Course: BT 305

Lab Session 5: Analysis of protein structures.

Designed peptides Vs Natural Proteins (Protein G and Trp Cage)

Last date of submission:

Aim: Estimate the solvent accessible surface area (SASA) of the designed peptides as well as Protein G (1PGB.pdb) and Trp Cage (1L2Y.pdb)

Note: Test set: Designed peptides means alpha helix, beta sheet you have designed

Work: 1.Design an alpha helix and beta sheet using PROSS and Ribosome
2. Download 1PGB.pdb and 1L2Y.pdb

The objectives of current session are as follows:

1. What is the total relative solvent accessible surface area of the each (total 4) protein/peptide molecule in the test set.

2. What is the average per residue solvent accessible surface area of four test proteins.

3. Write down all four molecular systems in the increasing order of per residue SASA. What inference would you get from the magnitude of per residue SASA value.

4. If you change the probe radius from 1.4 to 1.0, how is it reflected in absolute and relative SASA values.

5. In protein G and Trp cage, you will notice that residue TRP has very low values of SASA. What could be the reason?

Materials and methods
Operating System: linux; Computational tool: VADAR