```
;
;     File 'membrane.top' was generated
;     By user: dpv (1019)
;     On host: node1.quantum.chem.uni-sofia.bg.
;     At date: Tue Aug 29 09:55:41 2017

;
;     This is a standalone topology file
;
;     Created by:
;                          :-) GROMACS - gmx pdb2gmx, 2016.3 (-:
;
;     Command line:
;       gmx pdb2gmx -f ../membrane_all_final.pdb -p membrane.top -i
membrane_restraints.itp -o membrane.gro
;     Force field was read from current directory or a relative path -
path added.
;

; Include forcefield parameters
#include "./charmm36.ff/forcefield.itp"

; Include chain topologies
#include "membrane.itp"
#include "protein.itp"

; Include water topology
#include "./charmm36.ff/tip3p.itp"

#ifdef POSRES_WATER
; Position restraint for each water oxygen
[ position_restraints ]
;  i funct       fcx        fcy        fcz
   1    1       1000       1000       1000
#endif

; Include topology for ions
#include "./charmm36.ff/ions.itp"

[ system ]
; Name
A membrane-protein system simulation

[ molecules ]
; Compound        #mols
Membrane            1
Protein             1
SOL             45732
NA                242
CL                190
```