



GROMACS 2023-2024: New features and improvements

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About GROMACS

- Molecular dynamics simulation package
- User-driven development
- High performance
 - Good scalability
 - GPU acceleration
 - Runs on most platforms and hardware
- Suite of analysis tools
- Tutorials
- Interfaces to other software
- Free Software

- General information: <https://www.gromacs.org>
- Documentation: <https://manual.gromacs.org>
- Tutorials: <https://tutorials.gromacs.org>
- Forums: <https://gromacs.bioexcel.eu>
- Development: <https://gitlab.com/gromacs/gromacs>

2024 release

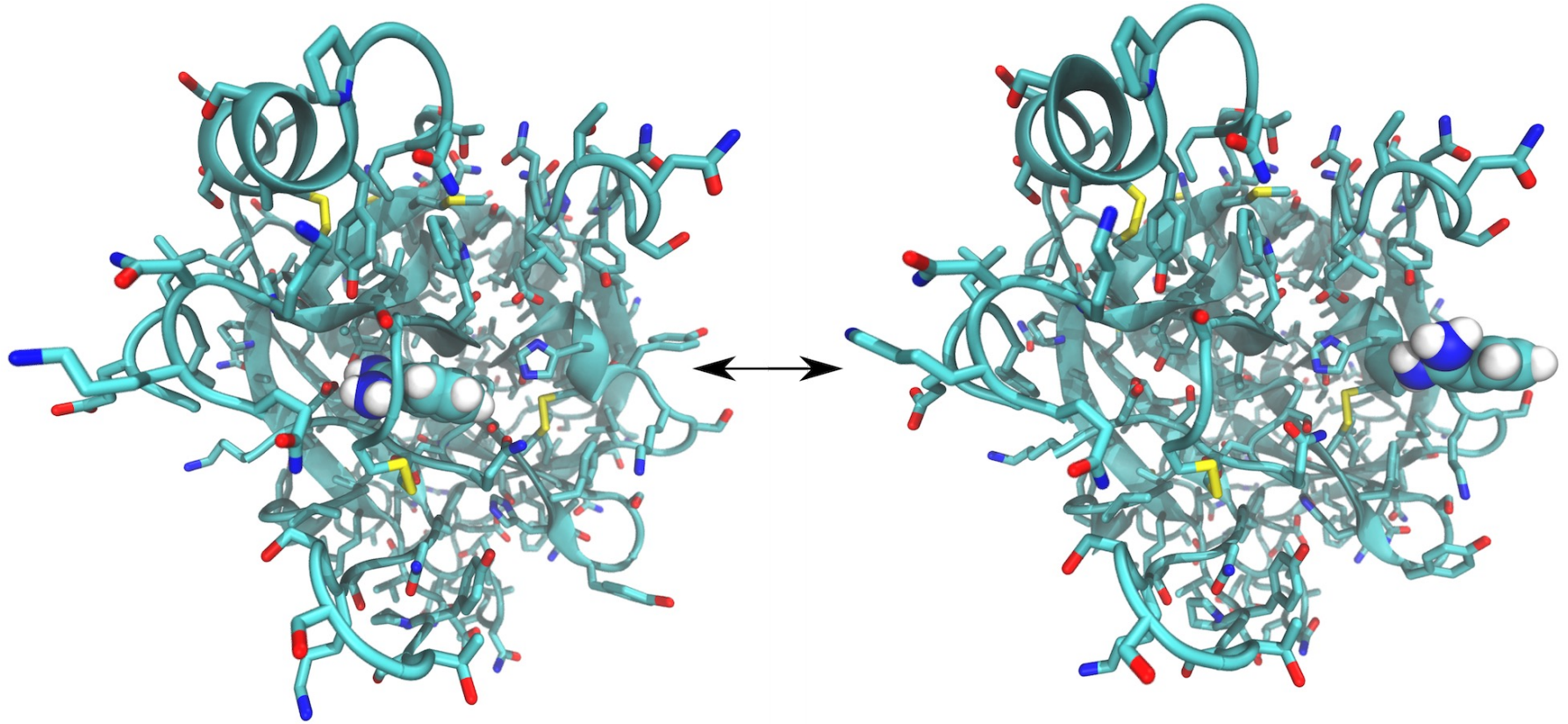
- 2024.0 was released January 30th
- 2024.1 was released February 28th

News in 2024

- Colvars integration
- AWH improvements
 - Automatic scaling of the target distribution
 - Improved control of the exponential growth of histograms
- Improved deform option, now suitable for calculating viscosities
- Reduced artifacts, on pressure, from Lennard-Jones pair interactions
- Performance improvements
 - Hydrogen mass repartitioning in `gmx grompp`
 - Configurable multi-GPU FFT options

