Time: 3 Hours **Marks: 75**

Q. 1 Attempt all multiple-choice questions (MCQ) **20M**

Sr No	Questions		Options
1	In target-based drug discovery, …….	**a**	biological (drug) targets are already established (or 'discovered') before lead discovery starts
		b	biological (drug) targets are established (or 'discovered') after lead discovery starts
		c	biological (drug) targets are not essential
		d	biological (drug) targets are confirmed after toxicity studies
2	Target identification is aimed at finding the _____ of a drug/pharmaceutical or other xenobiotic.	**a**	Structure
		b	Bioavailability
		c	Efficacy target
		d	Metabolism
3	Protein function array, will consist of thousands of native proteins _____	**a**	immobilized in a defined pattern.
		b	mobilized in random pattern
		c	mixed and mobilized in fixed wells
		d	are filled in 96 wells plate
4	Nucleic acid microarrays (genome chips) are generated by arraying _____ 'probes' onto a support matrix, and utilize the principle of specific base pairing to subsequently bind their complementary 'targets'.	**a**	Protein
		b	Enzyme
		c	ATP
		d	Nucleotide
5	The main problems in the development of siRNA-based drugs for therapeutic use are	**a**	high toxicity and longer half life
		b	nonspecificity and high toxicity
		c	the low efficiency of siRNA delivery to target cells and the degradation of siRNAs by nucleases in biological fluids
		d	high pH and high toxicity

6	Homology modelling is a procedure whereby	**a**	Due to low sequence similarity between protiens of unknown and known structure, the structure is predicted from first principle
		b	Due to high sequence similarity between protiens of unknown and known structure the same function is assumed for both
		c	Due to high sequence similarity between protiens of unknown and known structure the structure of the latter is used as a template to model the former
		d	A Protien of unknown structure is compared against a library of fold templates to find the best match
7	What is a domain?	**a**	A segment of protein structure that is autonomously stable.
		b	A stable, independent protein encoded by a single gene.
		c	The amino acid sequence of a polypeptide, listed from N-terminus to C-terminus.
		d	A complex structure composed of two or more tertiary structure subunits
8	……. is an essential element in High Throughput Screening.	**a**	Automation
		b	Manual transfer
		c	In vivo testing
		d	Toxicity testing
9	Which of the following approaches is considered under the 'Ligand based drug designing' ?	**a**	Molecular docking
		b	Pharmacophore modeling and QSAR modeling
		c	Rigid docking
		d	Molecular docking

10	It is TRUE for "a model of the biological target may be built based on the knowledge of what binds to it and this model in turn may be used to design new molecules."	**a**	Random screening of synthetic compounds
		b	Random screening of natural compounds
		c	Docking of lead compound
		d	Ligand Based Drug Designing
11	Which interaction is not used in FLOG conformation program	**a**	Hydrophobic
		b	Van der walls
		c	Hydrogen bonding
		d	Covalent
12	In which program ligand and receptor spheres are overlaid by means of a clique detection	**a**	Hammerhead
		b	FLOG
		c	FlexX
		d	DOCK
13	Which software program is involved in fitting and bridging of molecular fragments	**a**	SYNOPSIS
		b	SPROUT
		c	LEGEND
		d	LUDI
14	Scientist who has developed parabolic equation for extended hydrophobicity ranges	**a**	Ferguson
		b	Taft
		c	Wilson
		d	Hansch
15	In Rigid docking	**a**	Ligand is rigid and receptor is flexible
		b	Receptor is rigid and ligand is flexible
		c	Both receptor and ligand are flexible
		d	Both receptors and ligands are rigid
16	Esterification of Propranolol leads to ____	**a**	Taste masking
		b	Reduction in first pass metabolism
		c	Site -specific delivery
		d	Reduction in production cost

17	Which of the following will be a pharmaceutical application of prodrug	**a**	Enhancement of Bioavailability
		b	Reduction of toxicity
		c	Site-specific drug delivery
		d	Improvement of Odour
18	The advantage of erythromycin estolate over erythromycin is	**a**	Less bitter taste
		b	Prolong duration of action
		c	Cheap
		d	No drug drug interations
19	How is the improvement of a drug in case of taste is done?	**a**	Reducing drug solubility in saliva and lower affinity for taste receptors
		b	Increasing affinity for the taste receptors and making the drug sweet
		c	Increasing the drug solubility in the saliva
		d	Injecting the drug so no taste related problems
20	Prodrugs with two active compounds are known as _____	**a**	Mixed type prodrugs
		b	Pro-prodrugs
		c	Bioprecursors
		d	Mutual prodrug

Q 2. Attempt any Two question 20 M

1. Write a detailed note on the prediction of protein structure.
2. What are the different approaches for traditional drug design? Write a note on high-throughput screening processes.
3. Give a detailed account on De Novo drug design.

Q 3. Attempt any Seven questions 35M

1. Discuss in detail roles of siRNAs and Antisense Oligonucleotides in target identification.
2. Describe in detail the different types of docking methods used in the drug discovery process.
3. Write a note on principles involved in the design of prodrugs.
4. Write a note on Molecular Docking
5. Elaborate on concepts of Rational Drug Design.
6. What are advantages and disadvantages of combinatorial Chemistry?
7. Explain in detail structure based and ligand-based drug design.
8. Discuss in detail role of proteomics in target identification.
9. Describe various lead identification methods in drug design.

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