

SSH Secure Shell 3.2.9 (Build 283)
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This copy of SSH Secure Shell is a non-commercial version.
 This version does not include PKI and PKCS #11 functionality.

Last login: Mon Oct 27 10:29:57 2008 from phys9569.phys.tue.nl

-bash: Sample: command not found

andrea@nanopol:~> ls

```

:  bin          fftw-3.0.1.tar.gz  gromacs-3.3.3.tar.gz  lesstif-0.95.0.tar.gz  PS          tutor
:.. fftw-3.0.1  gromacs-3.3.3      lesstif-0.95.0      PDB          public_html

```

andrea@nanopol:~> cd PS

andrea@nanopol:~/PS> ls

```

32x80_equil_540_out.gro  dimer.gro      ffG43albon.itp      ffG43a1.hdb      ffG43a1-n_new.tdb
monomer.top             trimer.gro      #trimer.top.1#
32x80_equil_540_out.pdb  dimer.pdb      ffG43a1-c_new.tdb   ffG43a1.itp      ffG43a1-n.tdb
pdb2gmx.log             #trimer.gro.1#
32x80_equil_540_out.top  dimer.top      ffG43a1-c.tdb       ffG43a1nb.itp    ffG43a1.rtp      posre.itp
trimer.pdb
chain.pdb               ffG43a1.atp    ffG43a1.ddb         ffG43a1_new.hdb  monomer.pdb
#posre.itp.1#          trimer.top
andrea@nanopol:~/PS> less trimer.top

```

```

;
;      File 'trimer.top' was generated
;      By user: onbekend (0)
;      On host: onbekend
;      At date: Mon Oct 27 15:42:15 2008
;
;      This is your topology file
;      "Good Music Saves your Soul" (Lemmy)
;
; Include forcefield parameters
#include "ffG43a1.itp"

```

[moleculetype]

```

; Name          nrexcl
Protein         3

```

[atoms]

nr	type	resnr	residue	atom	cgnr	charge	mass	typeB	chargeB	massB
1	CH3	1	PS1	CH3	1	0	15.035	; qtot 0		
2	CH1	1	PS1	CH	1	0	13.019	; qtot 0		
3	C	1	PS1	CB	1	0	12.011	; qtot 0		
4	CR1	1	PS1	CG1	1	0	13.019	; qtot 0		
5	CR1	1	PS1	CG2	1	0	13.019	; qtot 0		
6	CR1	1	PS1	CG3	1	0	13.019	; qtot 0		
7	CR1	1	PS1	CG4	1	0	13.019	; qtot 0		
8	CR1	1	PS1	CG5	1	0	13.019	; qtot 0		
9	CH2	2	PS	CH2	2	0	14.027	; qtot 0		
10	CH1	2	PS	CH	2	0	13.019	; qtot 0		
11	C	2	PS	CB	2	0	12.011	; qtot 0		
12	CR1	2	PS	CG1	2	0	13.019	; qtot 0		
13	CR1	2	PS	CG2	2	0	13.019	; qtot 0		

14	CR1	2	PS	CG3	2	0	13.019	; qtot 0
15	CR1	2	PS	CG4	2	0	13.019	; qtot 0
16	CR1	2	PS	CG5	2	0	13.019	; qtot 0
17	CH2	3	PSN	CH2	3	0	14.027	; qtot 0
18	CH1	3	PSN	CH	3	0	13.019	; qtot 0
19	C	3	PSN	CB	3	0	12.011	; qtot 0
20	CR1	3	PSN	CG1	3	0	13.019	; qtot 0
21	CR1	3	PSN	CG2	3	0	13.019	; qtot 0
22	CR1	3	PSN	CG3	3	0	13.019	; qtot 0
23	CR1	3	PSN	CG4	3	0	13.019	; qtot 0
24	CR1	3	PSN	CG5	3	0	13.019	; qtot 0
25	CH3	3	PSN	CH3	3	0	15.035	; qtot 0

[bonds]

; ai	aj	funct	c0	c1	c2	c3
1	2	2	gb_26			
2	3	2	gb_26			
2	9	2	gb_26			
3	4	2	gb_15			
3	8	2	gb_15			
4	5	2	gb_15			
5	6	2	gb_15			
6	7	2	gb_15			
7	8	2	gb_15			
9	10	2	gb_26			
10	11	2	gb_26			
10	17	2	gb_26			
11	12	2	gb_15			
11	16	2	gb_15			
12	13	2	gb_15			
13	14	2	gb_15			
14	15	2	gb_15			
15	16	2	gb_15			
17	18	2	gb_26			
18	19	2	gb_26			
18	25	2	gb_26			
19	20	2	gb_15			
19	24	2	gb_15			
20	21	2	gb_15			
21	22	2	gb_15			
22	23	2	gb_15			
23	24	2	gb_15			

[pairs]