Native Colvars integration

- Use collective variables
 - Apply restraint or bias
 - Enhanced sampling



Input data from Aho N, Groenhof G, Buslaev P. ChemRxiv. 2023; doi:10.26434/chemrxiv-2023-2pqjs.
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Using Colvars from GROMACS

```
colvars-active      = true  
colvars-configfile = colvars.cfg
```



```
colvarsTrajFrequency 1000
indexFile ../../awh/awh_sw/index.ndx
```

```
colvar {
  name binding
  width 0.001

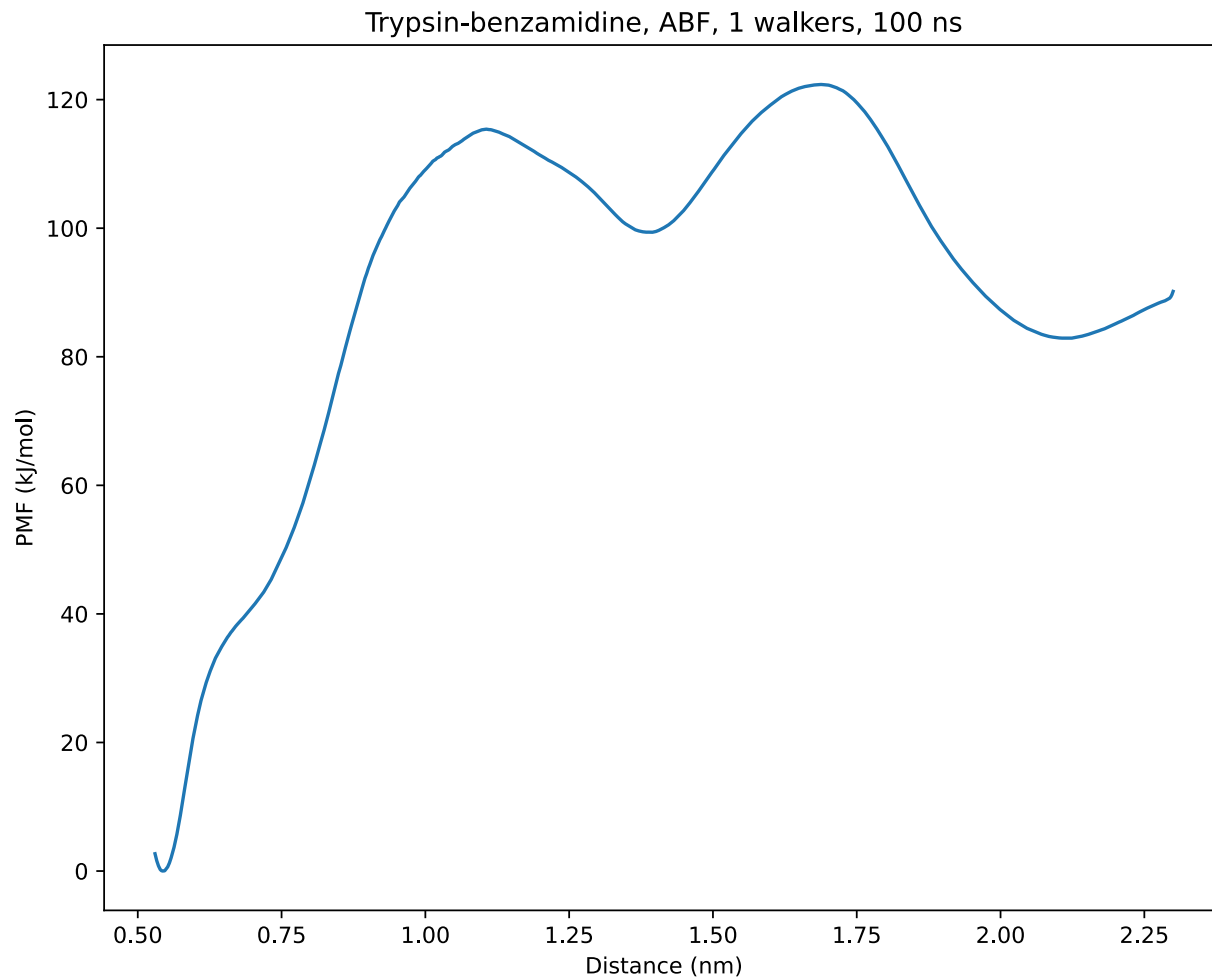
  lowerBoundary 0.53
  upperBoundary 2.3

  distanceZ {
    ref { indexGroup chainB }
    main { indexGroup chainA }
    axis (0.0, 0.0, 1.0)
  }
}
```

```
extendedLagrangian on
extendedFluctuation 0.005
}
```

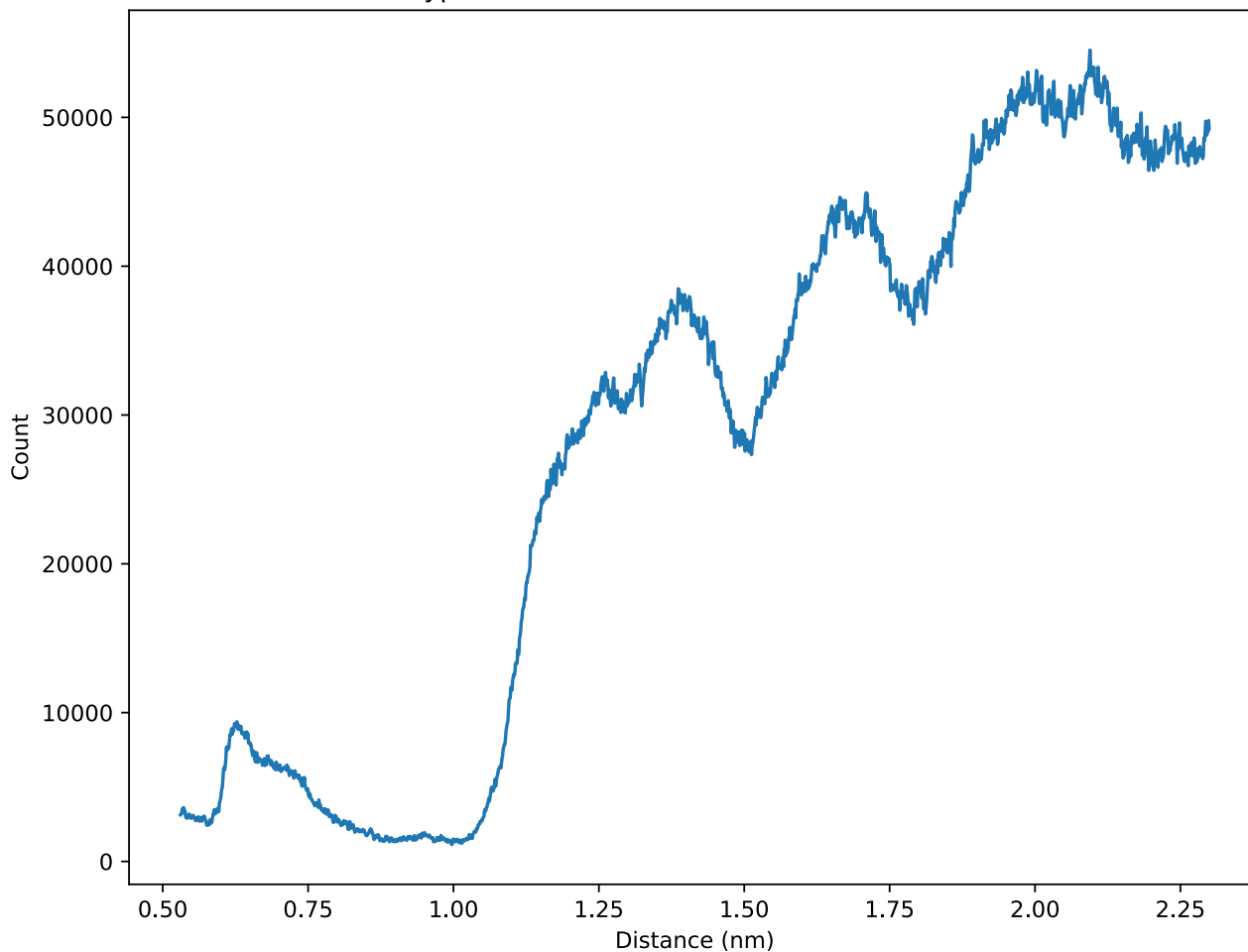
```
abf {
  colvars binding
  fullSamples 200
}
```

```
harmonicWalls {
  name wall_binding
  colvars binding
  lowerWalls 0.53
  upperWalls 2.3
  forceConstant 1
}
```

