

GROMACS - Bug #2480

pdb2gmx does not protonate correctly for united-atom Gromos

04/16/2018 06:19 PM - Mikko Huhtala

Status: New	
Priority: Normal	
Assignee: Mark Abraham	
Category: preprocessing (pdb2gmx,grompp)	
Target version: 2021	
Affected version - extra info:	Difficulty: uncategorized
Affected version: 2018	
Description	
<p>pdb2gmx builds ASPH residues without the HD2 hydrogen for Gromos 54a7. I changed manually the residue name of Asp95 in the PDB file 3GUU from ASP to ASPH and ran pdb2gmx. The result was a ASPH residue name both in the topology and the structure file, but both without the HD2 hydrogen, i.e. ASP structure, not ASPH. Changing His366 to HISA worked correctly, giving a correct HISA residue in the output. Edited PDB file included (3GUU A chain + crystal water, excluding heteroatoms, modified Asp95 and His366).</p> <p>Version: Gromacs 2018, single precision, Linux x86_64.</p> <p>Discussed on the mailing list: https://mailman-1.sys.kth.se/pipermail/gromacs.org_gmx-users/2018-April/119852.html</p>	

History

#1 - 05/09/2018 12:04 PM - Mikko Huhtala

Tested 2018.1, the issue is still there.

#2 - 05/09/2018 01:27 PM - Mikko Huhtala

Realized that the issue cuts both ways: renaming ASP to ASPH in the input will build a ASP topology, and having an actual ASPH with the hydrogen in the input is not recognized. I get the following error:

```
"Fatal error:
Atom HD2 in residue ASPH 61 was not found in rtp entry ASP with 9 atoms
while sorting atoms."
```

ASPH has 10 atoms, not 9. For some reason pdb2gmx tries to build an ASP residue with 9 atoms.

This is when selecting GROMOS96 54a7 in Gromacs 2018.1.

#3 - 05/09/2018 03:34 PM - Mark Abraham

What happens when you use `gmx pdb2gmx -asp`, which is the intended way for you to specify protonation states of such residues?

#4 - 05/10/2018 03:58 PM - Mikko Huhtala

That will work, but avoiding that was my whole point starting the thread on the mailing list. The manual entering of protonation states is a pain, if you need to e.g. input protonation calculated with another tool, or prepare multiple versions of the protein with residue substitutions etc. You want text input that's readable and scriptable.

#5 - 06/07/2018 01:02 PM - Mikko Huhtala

Work intervened, so I'm adding this comment late. I made another post weeks ago on the mailing list, and Justin Lemkul confirmed that pdb2gmx does behave inconsistently with different force fields. ASH gets built correctly for Amber and Charmm, but ASPH does not for Gromos and OPLS-AA. See

https://mailman-1.sys.kth.se/pipermail/gromacs.org_gmx-users/2018-May/120236.html

Justin Lemkul commented earlier that building the protonated states according to the force field residue name in the input PDB file is the expected behavior. I can't actually find an explicit statement of that anywhere in Gromacs documentation, but that may be just me. If the user is always expected to enter the protonation states manually, I think there should be at least a mention of it somewhere ("no guarantees on what happens to ASH/ASPH etc." or something to that effect). In any case, I think the current interactive interface is a very bad idea anyway - entering long lists of residues by hand. If you make one mistake, you have to start from the beginning. And the residues are not in the order of sequence, but by type, so using the output of a external protonation calculation tool manually becomes very inconvenient. E.g. my case happened to be a 430-residue protein

with 6 non-default protonation states across three different residue types (total > 40 residues). Preparing topologies for a wild type and a couple of mutants means going through the error-prone manual keying three times.

#6 - 06/07/2018 01:06 PM - Mark Abraham

- Target version set to 2018.2

We wholeheartedly agree that pdb2gmx needs an overhaul. I'll see what I can do on the minor points for 2018.2, but the structural issues will need more far-reaching re-design of system preparation workflows.

#7 - 06/13/2018 06:10 PM - Mark Abraham

- Category set to preprocessing (pdb2gmx.grompp)

- Assignee set to Mark Abraham

- Target version changed from 2018.2 to 2018.3

Will reconsider for 2018.3

#8 - 08/21/2018 10:38 AM - Paul Bauer

- Target version changed from 2018.3 to 2019

I changed the target version for this, as it involves more general work on how pdb2gmx works as Mark mentioned before.

#9 - 12/17/2018 01:27 PM - Paul Bauer

- Target version changed from 2019 to 2020

This work needs to be done in a future version

#10 - 12/20/2019 12:17 PM - Paul Bauer

- Target version changed from 2020 to 2021

Files

3guu_A.pdb	336 KB	04/16/2018	Mikko Huhtala
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