

Protein Model with Polarizability and Transferability (*proMPT*) Gromacs Tutorial for Glycophorin A (GpA) in Dodecyl-phosphocholine (DPC)

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* For the original paper, please see: Pei-Yin Lee, Abhilash Sahoo, and Silvina Matysiak. "Modulation of helical conformation of Glycophorin A by point mutations". *Manuscript in preparation*.
* Python3 and Gromacs 2019.4 are used.

[Create topology for protein]

Use "*create_indent.py*" to generate a CG conformation as an extended strand. Files needed to provide: "*seq.txt*". A file named "*protein.gro*" will be generated and this is our CG protein topology for one GpA monomer.

[Create force field parameter files]

1. File "*fixedff_MC1.itp*" is the force field file that can be generated from *ProMPT*. One modification is the addition of the bead type "MC1", which is the "C1" in MARTINI, but is different from the "C1" in *ProMPT*.
2. Use "*genitp_md.py*" to generate the itp file for protein. Files needed to provide: "*seq.txt*". A file named "*output.itp*" will be generated as the itp file for protein. Here we need to manually modify the table number for the backbone dihedral potential according to the desired secondary structure. In the [dihedral] section, the second to last value is the table number for the backbone dihedral. 1 is for alpha helix, 2 for 3-10 helix, 4 for beta-sheet, and 6 for double-well (same preference for alpha helix and beta sheet). Currently only alpha helix, 3-10 helix, and beta sheet automation based on the pdb file is implemented. We recommend to check the [dihedral] section before running simulations to make sure the assigned secondary structure is desired. Here the second to last column should be 1 and the last column should be 10 (the force constant).
3. "*dpc_MC1.itp*" is the force field file for DPC and "*water.em.itp*"/"*water.md.itp*" are the force field files for water and they are from MARTINI.

[Construct the GpA system in a DPC/water box]

1. Create two boxes separately that contains one GpA monomer in a box:
`gmx_mpi editconf -f protein.gro -o monomer_box1.gro -bt cubic -center 4 2 6 -box 8 8 8 -princ`
`gmx_mpi editconf -f protein.gro -o monomer_box2.gro -bt cubic -center 4 6 2 -box 8 8 8 -princ`
2. Construct the final box:
Concatenate monomer_box1.gro and monomer_box2.gro together and make the file as *monomers.gro*.

3. Insert 80 DPC micelle:

`gmx_mpi insert-molecules -f monomers.gro -ci dpc.gro -o box1.gro -bt cubic -nmol 80`

4. Solvate 3000 water molecules:

`gmx_mpi solvate -cp box1.gro -cs water_001.npt.gro -o ready.gro -p newprotein.top -maxsol 3000` Here the “*water_001.npt.gro*” is taken from MARTINI.

[Energy minimization]

1. `gmx_mpi grompp -f em.mdp -c ready.gro -p newprotein.top -o em.tpr`

2. `gmx_mpi mdrun -s em.tpr -c em.gro -tableb ./table_a/* ./table_d* -v` Here the angular potential and the dihedral potential files need to be provided

[NPT equilibration]

1. First need to change “*water.em.itp*” to “*water.md.itp*” in “*newprotein.top*”.

2. `gmx_mpi grompp -f npt_posres_befion.mdp -p newprotein.top -c em.gro -o npt.tpr -maxwarn 1 -r em.gro -r em.gro -n index.ndx`

Here the index.ndx needs to be provided because the application of C α -H interaction that the GxxxG region residues need to be identified.

3. `mpirun gmx_mpi mdrun -s npt.tpr -cpi state.cpt -tableb ./table_a/table_a*.xvg ./table_d*.xvg -tablep table.xvg -deffnm npt_eq`

[MD production run]

1. `gmx_mpi grompp -f md.mdp -p newprotein.top -c npteq.gro -o md.tpr`

2. `mpirun gmx_mpi mdrun -s md.tpr -cpi npt_eq.cpt -tableb ./table_a/table_a*.xvg ./table_d*.xvg -tablep table.xvg -deffnm md`