DBY-MPL-203-T Seat No. _____

M. P. M. (Sem. II) Examination

July - 2022

Principles of Drug Discovery : MPL203T

Time : **3** Hours] [Total Marks : **75**

Instruction : Figure to the right indicates full marks.

1 Answer the following questions : **20**

(A) Differentiate HIT from Lead molecule.

(B) Enlist various levels of Protein structure.

(C) What is siRNA ?

(D) Enlist various *In silico* methods of drug discovery process.

(E) What are different types docking studies ?

(F) Name the full form of COMSIA & COMFA.

(G) Explain the term : PHARMACOPHORE.

(H) What is de Novo drug design ?

(I) Enlist different types of assay technique we can use to identify the HIT.

(J) Explain the meaning of Homology modelling.

2 Answer the following questions : (ANY **TWO**) **20**

(A) Explain High throughput screening with enough detail.

(B) Differentiate traditional drug discovery process from rational drug discovery process.

(C) Make a note on Docking study as a part of drug discovery process.

3 Answer the following questions : (ANY **SEVEN**) **35**

(A) Discuss the role of Bioinformatics in lead identification.

(B) Draw suitable flow chart of modern drug discovery process.

(C) Explain various Combinatorial chemistry method for lead identification.

(D) Discuss X-ray crystallography and NMR technique in protein structure prediction.

(E) Make a note on Hansch analysis.

(F) Differentiate SAR from QSAR.

(G) Elaborate role of transgenic animals in target validation.

(H) Make a detailed note on Rational drug design methods.

(I) What is partial least square analysis (PLS) ? Explain in detail.