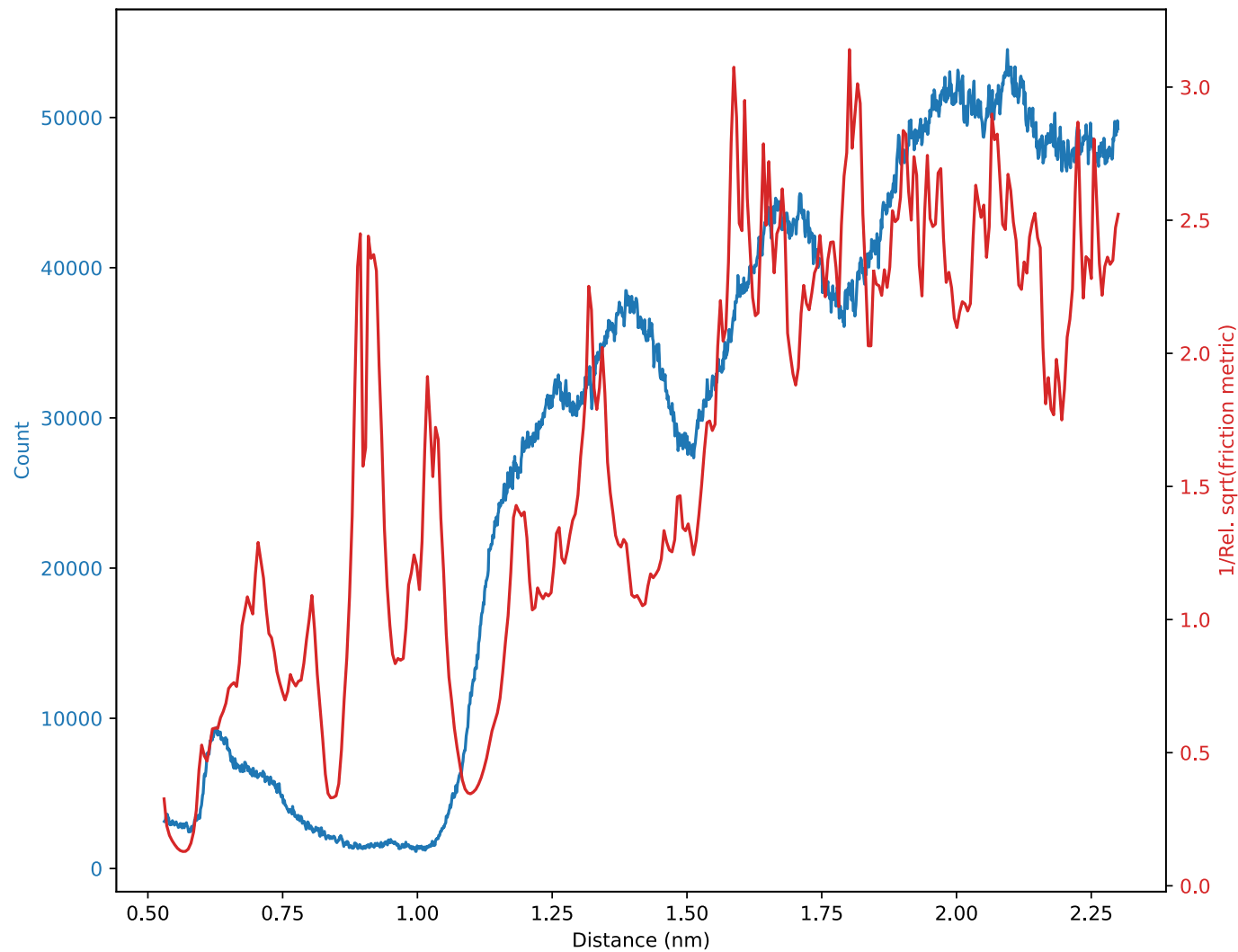


Input data from Aho N, Groenhof G, Buslaev P. ChemRxiv. 2023; doi:10.26434/chemrxiv-2023-2pqls.
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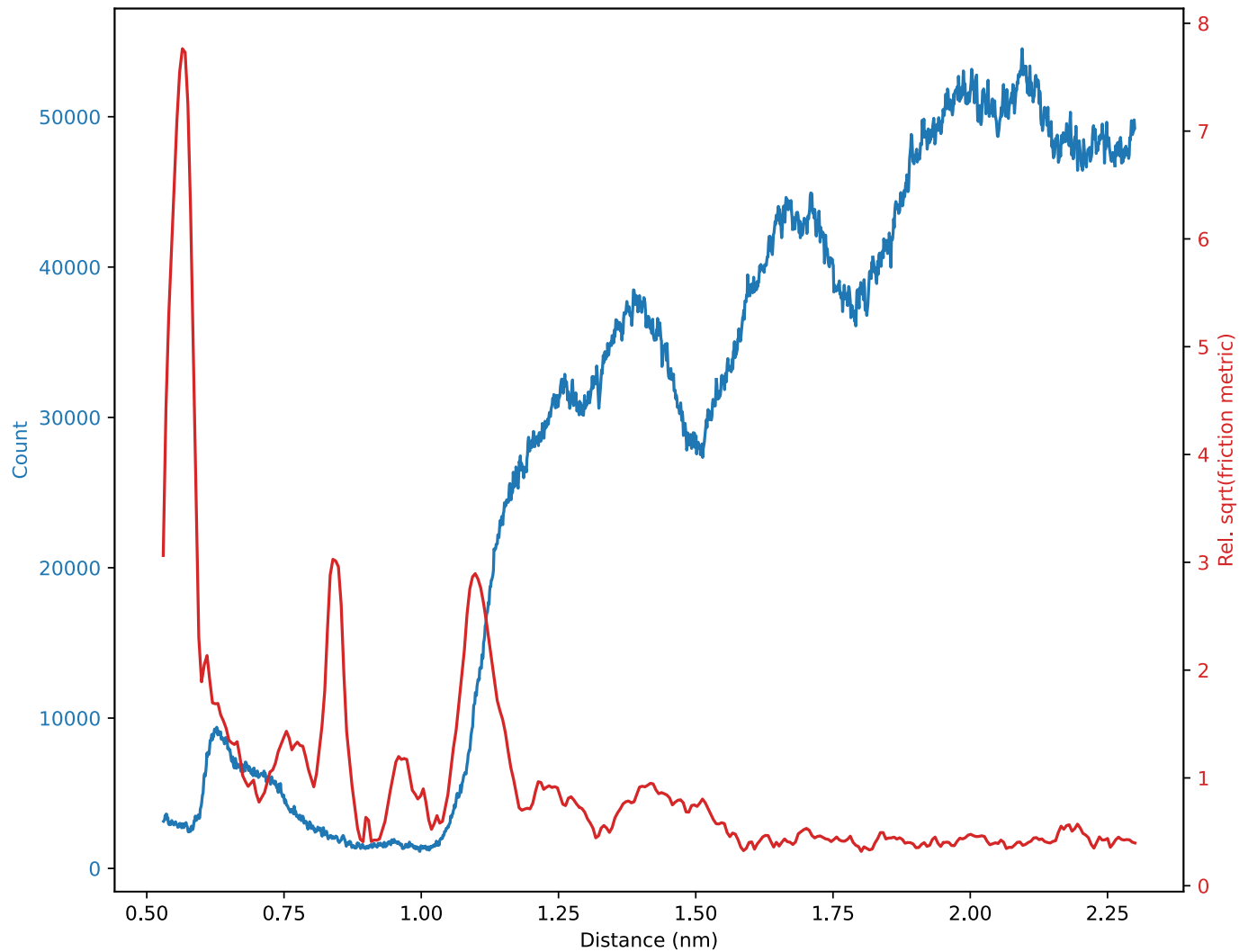
