Week 6

1. In Protein Data Bank, most of the known three-dimensional structures of proteins are determined by the method, _____
   a. Circular Dichroism
   b. NMR spectroscopy
   c. X-ray crystallography
   d. Cryo-Electron microscopy
2. Temperature factors of less than 75 in a protein structure shows that the atom is _____
   a. Rigid
   b. Flexible
   c. Located in a fixed position
   d. None of the above
3. From the given contact map, which of the following residues form long-range contacts?
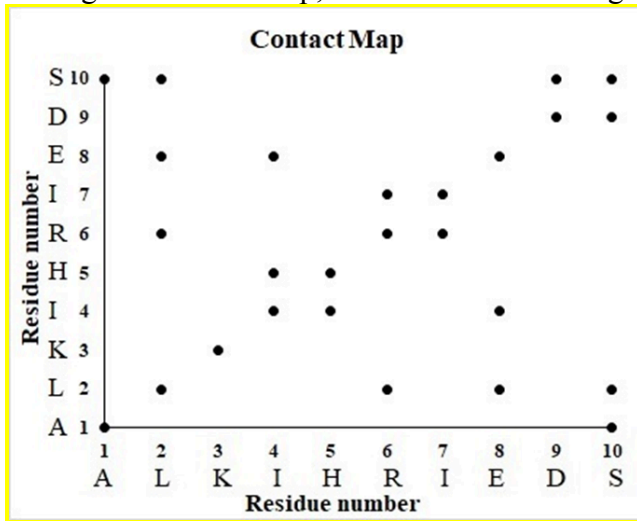
   a. I4 and E8
   b. D9 and S10
   c. K3 and S10
   d. L2 and E8
4. Which method provides the information on atomic level solvent accessibility?
   a. HBPLUS
   b. NACCESS
   c. DSSP
   d. ASAview
5. Which of the following is not a protein visualization software?
   a. Pymol
   b. Rasmol
   c. Jmol
   d. None of the above
6. Proteins with segregation of alpha helices and beta strands belong to _____ class

a. All alpha class
b. All beta class
c. **Alpha+Beta class**
d. Alpha/Beta class

7. If the atoms of a particular residue have an occupancy of less than 1, it implies that
   a. **The residue is said to assume alternate conformations.**
   b. The residue is missing in some cases.
   c. The residue is flexible.
   d. The residue is not conserved.
8. Which databases contain information on structural classes of proteins?
   a. SCOP and UniProt
   b. CATH and EMBL
   c. **SCOP and CATH**
   d. DALI and CATH
9. Extended state accessible surface area (ASA) of a residue X can be obtained from the ASA of tripeptides,
   a. **Gly-X-Gly**
   b. Gly-X-Ala
   c. Lys-X-Lys
   d. Ala-X-Gly
10. X-ray crystallography provides information on _____ to determine protein three-dimensional structures?
    a. **Electron density map**
    b. X, Y, Z coordinates
    c. Alpha helices and beta strands
    d. Sequence alignment