Roll No. Total No. of Pages : 01

Total No. of Questions : 06

M.Pharmacy(Pharmacology) (2017 Batch) (Sem.–2)

PRINCIPLES OF DRUG DISCOVERY

Subject Code : MPL-203T

Paper ID : [74945]

Time : 3 Hrs. Max. Marks: 75

INSTRUCTIONS TO CANDIDATES :

1. **Attempt any FIVE questions out of SIX questions.**
2. **Each question carries FIFTEEN marks.**

Q1 a. What is proteomics? Describe its role in drug discovery. (7.5)

b. Discuss the role of protein microarrays in target identification and validation. (7.5)

Q2 a. What criteria should be satisfied by the reactions when used in designing a combinatorial sequence? (5)

b. Compare single and multiple sequence alignment protocol in homology modeling. (5)

c. Give outlines for *in silico* lead identification techniques. (5)

Q3 a. Compare modern rational drug designing to traditional approaches. (5)

b. How to determine bioactive conformations of ligand molecules prepared for pharmacophore mapping? (5)

c. What is a traditional method to evaluate drug likeness of newly synthesized compounds? (5)

Q4 a. What is induced fit docking analysis? (5)

b. Describe mixed model of traditional QSAR. (5)

c. How to quantify electrostatic interactions to derive traditional QSAR models. (5)

Q5 a. What is stepwise multiple linear regression (SMLR) analysis? Name various statistical parameters used to select the best QSAR model derived from SMLR. (5)

b. Give outline of CoMFA methodology. Discuss contour analysis of CoMFA model. (10)

Q6 a. Describe the ideal properties of prodrugs. (5)

b. By citing suitable examples, describe the applications of prodrugs in reducing toxicity of the drug molecules. (10)