Trypsin-benzamidine, ABF, 1 walker, 100 ns



Input data from Aho N, Groenhof G, Buslaev P. ChemRxiv. 2023; doi:10.26434/chemrxiv-2023-2pqls.
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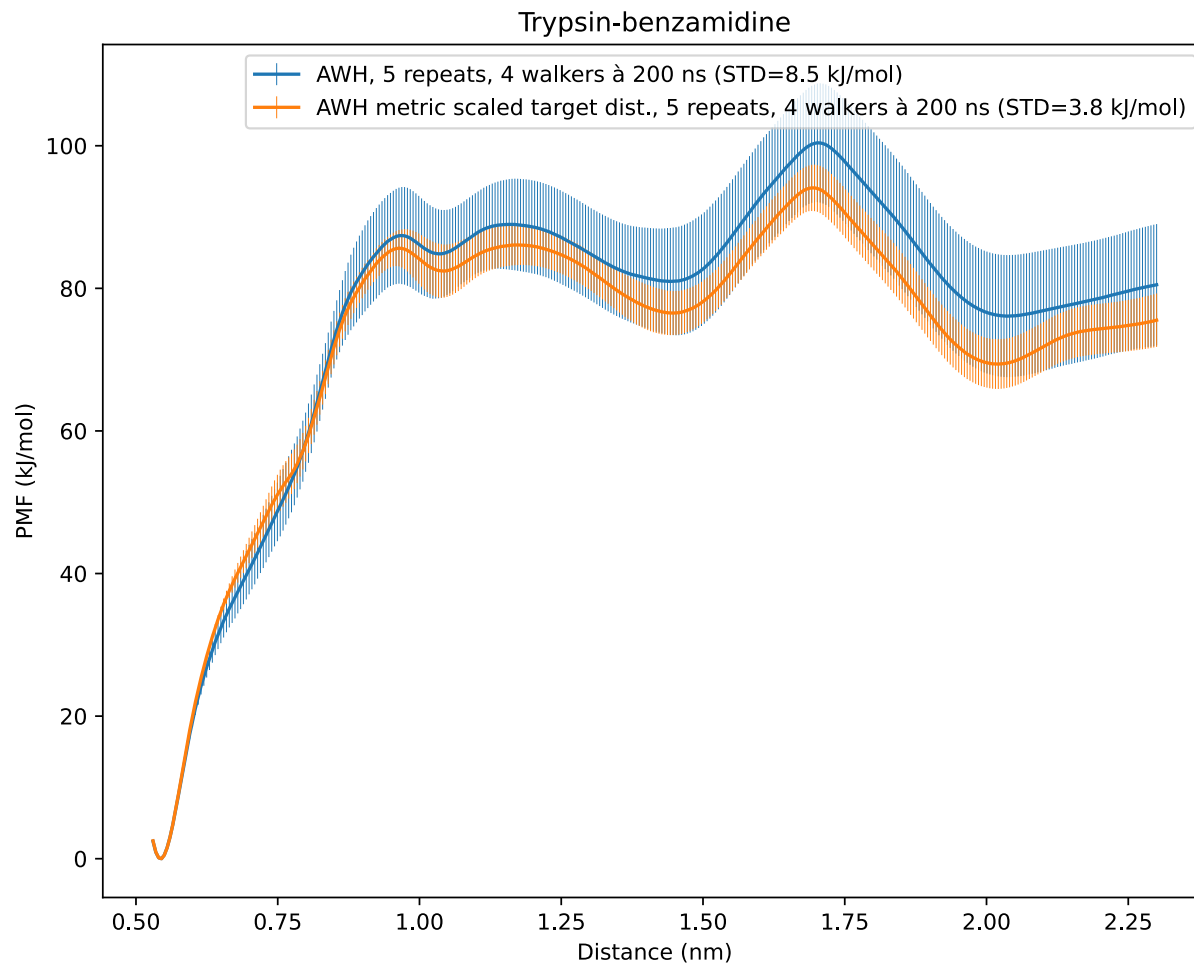


