Fatal error molecule type sol contains no atoms gromacs

GROMACSGROMACS,,??, ...

GROMACS,?,, ...

T-Coupling group XXX has fewer than 10% of the atoms¶. It is possible to specify separate thermostats (temperature coupling groups) for every molecule type within a ...

GROMACS version: 2020.2 GROMACS modification: No Hello, I am trying to follow the Protein-Ligand Complex tutorial but I end up in a problem and I don"t understand ...

Gromacs,: No line with molecule type "SOL" found the [molecule] section of file topol ? ...

[atomtypes] [system] [molecules] ?top,itp?itp [atomtypes] itp ...

2.6k,6,4?gromacs,:Fatal error:No line with moleculetype "SOL" found the ...

,gromacs: No such moleculetype SOL? sobtop p.gro,gromacs, ...

-,gmx grompp,No molecules were defined in the system,gro,? ...

: [atomtypes] [moleculetype],atometype not found,amber, [...

(genionion.tpr),"NoSOL"? SOL,"""? ...

Excluding 2 bonded neighbours molecule type "SOL" Excluding 1 bonded neighbours molecule type "NA" turning H bonds into constraints... NOTE 1 [file topol , line ...

Fatal error: No such moleculetype XXX¶ Each type of molecule in your [molecules] section of your top file must have a corresponding [moleculetype] section defined previously, ...

Fatal error: There were 4 missing atoms in molecule Protein_chain_A, if you want to use this incomplete topology anyhow, use the option -missing *.pdb*.rtp ...

I ran gromacs with command: grompp -f ions.mdp -c protein a_solv.gro -p topol -o ions.tpr. and yielded a Fatal error: Correct the number of coordinates in coordinate file (protein a.gro, 36891 ...

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No default Proper Dih. types. ERROR 2 [file sin p, line 344]: No default Proper Dih. types. Excluding 3 bonded neighbours molecule type "Protein_chain_A" Excluding 3 ...

Fatal error: No such moleculetype XXX# Each type of molecule in your [molecules] section of your top file must have a corresponding [moleculetype] section defined previously, ...

Solvent box contains 99373 atoms in 28208 residues Removed 12253 solvent atoms due to solvent-solvent overlap Removed 5122 solvent atoms due to solute-solvent ...

However, after the solvation stage, I keep encountering this error when I try to run the command: "gmx grompp -f ions.mdp -c solvated.gro -p topol -o ions.tpr" The error: ...

I am facing a problem between different versions of gromacs for gmx pdb2gmx. I have a protein-ligand system, I did all the necessary steps mentioned in gromacs manual for ...

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