; ai	aj	funct	c0	c1	c2	c3
1	4	1				
1	8	1				
1	10	1				
2	5	1				
2	7	1				
2	11	1				
2	17	1				
3	6	1				
3	10	1				
4	7	1				
4	9	1				
5	8	1				
8	9	1				
9	12	1				
9	16	1				
9	18	1				
10	13	1				
10	15	1				
10	19	1				
10	25	1				
11	14	1				
11	18	1				
12	15	1				
12	17	1				
13	16	1				
16	17	1				
17	20	1				
17	24	1				
18	21	1				

18	23	1
19	22	1
20	23	1
20	25	1
21	24	1
24	25	1

[angles]

; ai	aj	ak	funct		c0	c1	c2	c3
1	2	3	2	ga_12				
1	2	9	2	ga_12				
3	2	9	2	ga_12				
2	3	4	2	ga_26				
2	3	8	2	ga_26				
4	3	8	2	ga_26				
3	4	5	2	ga_26				
4	5	6	2	ga_26				
5	6	7	2	ga_26				
6	7	8	2	ga_26				
3	8	7	2	ga_26				
2	9	10	2	ga_12				
9	10	11	2	ga_12				
9	10	17	2	ga_12				
11	10	17	2	ga_12				
10	11	12	2	ga_26				
10	11	16	2	ga_26				
12	11	16	2	ga_26				
11	12	13	2	ga_26				
12	13	14	2	ga_26				
13	14	15	2	ga_26				
14	15	16	2	ga_26				
11	16	15	2	ga_26				
10	17	18	2	ga_12				
17	18	19	2	ga_12				
17	18	25	2	ga_12				
19	18	25	2	ga_12				
18	19	20	2	ga_26				
18	19	24	2	ga_26				
20	19	24	2	ga_26				
19	20	21	2	ga_26				
20	21	22	2	ga_26				
21	22	23	2	ga_26				
22	23	24	2	ga_26				
19	24	23	2	ga_26				

[dihedrals]

; ai	aj	ak	al	funct		c0	c1	c2	c3	c4
	c5									
1	2	3	4	1	gd_1					
1	2	3	8	1	gd_1					
9	2	3	4	1	gd_1					
9	2	3	8	1	gd_1					
1	2	9	10	1	gd_16					
3	2	9	10	1	gd_16					
2	3	4	5	1						
2	3	8	7	1						
2	9	10	11	1	gd_16					
9	10	11	12	1	gd_1					
9	10	11	16	1	gd_1					
17	10	11	12	1	gd_1					
17	10	11	16	1	gd_1					
9	10	17	18	1	gd_16					
11	10	17	18	1	gd_16					
10	11	12	13	1						
10	11	16	15	1						
10	17	18	19	1	gd_16					
10	17	18	25	1	gd_16					
17	18	19	20	1	gd_1					
17	18	19	24	1	gd_1					
25	18	19	20	1	gd_1					
25	18	19	24	1	gd_1					
18	19	20	21	1						
18	19	24	23	1						

```
[ dihedrals ]
; ai aj ak al funct c0 c1 c2 c3
1 9 3 2 2 gi_1
2 8 4 3 2 gi_1
2 9 1 3 2 gi_1
2 1 3 9 2 gi_1
3 8 2 4 2 gi_1
3 4 5 6 2 gi_1
3 8 7 6 2 gi_1
3 2 4 8 2 gi_1
4 3 8 7 2 gi_1
4 5 6 7 2 gi_1
5 4 3 8 2 gi_1
5 6 7 8 2 gi_1
9 17 11 10 2 gi_1
10 16 12 11 2 gi_1
10 17 9 11 2 gi_1
10 9 11 17 2 gi_1
11 16 10 12 2 gi_1
11 12 13 14 2 gi_1
11 16 15 14 2 gi_1
11 10 12 16 2 gi_1
12 11 16 15 2 gi_1
12 13 14 15 2 gi_1
13 12 11 16 2 gi_1
13 14 15 16 2 gi_1
17 25 19 18 2 gi_1
18 24 20 19 2 gi_1
18 25 17 19 2 gi_1
18 17 19 25 2 gi_1
19 24 18 20 2 gi_1
19 20 21 22 2 gi_1
19 24 23 22 2 gi_1
19 18 20 24 2 gi_1
20 19 24 23 2 gi_1
20 21 22 23 2 gi_1
21 20 19 24 2 gi_1
21 22 23 24 2 gi_1
```

```
; Include Position restraint file
#ifdef POSRES
#include "posre.itp"
#endif
```

```
; Include water topology
#include "spc.itp"
```

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

```
; Include generic topology for ions
#include "ions.itp"
```

```
[ system ]
; Name
Protein
```

```
[ molecules ]
; Compound #mols
Protein 1
trimer.top lines 204-242/242 (END)
```

