## BIRLA INSTITUTE OF TECHNOLOGY, MESRA, RANCHI (END SEMESTER EXAMINATION)

CLASS: MPharm BRANCH: PHARMACY TIME: 3.00 Hours		SUP IECT, MDI 202T Dringinles of Drug Discovery	SEMESTER: II SESSION: SP/22 FULL MARK: 75	
		SUBJECT: MPL2031 Principles of Drug Discovery		
INSTRUCTIONS: 1. Attempt any 5 questions 2. The missing data, if any, may be assumed suitably. 3. Before attempting the question paper, be sure that you have got the correct question paper. 4. Tables/Data hand book/Graph paper etc. to be supplied to the candidates in the examination hall.				
1a. 1b.	Describe different st Define Antisense te identification and va	teps of modern drug discovery process. echnology. Explain the application of antisense techno alidation.	logy in target	[7] [8]
2a. 2b.	Define microarrays. Explain the role of microarrays in target discovery. Explain the role of Transgenic animals in modern drug discovery process.		[7] [8]	
3a. 3b.	Compare Homology and Threading modelling for the prediction of protein structure. Define the basic principal of NMR. Describe the application of NMR in Drug Discovery Process.		[7] [8]	
4a. 4b.	Define RNA interference. Describe siRNA in detail. Which regression-based approaches are widely used in QSAR? Describe any ONE of them.		[7] [8]	
5a. 5b.	What are the differences between manual and automatic docking. How the physicochemical properties of drugs are expressed numerically in quantitative structure activity relationship (QSAR) studies? Why the logarithmic graph of biological activity versus partition coefficient shows a parabolic relationship?		[7] [3+5]	
6a. 6b.	What are the differences between structure activity relationship and QSAR? Explain QSAR by Hansch analysis. How COMFA is used in 3-D QSAR approach? How COMSIA is advantageous over COMFA?		[2+5] [6+2]	
7a. 7b.	Discuss the applicat case. State the properties	tions of QSAR in prodrug designing with suitable example of an ideal prodrug. Write a note on drug likeliness scree	mples in each ening.	[7] [3+5]
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