

Question Paper

Exam Date & Time: 11-Jul-2023 (10:00 AM - 01:00 PM)



MANIPAL ACADEMY OF HIGHER EDUCATION

Computer Aided Drug Design [PCH-BP807ET-S3]

Marks: 75

Duration: 180 mins.

I Multiple Choice Questions (MCQs)

Answer all the questions.

Section Duration: 30 mins

1) Which of the following is not a strategy in identifying a drug target? (1)

[Analysis of pathophysiology](#)

[Analysis of mechanism of action of existing therapeutic drugs](#)

[Analysis of SAR](#)

[Trawling the genome](#)

2) What are Disease genes? (1)

[Genes whose altered expression is thought to be involved in the development of the disease state](#)

[Genes that encode functional proteins, whose activity is altered](#)

[Genes, mutations of which cause or predispose to the development of human disease](#)

[All of the above](#)

3) Which of the following is not a "Rule of Five" (Ro5) for drug-likeness filter? (1)

[molecular weight less than 500 Da](#)

[number of hydrogen bond donors equal or more than 5](#)

[number of hydrogen bond acceptors less than 10](#)

[calculated Log P less than 5.0](#)

4) For selection of a 3D structure of a target protein for molecular docking studies what is preferred resolution? (1)

[Less than 3.0 Å](#)

[More than 3.5](#)

[Å](#)

[Less than 2.5 Å](#)

[Less than 1 Å](#)

5) What is scaffold hopping? (1)

[screening in order to predict pharmacological profiles for lead structures in silico](#)
[identification of chemical features for a specific binding site](#)
[extracting common chemical features from set of active ligands](#)
[identification of novel scaffolds that have not been associated with the target of interest](#)

6) De Novo Design can be used to (1)

[generate ligand structures to virgin targets](#)
[generate ligand structures from molecular fragments bound into the site](#)
[generate alternative chemotypes to known active compounds](#)
[All of the above](#)

7) Which of the following strategy is not a divide-and-conquer approach in De novo drug design? (1)

[Ligand Growing](#)
[Ligand Morphing](#)
[Ligand Linking](#)
[Lattice based methods](#)

8) AMBER is the force field used for the simulation for the following (1)

[Proteins](#)
[Nucleic acids and Proteins](#)
[Carbohydrates](#)
[All of the above](#)

9) Microarray provides massive amount of data about the following (1)

[Gene activity in the presence of certain biological samples under specific conditions](#)
[Protein activity in the presence of certain biological samples under specific conditions](#)
[Protein activity in the absence of certain biological samples under specific conditions](#)
[Gene activity in the absence of certain biological samples under specific conditions](#)

10) MM1 force field is applied only to (1)

[Saccharides](#)
[Hydrocarbons](#)
[Nucleotides](#)
[Proteins](#)

11) Molecular dynamics can be used to generate a variety of different conformations by 'heating' the molecule to (1)

[500 K](#)
[600 K](#)
[700 K](#)
[900 K](#)

- 12) Software used to study protein ligand docking is: (1)
- [SPORE](#)
 - [H++](#)
 - [PHASE](#)
 - [GOLD](#)
- 13) Quantum mechanics describes molecules in terms of interactions among the following. (1)
- [Nuclei and molecular geometry](#)
 - [Electrons and Molecular geometry](#)
 - [Nuclei and Electrons](#)
 - [Nuclei, Electrons and Molecular geometry](#)
- 14) The most common program for structure drawing is (1)
- [CORINA](#)
 - [Dragon](#)
 - [UNIPROT](#)
 - [FT map](#)
- 15) Main advantage of using COMFA in drug discovery (1)
- [Fast and inexpensive method](#)
 - [Can predict the bioactivity of molecules without the need of experimental testing](#)
 - [Can predict the toxicity of molecules](#)
 - [Can predict the optimal condition for synthesising a molecule](#)
- 16) COMSIA is based on the principle of (1)
- [Molecular docking](#)
 - [Molecular dynamic simulation](#)
 - [QSAR](#)
 - [3D-QSAR](#)
- 17) Silameprobamate is an example of bioisosteric replacement of (1)
- [N for C](#)
 - [Si for N](#)
 - [Si for C](#)
 - [S for](#)
 - [N](#)
- 18) =C=, =N= and =P= are examples of (1)
- [Tetravalent classical isosters](#)
 - [Tetravalent non-classical isosters](#)
 - [Divalent classical isosters](#)
 - [Divalent non-classical isosters](#)
- 19) Following change are expected from Bioisosteric replacement (1)
- [Structural changes](#)
 - [Change in receptor interaction](#)
 - [Change in Pharmacokinetic properties](#)
 - [All the above](#)
- 20) Which of the following is a characteristics of Lipophilic molecules (1)

[They have high water solubility](#)
[They tend to be polar and dissociates into ions](#)
[They can diffuse across cell membranes](#)
[They do not interact with biological membrane](#)

II Long Answers

Answer all the questions.

- 21) Enlist the various methods used for lead discovery add a note on lead optimization (5)
- A)
- B) Write a note on selection of 3D structure of a protein and site map analysis for molecular docking (5)
- 22) Write Hansch equation? What are the advantages of this equation in QSAR? (4)
- A)
- B) With the help of a case study, explain the alteration of physicochemical properties by classical bioisosterism (6)

III Short Answers

Answer all the questions.

- 23) What is De novo drug design? Explain divide and conquer ligand build up strategies for in situ De novo drug design. (5)
- 24) Explain the fundamental steps in Pharmacophore modelling (5)
- 25) How is Bioinformatics useful in new drug discovery program. Define HTS and Combinatorial chemistry in new drug discovery (5)
- 26) Mention the software used in drug discovery program. Enlist various chemical databases. Mention their applications (5)
- 27) Explain the principles of quantum mechanics. What is energy minimisation? Define local and global energy minima (5)
- 28) Explain the principle of Molecular mechanics. What is Force field and Molecular dynamics ? Mention their relevance in molecular mechanics (5)
- 29) Enumerate the fundamental steps of the CoMFA methodology (5)

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