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M. PHARMA.

THEORY EXAMINATION (SEM–II) 2016-17

PRINCIPLES OF DRUG DISCOVERY METHODS

Time : 3 Hours ***Max. Marks : 70***

Note : *Be precise in your answer. In case of numerical problem assume data wherever not provided.*

SECTION- A

1. Attempt all parts of this Section : **7×2=14**

(a) Discuss the role of genomics in target discovery.

(b) Define regression analysis.

(c) What is the role of "log p" in QSAR?

(d) Discuss the application of X-ray crystallography in protein structure prediction.

(e) Discuss the major differences between traditional and rational drug design.

(f) Discuss the concept of pharmacophore mapping.

(g) Comparative molecular similarity index analysis (CoMSIA)

SECTION- B

2. Attempt any three parts of the following : **3×7=21**

(a) Explain 'an overview of modern drug discovery process'. What is the role of lead optimization in drug discovery process?

(b) Explain threading and homology modelling method in protein structure.

(c) What are the benefits of Pharmacophore based approaches of drug design? Explain with special example.

(d) Discuss in detail about "Hammet Substituent Constant".

(e) Discuss the advantages of 3D-QSAR over 2D-QSAR..

SECTION- C

3. Attempt all questions in this section : **5×7=35**

(a) Define combinatorial chemistry. Discuss in detail about solid phase synthesis in lead identification.

(b) Discuss in detail about high throughput screening with suitable example.

(c) Explain 'Hansch Analysis' in Quantitative Structure Activity relationship.

(d) Discuss the pharmacophore based approaches in rational drug design.

(e) Define prodrug and discuss the rationale of prodrug design to improve patient acceptability.