**SB – Assignment 3**

**Q1)**

**The technique used in the May et al (2014) paper for calculating the PMF is constraint force integration.**

* *In general terms, describe the main differences between constraint force integration and umbrella sampling.*
* *Can you name some underlying assumptions of both methods?*
* *Are these assumptions discussed in the paper and Wikipedia page?*

**Q2)**

**Open the 1VET structure in your favorite PDB viewer.**

* *How many chains are present in the structure?*

There are two chains present in the structure.

* *What is the dominant secondary structure type?*

With 37% helical structure type (6 helices; 46 residues) and 29% beta sheet

structure type (5 strands; 37 residues) the most dominant structure type is likely

to be helical.

* Locate the interface region. How many of each type of secondary structure elements (strand, helix, coil) are involved in the interaction?

There are a total of 12 contact pairs involved in the interaction, see below, of which there are (counted by the number of contact residues within secondary structures) 5 strands, 3 helices and 6 coils.

atom1 atom2 overlap distance

HOH 251.A O PRO 41.A CB 0.834 2.506

THR 57.A CG2 ASN 68.A OD1 0.734 2.566

HOH 209.B O VAL 99.B CG1 0.710 2.630

MET 103.B CB HOH 209.B O 0.703 2.637

ALA 54.B CA ARG 58.B NH2 0.700 2.820

HOH 235.A O LYS 119.A CB 0.677 2.663

LEU 31.B CG HOH 233.B O 0.662 2.678

HOH 171.A O ILE 118.A CG1 0.632 2.708

ASP 57.B CB ARG 58.B NH2 0.619 2.901

HOH 226.B O LEU 63.A CD2 0.609 2.731

LEU 5.A CD2 LEU 9.A CD1 0.607 3.153

HOH 141.A O HIS 20.A CD2 0.604 2.616

Q3)

Use g\_confrms to fit the starting and minimized structures on top of each other for easy comparison:

*G\_confrms -f1 conf.gro -f2 confout.gro*

When you are asked for group(s) to work on, select Protein.

* The output file fit.pdb will contain both structures, open it in your protein viewer. Can you now see any differences?
* The tool also calculates the RMSD, look it up in the output. How large is it?

Root mean square deviation after lsq fit = 0.00986369 nm

* Explain if your observation makes sense, knowing that the energy minimization optimizes the structure to a local minimum?