Input data from Aho N, Groenhof G, Buslaev P. ChemRxiv. 2023; doi:10.26434/chemrxiv-2023-2pqls.
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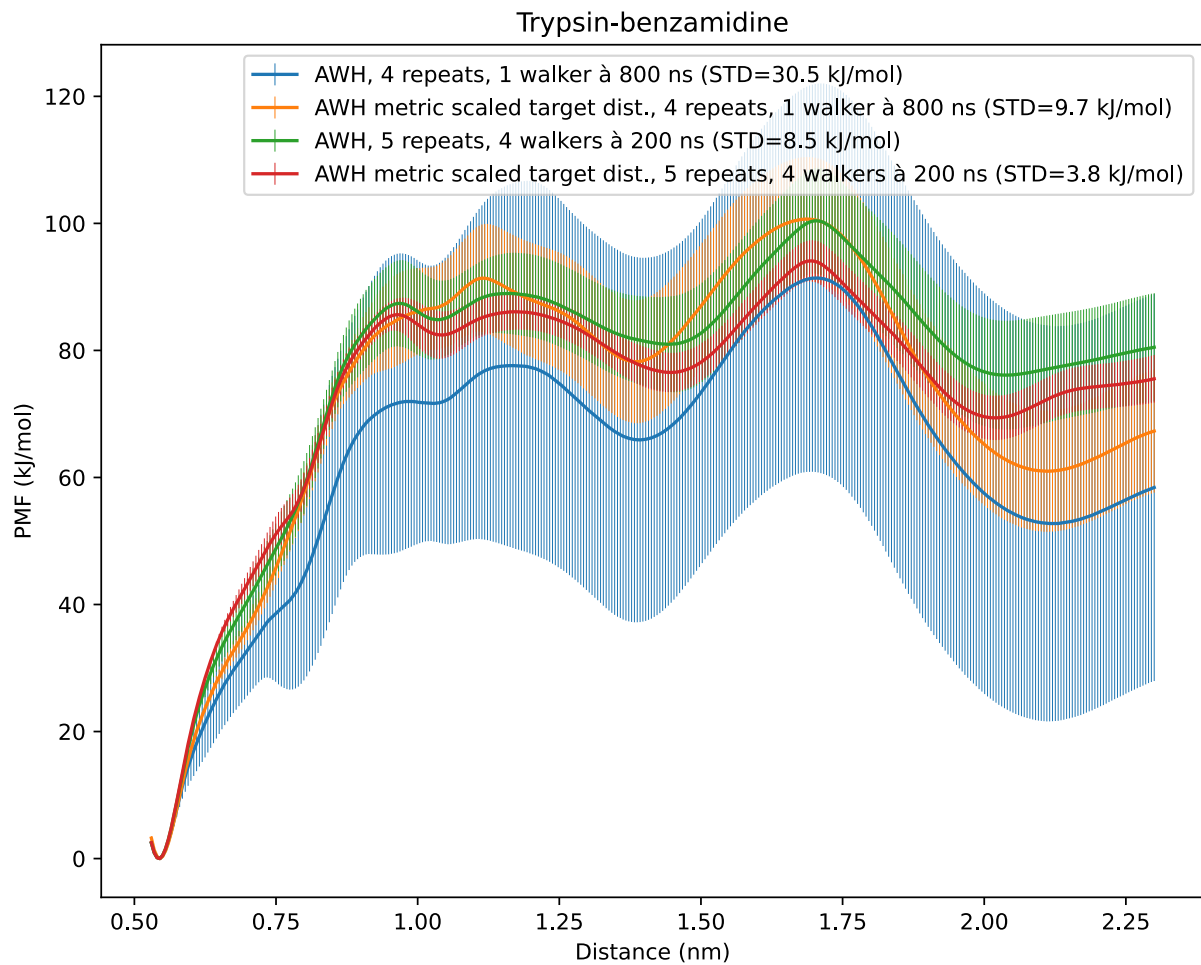
Accelerated Weight Histogram (AWH) method

- Automatic scaling of the target distribution based on the AWH friction metric

`awh1-target-metric-scaling = yes`



Input data from Aho N, Groenhof G, Buslaev P. ChemRxiv. 2023; doi:10.26434/chemrxiv-2023-2pqls.
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Input data from Aho N, Groenhof G, Buslaev P. ChemRxiv. 2023; doi:10.26434/chemrxiv-2023-2pqls.
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Accelerated Weight Histogram (AWH) method

