visualization tools

Q.6 Answer the following: (Any **TWO**) **(10)**

a) What do you mean by Trasncriptomics? Explain importance of this field with example.
b) Write a note on DNA Microarray technology.
c) Describe in detail RNA chips.

Q.7 Write notes on: (Any **TWO**) **(10)**

a) CATH
b) BLOCK
c) SCOP

Q.8 Explain the protein Expression Analysis methods in detail. **(10)**

OR

Write Automation of proteomic analysis. Enlist its applications in clinical and biomedical field.

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