

## UNIVERSITY OF PETROLEUM AND ENERGY STUDIES

## **End Semester Examination, December 2021**

**Course: Drug Discovery and Development** 

**Program: MSc (Clinical Research)** 

**Course Code: HSCR7006** 

Semester: I Duration: 03 hr Max. Marks: 100

	SECTION A		СО
	(Type the answers in test box)		
		30 Marilan	
01	Which of the following annuage is considered under the Higand based	Marks)	001
Q1	Which of the following approach is considered under the 'Ligand based	1.5	CO1
	drug designing?		
	a) Molecular docking b) Pharmacophore modeling c) QSAR Modeling d) b and c both		
	c) QSAR Wodeling and c both		
Q2	Which of the following sets contains all aromatic residues?	1.5	CO1
Q2	a) G, D, N, E b) I, V, L, M	1.5	001
	c) R, K, H d) F, Y, W		
Q3	Which type of data base EBI is?	1.5	CO2
Q3	a) Protein db b) Pathway db	1.5	002
	c) Nucleotide db d) Specialized db		
Q4	'Procheck' tool is use for	1.5	CO1
ζ'	a) Alignment b) Protein Validation	1.0	
	c) Simulation d) None of these		
Q5	Two sequences are said to be homologous if:	1.5	CO3
Q3	a) they have diverged from a common ancestor.	1.5	003
	b) their alignments share 30% identity or more.		
	c) they belong to the same fold family.		
	d) they have converged to share similar functional properties.		
Q6	Which of the following method used for virtual screening?	1.5	CO1
	a) ADMET analyses b) QSAR modeling		
	c) Pharmacophore modeling d) All of the above		
Q7	CoMFA method is used for	1.5	CO4
	a) 4D-QSAR b) 3D-QSAR		
	c) 5D-QSAR d) 6D-QSAR		
Q8	With homology modelling, if there are major errors in the template, the	1.5	CO2
	model will:		
	a) be very good b) be just as good as the template		
	c) be unable to be built using current modelling programs		
	d) be completely wrong	1.7	GOA
Q9	Lipinski's rule of five is used for	1.5	CO3
	a) Docking b) Similarity search c) Drug likeness d) Dynamics simulation		
010	c) Drug likeness d) Dynamics simulation Which of these is gene prediction algorithm?	1.5	CO2
\Q10	a) UPGMA  b) Hidden Markov Model	1.5	CO2
	c) Maximum parsimony d) None of these		
Q11	Identify the kind of interactions that are typically involved in binding a	1.5	CO2
VII	drug to the binding site of a protein.	1.5	002
	urug to the binding site of a protein.		İ

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	a) van der Waals interactions				
	b) ionic bonds				
	c) hydrogen bonds				
010	d) a combination of all of the above	1.5	CO2		
Q12	Which of the following descriptions most accurately describes binding			CO2	
	sites and binding regions?				
	a) a binding site is part of a binding region				
	b) a binding region is part of a binding site				
	c) a binding region is the same as a binding site				
	d) a binding region is on a drug whereas a binding site is on a				
0.10	macromolecular target			004	
Q13	What is meant by ADME in pharmacok	inetics?	1.5	CO4	
	a) Affinity, dosage, marketing, efficacy				
	b) Absorption, distribution, metabolism, ex				
	<ul><li>c) Agonism, dependence, mobility, efficiency</li><li>d) Antagonism, deficiency, mean, efflux</li></ul>				
Q14	Which of the following statements best of	lescribes an induced fit?	1.5	CO1	
	a) the process by which a binding site alter				
	accept a drug	ı ,			
	b) the process by which a drug adopts the correct binding conformation before entering a binding site c) the process by which binding of a drug to a binding site alters the shape of the binding site				
	d) the process by which a binding site alters the shape of the drug into the				
	binding conformation before binding				
015		lished before the seems for a	1.5	CO2	
Q13	Which of the following needs to be established before the search for a			CO2	
	lead compound takes place?	matuma activity malationships			
		ructure-activity relationships			
016	c) a bioassay d) pa		1.5	CO4	
Q16	What is the term used for the automated in vitro testing of large			CO4	
	numbers of compounds using genetically				
		gh throughput screening			
	c) multi-screening d) na				
Q17	There are several sources and methods	_	1.5	CO2	
	Which of the following is most likely to lead to the discovery of a				
	complex structure quite unlike any othe	r previously discovered?			
	a) combinatorial chemistry b) da	atabase mining			
	c) screening plant extracts d) m	e too drugs			
Q18	What is the term used for drugs that are similar in structure to a known			CO3	
	drug and which are used for the same purpose?				
		ne-too' drugs			
	, 10	nalogue' drugs			
Q19	What is the term used for small molecul		1.5	CO2	
	of a binding site?				
	_	somers			
		pitopes			
020	Q20 The software which is not used for molecular docking?			CO3	
\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	a) Auto Dock b) Gold		1.5		
	,	Chemdraw			
1	p) Onde a) C	Hemulaw			

	SECTION B (Scan and upload)	(4Qx5M =20 Marks)	CO
	Short Answer Type Question (5 marks each)		
Q1	<ul><li>a) What is QSAR?</li><li>b) Explain the importance of QSAR for lead optimization.</li></ul>	1+4	CO1
Q2	<ul><li>a) What are the needs of drug discovery?</li><li>b) Illustrate the process used for drug discovery?</li></ul>	2+3	CO3
Q3	<ul><li>a) What is molecular docking?</li><li>b) How this technique can be utilized to predict binding affinity of new biologically active molecules?</li></ul>	2+3	CO2
Q4	Write a short note on target based virtual high throughput screening.	5	CO4
	SECTION C (Scan and upload)	(2Qx15 M=30 Marks)	СО
	Two case studies 15 marks each subsection		
Q1	<ul><li>a) What is role of fragment-based drug discovery?</li><li>b) Describe the method of fragment-based drug discovery by giving an example.</li><li>c)Illustrate the advantage and disadvantages of pharmacophore mapping.</li></ul>	3+6+6	CO1
Q2	<ul><li>a) What do you mean by rational drug design?</li><li>b) Ranitidine (Zantac) is a medicine that reduce indigestion, heartburn and acid reflux. Describe the steps which were utilized to discover this drug via rational drug design approach?</li><li>c) Briefly discuss the types of rational drug design methods used for developing new drug like molecules.</li></ul>	3+7+5	CO4
	SECTION- D (Scan and upload)	(2Qx10 M=20 Marks)	СО
	Long Answer type Question	wiai KS)	
Q1	<ul><li>a) Discuss the importance of homology modelling?</li><li>b) Briefly describe the method ofhomology modelling of a targeted protein.</li></ul>	4+6	CO2
Q2	<ul><li>a) Write down the different characteristics of drug target.</li><li>b) What is the role of proteomics intarget identification.</li></ul>	4+6	CO3