Quiz
Chapter 4-7
Docking

Full Marks: 10 Time: 10 min

1. Which one is a free tool for docking?

a) GOLD b) GLIDE c) SCHRODINGER d) SWISS DOCK

2. Which one of the following is a software to read protein?

c) UCSF Chimera b) PyMOL c) Rasmol d)All of these

3. .mol2 is a format to save

a) Protein b) Ligand c) Both of these d) None of these

4. Which one of the following is suppressed in PDB derived protein structure but required to add explicitly during docking?

a) All bonds in protein b) All Amino acid residues in protein c) All hydrogens of protein d) All –COOH terminals in protein

5. In docking, which one is true?

a) Protein-flexible, ligand-rigid b) Both protein and ligands are flexible c) Protein-rigid, ligand flexible d) All of these

6. Which one of the following is preferentially the output format of docking energy (binding energy)?

a) ΔG b) ΔH c) ΔA d) ΔG/ΔH

7. in SWISSDOCK, conformers of a specific docking generated ligand is categorized as

a) most fitting to lowest fitting b) Lowest fitting to most fitting c) Highest potential energy to lowest potential energy d) None of these

8. The favorable conformations generated by SWISS DOCK can be analyzed by

a) UCSF Chimera b) Chem Draw c) JMol d) ISIS DRAW

9. The most favorable bonding between ligand and protein is

a) Covalent bonding b) Metal Binding c) vander Waals Bonding d) Hydrogen bonding

10. The inbound ligand in PDB protein helps in

a) intiate the ligand protein interaction b) solvating the protein while docking c) helping in determining the binding pocket within the protein d) helping in determining the conformation of the interacting ligand