

Issues

#	Project	Tracker	Status	Priority	Subject	Assignee	Updated	Target version
49	GROMACS	Bug	Closed	High	Wrong image convention for evaluating dummy atoms.	David van der Spoel	04/01/2006 08:22 PM	3.3
39	GROMACS	Bug	Closed	High	Generation of initial velocities counts dummy atoms as normal atoms.	Erik Lindahl	01/01/2006 10:06 PM	3.3
35	GROMACS	Bug	Closed	High	trjconv does not read velocities from g96 file.	Erik Lindahl	12/08/2005 09:58 PM	3.3
18	GROMACS	Bug	Closed	Low	Implement position rescaling with Rahman Parrinello barostat.	Erik Lindahl	07/23/2007 04:38 PM	CVS
17	GROMACS	Bug	Closed	High	Double precision gromacs truncates in memory coordinates to single precision when writting XTC file.	Erik Lindahl	10/06/2005 06:51 PM	3.2.1
16	GROMACS	Bug	Closed	High	Issue an error if pme_order < fourier_nx/y/z	Erik Lindahl	10/03/2005 09:30 PM	3.2.1
14	GROMACS	Bug	Closed	Normal	Rahman Parrinello barostat not accurate for the anisotropic case.	Erik Lindahl	07/23/2007 04:15 PM	CVS
12	GROMACS	Bug	Closed	Low	Forces between frozen particles contribute to pressure.	Erik Lindahl	09/12/2005 11:41 PM	3.2.1
11	GROMACS	Bug	Closed	High	ngmx exit confirmation is broken	David van der Spoel	09/21/2005 10:29 PM	3.2.1