

Day: Wednesday Time 02:00 PM-05:00 PM Date: 01-12-2021 Max. Marks: 75 W-20787-2021 N.B.: 1) Q. No.1 and Q. No.5 are COMPULSORY. Out of remaining questions attempt **ANY TWO** questions from each section. Answer to both the sections should be written in **SEPARATE** answer book. 2) 3) Figures to the right indicate FULL marks. **SECTION-I** Q.1 What do you main by pharmacophore? Describe the process of development (08) of pharmacophore model. What is Homology modeling and criteria for determining protein structure (07) **Q.2** computationally? Explain the process of determination of protein structure by homology (08) modeling. Highlight the quality check of built protein model What is load in drug discovery process? Describe in detail with example the (15) Q.3 lead identification process. **Q.4** Write short notes on **ANY TWO** of the following. (15)Different phases of clinical trials a)

SECTION-II

- Q.5 What is prodrug concept? how prodrug helps in developing poorly soluble (07) drugs
- Q.6 What are different statistical parameters considered in QSAR and describe their mathematical expressions. What are the differences between 2D and 3D QSAR
- Q.7 What do you mean by molecular docking and list out types? Write in detail (15) scoring functions of docking tools.
- Q.8 Write short notes on ANY TWO of the following: (15)
 - a) Physicochemical properties of QSAR

Target identification and validation

Antisense Technology

b)

c)

- b) Hansch model with examples
- c) Practical consideration of prodrug design

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