

```
title                = relaxation in ana ensemble with constant
surface tension

integrator           = md ; Leap-frog integrator
tinit               = 0.0
dt                  = 0.002
nsteps              = 500000

; number of steps for center of mass motion removal
comm_mode           = Linear
nstcomm             = 10
comm_grps           = System

; Output frequency for coords (x), velocities (v) and forces (f)
nstxout             = 5000
nstvout             = 10000
nstfout             = 0
; Output frequency for energies to log file and energy file
nstlog              = 5000
nstenergy           = 500

; NEIGHBORSEARCHING PARAMETERS
nstlist             = 10
nstcalcenergy       = 10
rlist               = 1.2
ns_type             = grid

; Output frequency and precision for xtc file
;nstxtcout          = 500
;xtc_precision      = 50

; Periodic boundary conditions: xyz or none
pbc                 = xyz
cutoff-scheme       = verlet

; Method for doing electrostatics
coulombtype         = PME
rcoulomb            = 1.2
rcoulomb_switch     = 1.0
fourierspacing      = 0.12
pme_order           = 4
optimize_fft        = yes

; Method for doing Van der Waals
vdwtype             = Cut-off
vdw_modifier        = Force-switch
rvdw                = 1.2
rvdw_switch         = 1.0
DispCorr            = no

; Temperature coupling
tcoupl              = V-rescale
tc_grps             = NA CL SOL MEM Protein
tau_t               = 0.1 0.1 0.1 0.1 0.1
```

```
ref_t          = 310 310 310 310 310

; Pressure coupling
pcoupl        = Berendsen
pcoupltype    = surface-tension
tau_p         = 1.0
ref_p         = 220 1.0
compressibility = 4.5e-05 4.5e-5

; GENERATE VELOCITIES FOR STARTUP RUN
gen_vel       = no

; OPTIONS FOR BONDS
constraints   = hbonds

; Type of constraint algorithm
constraint_algorithm = lincs

; Highest order in the expansion of the constraint coupling matrix
lincs_order   = 4
lincs_iter    = 4

; Lincs will write a warning to the stderr if in one step a bond
lincs_warnangle = 30
```