- Set the exponential growth factor during the initial stage

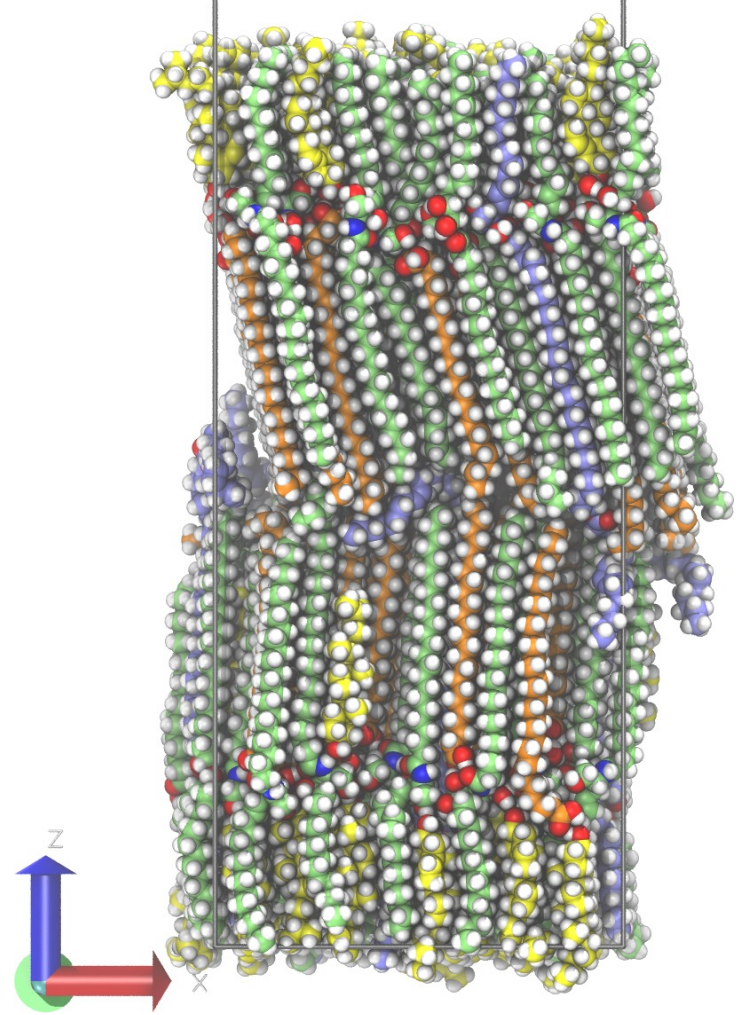
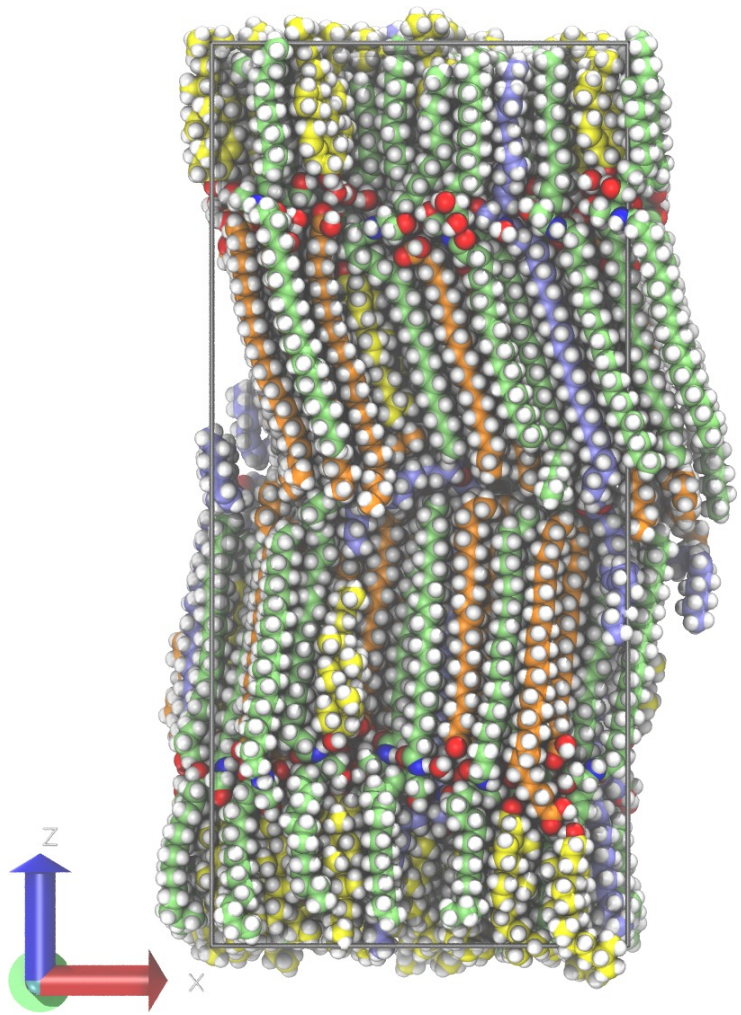
`awh1-growth-factor = 2`

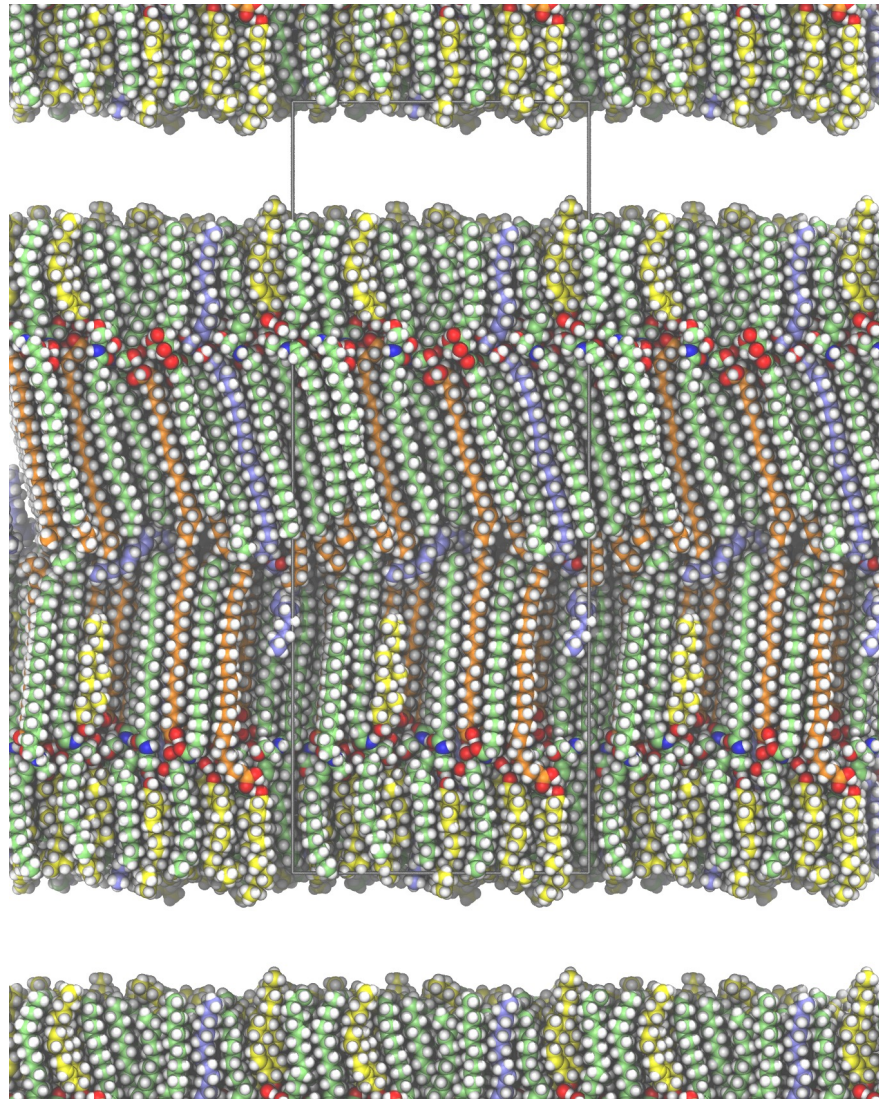
Box deformation and viscosity calculations

- The deform option now only deforms the box without modifying particle positions.
- Uses a velocity profile (flow field), that can be automatically generated at the beginning of the simulation.

