

Day: Monday
Date: 15-04-2019

Time: 10:00 AM TO 1:00 P.M.
Max. Marks: 60

S-2019-1510

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.
- 4) Draw neat labeled diagrams **WHEREVER** necessary.

SECTION-I

- Q.1** Differentiate with **TWO** points: (10)
i) High and low resolution maps ii) RFLP and RAPD
iii) EST and STS iv) OMIM and OMIA
v) Pseudo genes and Junked DNA
- Q.2** Write short notes on: (Any **TWO**) (10)
a) Line and Sine
b) MGD
c) CEPH reference pedigree
- Q.3** Answer the following (Any **TWO**) (10)
a) Explain the different types of genetic maps.
b) Explain the different types of physical maps.
c) Write briefly about Map viewer applications.
- Q.4** Explain in detail HGP. Discuss about features, expected outcomes and the era after the completion of HGP. (10)

OR

Explain Transposable elements and sequence repeats in brief.

SECTION-II

- Q.5** Define: (10)
a) C value paradox
b) Repetition frequency
c) Housekeeping genes
d) RNA splicing
e) Upstream flanking region
- Q.6** Answer the following: (Any **TWO**) (10)
a) Explain RNA chip technology.
b) Describe the concept of Chromosomal rearrangement.
c) State the basis of gene clustering with example.
- Q.7** Write notes on: (Any **TWO**) (10)
a) Comparative genomics
b) Motif, pattern and PROSITE
c) Integrated proteome analysis
- Q.8** Explain High throughput proteomics analysis. (10)

OR

Explain organ and spatio temporal comparison. Also comment on intra and cross species proteomics analysis comparison.