MPL 203 T

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M. PHARMACY (Regular) DEGREE EXAMINATIONS, DECEMBER-2022

Second Semester

PHARMACOLOGY

PRINCIPLES OF DRUG DISCOVERY

Time : **Three Hours** Maximum : 75 Marks

SECTION - A

Answer any FIVE Questions. **5x5 = 25 M**

1. Write a note on Zinc finger proteins.
2. Give an account on assay development for Hit identification.
3. Compare and contrast Traditional drug design and Rational drug design.
4. Write a short note on Hansch analysis.
5. Give a detailed note on Partial Least Square analysis (PLS).
6. What is SiRNA ? Explain its role in drug discovery.
7. Define Molecular docking and add a note on Rigid and Flexible docking.

SECTION - B

Answer any FIVE Questions. **5x10 = 50 M**

8. Explain the following :
   a) Anti sense technologies.
   b) Economics of drug discovery.
9. Discuss the applications of
   a) X-ray crystallography in protein structure prediction.
   b) Combinational chemistry.

10. Write a note on

    a) Pharmacophore Mapping.

    b) High throughput screening.

11. Give a detailed note on De novo drug design.

12. Discuss on the prodrug strategies to improve patient acceptability, drug solubility and site specific delivery of drugs.

13. Write a note on 3D - QSAR approaches in drug design.

14. Discuss the computational methods for prediction of protein structure.

MPL 203 T

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M. PHARMACY (REGULAR) DEGREE EXAMINATIONS, JANUARY-2022

Second Semester

PHARMACOLOGY

PRINCIPLES OF DRUG DISCOVERY

Time : **Three Hours** Maximum : **75** Marks

SECTION - A

Answer any FIVE Questions. **5x5 = 25 M**

1. Explain the role of Nucleic acid microarrays in drug discovery.
2. Describe the homology modeling method in prediction of protein structure.
3. Differentiate Traditional and Rational drug design.
4. Write a brief note on De novo drug design.
5. Explain the application iof prodrugs for site specific delivery and sustained drug action.
6. Explain the assay development for hit identification.
7. Discuss SAR vs QSAR.

SECTION - B

Answer any FIVE Questions. **5x10 = 50 M**

8. Write a detailed note on Antisense technologies in drug discovery.
9. Explain Lead optimization and add a note on economics of drug discovery.
10. Write a note on
    a) High thoroughput screening.
    b) Pharmacophore Mapping.
11. Explain Free Wilson Analysis.
12. Write a note on
    a) Partial least Square Analysis.
    b) COMFA.
13. Discuss the application of NMR and X-ray crystallography in protein structure prediction.
14. Give an account on Drug likeness screening.

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M.PHARMACY (Regular) DEGREE EXAMINATIONS, AUGUST-2019

Second Semester

PHARMACOLOGY

PRINCIPLES OF DRUG DISCOVERY

Time: Three Hours **Maximum marks:75**

SECTION-A

Answer any FIVE of the following. **5X5=25M**

1. Explain the differences between domain and motif in a protein giving suitable examples.
2. Why virtual screening is preferred over High throughput screening.
3. Discuss the significance of molecular docking in structure based drug design.
4. Explain the objectives of prodrug concept.
5. Mention the role of proteomics in target validation.
6. Add a note on physicochemical parameters useful to develop QSAR equation.
7. Write briefly about various statistical methods used in QSAR techniques.

SECTION-B

Answer any FIVE of the following. **5X10=50M**

8. Explain in detail about various steps involved in target validation.
9. Explain the methodology, applications and limitations of Hansch analysis.
10. Enlist and discuss about various established assay techniques in high throughput screening for lead identification.
11. Discuss about the prodrug strategies to deliver site specific drugs and sustained drug action.
12. Add a detailed note on pharmacophore based screening in drug development process.

P.T.O

13. Write about

a) Methodology and applications of COMFA

b) Zinc-finger proteins

14. Discuss on

a) Role of X-ray crystallography in protein structure prediction.

b) Threading

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M.PHARMACY (Supple) DEGREE EXAMINATIONS, FEB/MAR-2020

Second Semester

M.PHARMACY

PHARMACOLOGY

PRINCIPLES OF DRUG DISCOVERY

Time: Three Hours

Maximum marks:75

SECTION-A

Answer any FIVE Questions **5X5=25M**

1. Discuss about COMFA. How it differs from COMSIA.
2. Explain the concept of pharmacophore mapping in drug design.
3. Discuss about the prodrug strategies to improve absorption and distribution.
4. Explain the importance of NMR techniques in protein structure predictions.
5. Enumerate the role of siRNAs in target validation.
6. Discuss the methodology, applications and limitations of Free-wilson analysis.
7. Explain the role of nucleic acid microarrays target identification and validation.

SECTION-B

Answer any FIVE Questions **5X10=50M**

8. Discuss about the objective, mechanism of action and diseases targeted by antisense oligonucleotides.
9. Explain the role of combinational chemistry in lead identification process.
10. Describe the concept of structure-based pharmacophore approaches and their applications in drug discovery.
11. Briefly outline the methodology involved in various docking studies. Which technique is more accurate.

P.T.O

12. Discuss the role of transgenic animals in target validation.

13. Explain the procedure involved in structural prediction of protein by homology modeling.

14. Write a note on

    a) Drug likeness screening

    b) Physicochemical parameters in QSAR.