- MDP example

```
deform          = 0 0 0.001 0 0 0  
deform-init-flow = yes
```

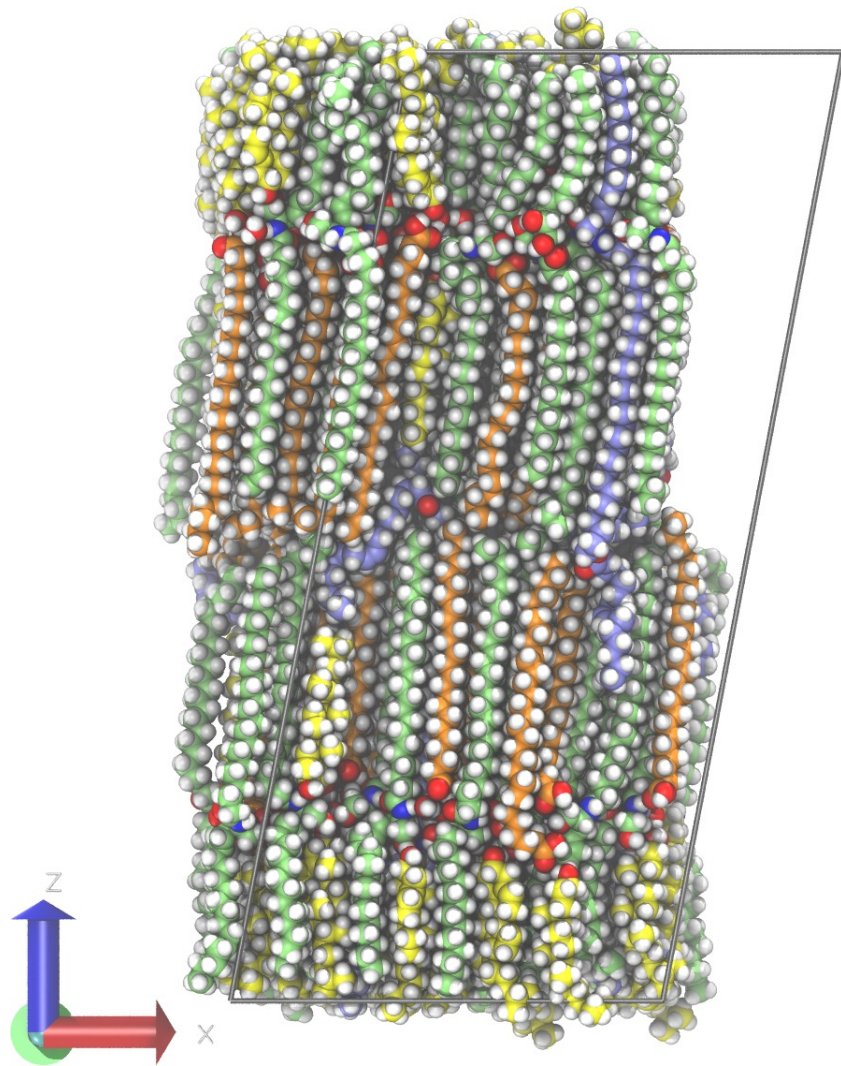
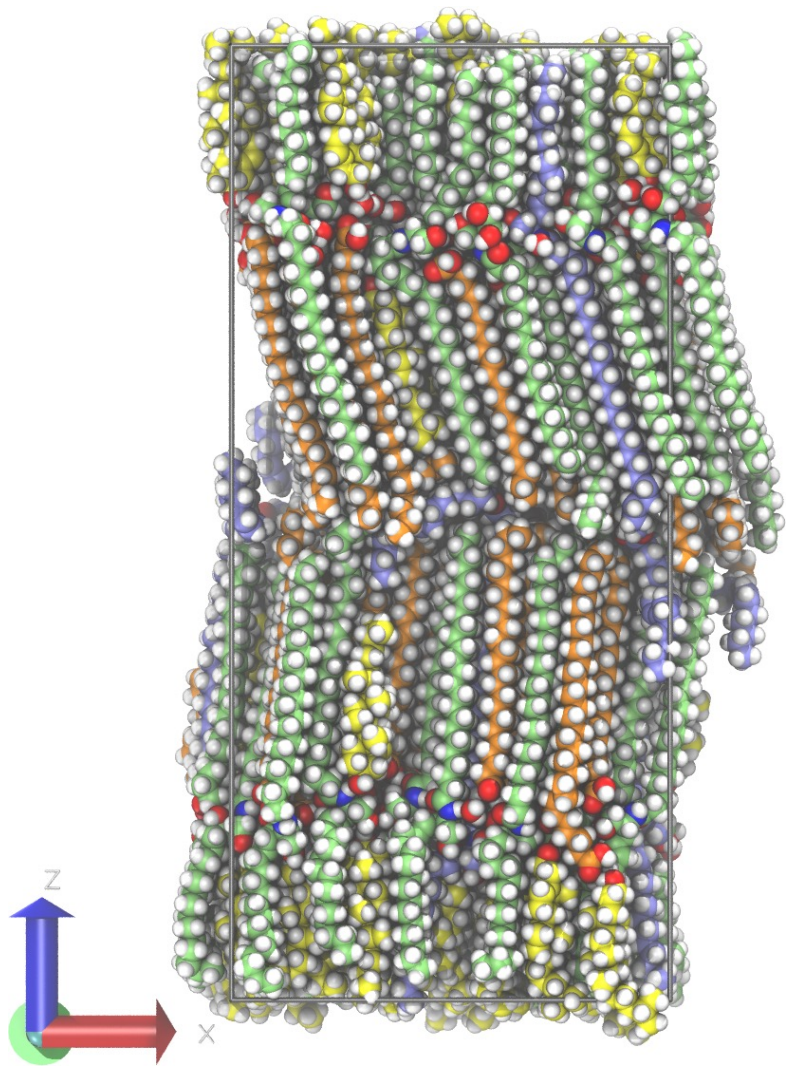


