PAPER ID-311205

Subject Code: BP807ET

Roll No: | | | | | | | | | | | | | |

BPHARM
(SEM VIII) THEORY EXAMINATION 2024-25
COMPUTER AIDED DRUG DESIGN

TIME: 3 HRS **M.MARKS: 75**

Note: 1. Attempt all Sections. If require any missing data; then choose suitably.

SECTION A

1. Attempt *all* questions in brief. **10 x 2 = 20**

a.	How lead molecule play a vital role in drug discovery?
b.	What do you understand from non-random screening?
c.	Write the importance of *de novo* drug design.
d.	Write the importance of partition coefficient.
e.	Write the outcomes of docking based screening.
f.	Write the purpose of conformational analysis.
g.	Define Pharmacophore mapping.
h.	Write the applications of bio-informatics.
i.	Define random screening.
j.	Define COMSIA.

SECTION B

2. Attempt any *two* parts of the following: **2 x 10 = 20**

a.	Give the stages of drug discovery and development.
b.	Write the history and development of QSAR.
c.	Discuss the energy minimization methods.

SECTION C

3. Attempt any *five* parts of the following: **7 x 5 = 35**

a.	How traditional medicines become the source of drug discovery? Explain.
b.	Describe the physicochemical parameters used in QSAR studies.
c.	Compare between rigid docking and flexible docking.
d.	Write the role of ADME databases in drug discovery.
e.	Write a note on bio-isosterism.
f.	Explain lead discovery based on clinical observation.
g.	Describe principle and applications of COMFA.