

START

## System Preparation

GET YOUR PDB  
(RCSB, literature, etc.)

pippo.pdb

PREPARE FILE FOR GMX  
(pdb2gmx)

conf.gro  
topol.top  
posre.itp

GENERATE BOX  
(editconf)

box.gro

ADD WATER  
(solvate)

solv.gro

ADD IONS  
(grompp + genion)

ions.gro

1em.gro  
1em.xtc  
1em.trr  
1em.edr  
1em.cpt  
1em.log

## Simulation

ENERGY MINIMIZATION  
(grompp + mdrun)

POSITION RESTRAINTS  
EQUILIBRATION  
(grompp + mdrun)

2nvt.gro  
2nvt.xtc  
2nvt.trr  
2nvt.edr  
2nvt.cpt  
2nvt.log

PRODUCTION  
(grompp + mdrun)

3md.gro  
3md.xtc  
3md.trr  
3md.edr  
3md.cpt  
3md.log

ANALYSIS  
(rms, cluster, rmsf, gyrate,  
distance, mindist, ..)

END

RCSB  
**PDB**  
PROTEIN DATA BANK

