

# COMMANDS TO RUN MDS OF PROTEIN-LIGAND COMPLEX

## Step-1: Preparation of protein and ligand.

➤ Use Discovery studio software.

## Step-2: Preparation of protein topology file

```
gmx pdb2gmx -f receptor.pdb -o receptor.gro
```

## Step-3: Preparation of ligand topology file.

➤ Use the Swiss Param online server.

Use the below command to generate the ligand.gro file

```
gmx editconf -f LIG.pdb -o lig.gro
```

## Step-4:

1. Merging of the receptor.gro and ligand.gro file to create the complex.gro file.
2. Modification of topol.top file.

## Step-5: Solvation

```
gmx editconf -f complex.gro -o newbox.gro -bt dodecahedron -d 1.0
```

Once the above command is executed, run the following command

```
gmx solvate -cp newbox.gro -cs spc216.gro -p topol.top -o solv.gro
```

## Step-6: Ionization

```
gmx grompp -f ions.mdp -c solv.gro -p topol.top -o ions.tpr
```

Once the above command is executed, run the following command

```
gmx genion -s ions.tpr -o solv_ions.gro -p topol.top -pname NA -nname CL -neutral
```

### Step-7: Energy Minimization

```
gmx grompp -f em.mdp -c solv_ions.gro -p topol.top -o em.tpr
```

Once the above command is executed, run the following command

```
gmx mdrun -v -deffnm em
```

### Step-8: Ligand Restrain

```
gmx make_ndx -f lig.gro -o index_lig.ndx
```

Once the above command is executed, run the following command

```
gmx genrestr -f lig.gro -n index_lig.ndx -o posre_lig.itp -fc 1000 1000 1000
```

### Step-9: Modification of topol.top file.

### Step-10: Generation of Thermostat.

```
gmx make_ndx -f em.gro -o index.ndx
```

### Step-11: Equilibration

#### Temperature equilibration:

```
gmx grompp -f nvt.mdp -c em.gro -r em.gro -p topol.top -n index.ndx -o nvt.tpr
```

Once the above command is executed, run the following command

```
gmx mdrun -v -deffnm nvt
```

#### Pressure equilibration:

```
gmx grompp -f npt.mdp -c nvt.gro -t nvt.cpt -r nvt.gro -p topol.top -n index.ndx  
-o npt.tpr
```

Once the above command is executed, run the following command

```
gmx mdrun -v -deffnm npt
```

### **Step-12: MD run**

```
gmx grompp -f md.mdp -c npt.gro -t npt.cpt -p topol.top -n index.ndx -o md.tpr
```

Once the above command is executed, run the following command

```
gmx mdrun -v -deffnm md
```