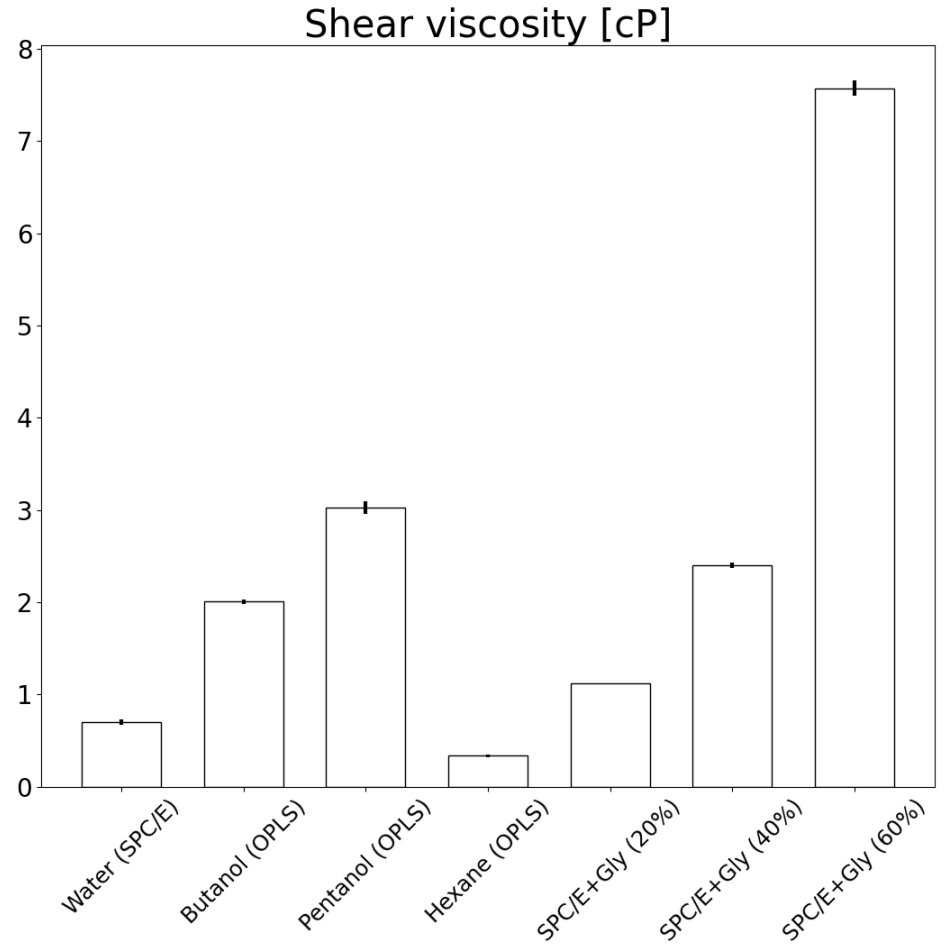
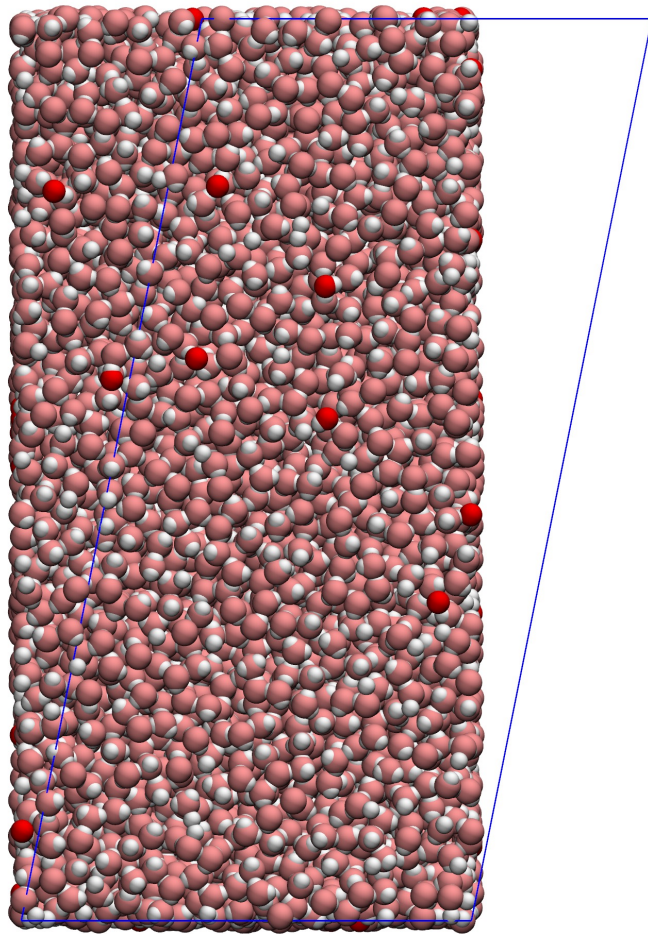


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- MDP example

```
deform          = 0 0 0 0 0.001 0  
deform-init-flow = yes
```





- Reduced artifacts from LJ interactions on the pressure
 - The Verlet pair list buffer was based only on energy drift.
 - Missing Lennard-Jones interactions could lead to incorrectly increasing pressure over the life time of the pairlist.
 - Affected systems without charge.
- Can lead to a slight performance loss, especially for coarse-grained systems.
- The tolerance to pressure deviation over the lifetime of the pair list can be set by an mdp parameter:

```
verlet-buffer-pressure-tolerance (0.5) [bar]
```

Performance improvements 2023

- Major SYCL GPU extensions
 - Working on important HPC platforms
- CUDA Graphs
 - When all force and updates are run on GPU
 - Record activities to a graph
 - Reduced overhead when launching a graph instead of each activity
 - Enabled using `GMX_CUDA_GRAPH` environment variable
- PME decomposition support with CUDA and SYCL
- Updates run on GPU by default
- Higher default coupling intervals for thermostats and barostats

Performance improvements 2024

- Hydrogen mass repartitioning in gmx grompp
 - New mdp option
`mass-repartitioning-factor = 1`
- HeFFTe multi-GPU FFT plan options are configurable
 - Using environment variables
 - Users can find and use suitable settings for their setup.

Contributors to the 2024 release

Mark Abraham	Andrey Alekseenko	Vladimir Basov
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