

GROMACS - Bug #2907

Gromacs autocompletion appears to be broken with ZSH

03/27/2019 11:19 AM - Daniel Bauer

Status: New	
Priority: Normal	
Assignee:	
Category: documentation	
Target version:	
Affected version - extra info:	Difficulty: uncategorized
Affected version: 2018.3	

Description

Hello,

It appears that gromacs autocompletion is at least partially broken when using zsh. It does not complete filenames. Here is a little example:

Bash:

```
bauer@t480s:~$ ls -l | grep xe
-rw-r--r--  1 bauer bauer    387 Dec 10 10:39 xe.gro
-rw-r--r--  1 bauer bauer    571 Dec 10 10:36 xe.pdb
```

```
bauer@t480s:~$ source /opt/gromacs-2018/bin/GMXRC
# this gives me working autocompletion for editconf, -f and also finds xe.pdb when typing x<TAB>
bauer@t480s:~$ gmx editconf -f xe.pdb
```

ZSH:

```
t480s% source /opt/gromacs-2018/bin/GMXRC
# this gives me working autocompletion for editconf and -f, however, autocompletion of files (xe.p
db) is not working
t480s% gmx editconf -f xe<TAB>
```

All this was done with a minimal .zshrc/.bashrc and no plugins, customizations or whatsoever (except loading compinit in .zshrc). From a short glance over the code of gmx-autocompletion.bash it appears that the variable "\$p\$" that is responsible for the next switch statement is not populated in zsh for some reason (I wasn't able to find out why). Please let me know if more information is needed.

History

#1 - 07/16/2019 04:46 AM - Floris van Eerden

I have the same issue... Did anybody by any chance find a solution?