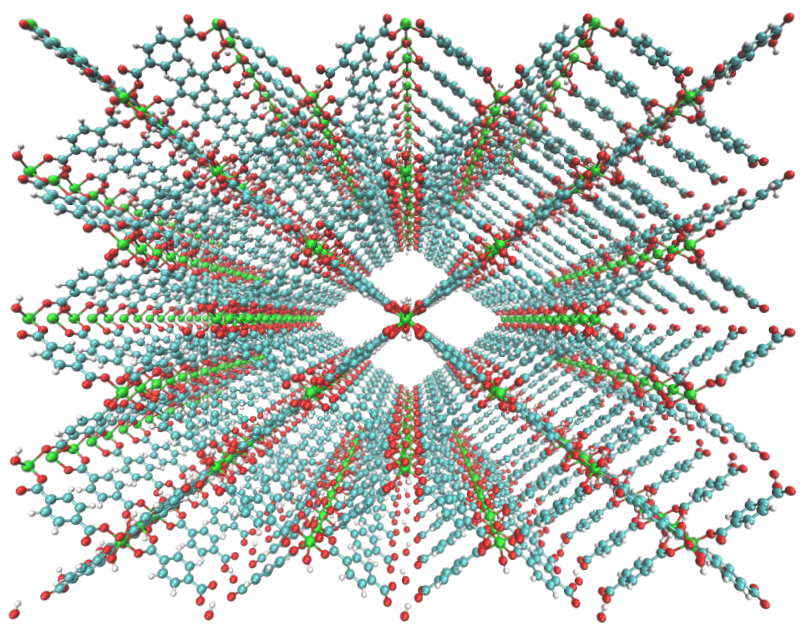


## Studied material: MIL-53(AI)



MIL-53 is a metal-organic framework. It exhibits breathing behaviour: A transition between a narrow-pore (np) and a large-pore (lp) configuration under adsorption of molecules or other stimuli.

## Research question

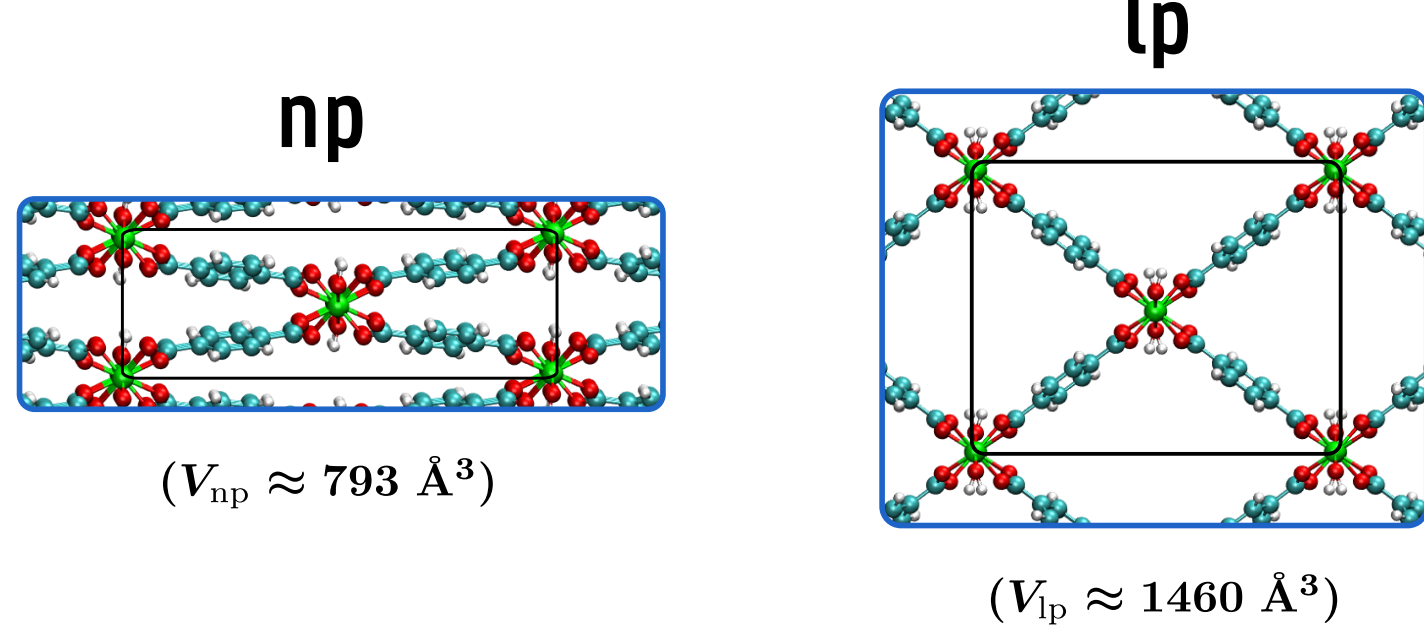
What is the stability of the structure at 300 K and at a given pressure?  
 A free energy profile as a function of the volume  $V$  is needed.  
 Three methods exist:  
 1. Thermodynamic integration  
 2. Normal mode analysis / Principal component analysis  
 3. Metadynamics  
 How to treat the unit cell in simulations?  
 Is the ensemble important?  
 What is the most efficient simulation method?

## Computational details

We perform molecular dynamics with a classical force field [1] using the code Yaff [2].

We apply periodic boundary conditions to a double unit cell with a fixed number of particles (152), a NHC thermostat (300 K) [3], and a MTK barostat [4].

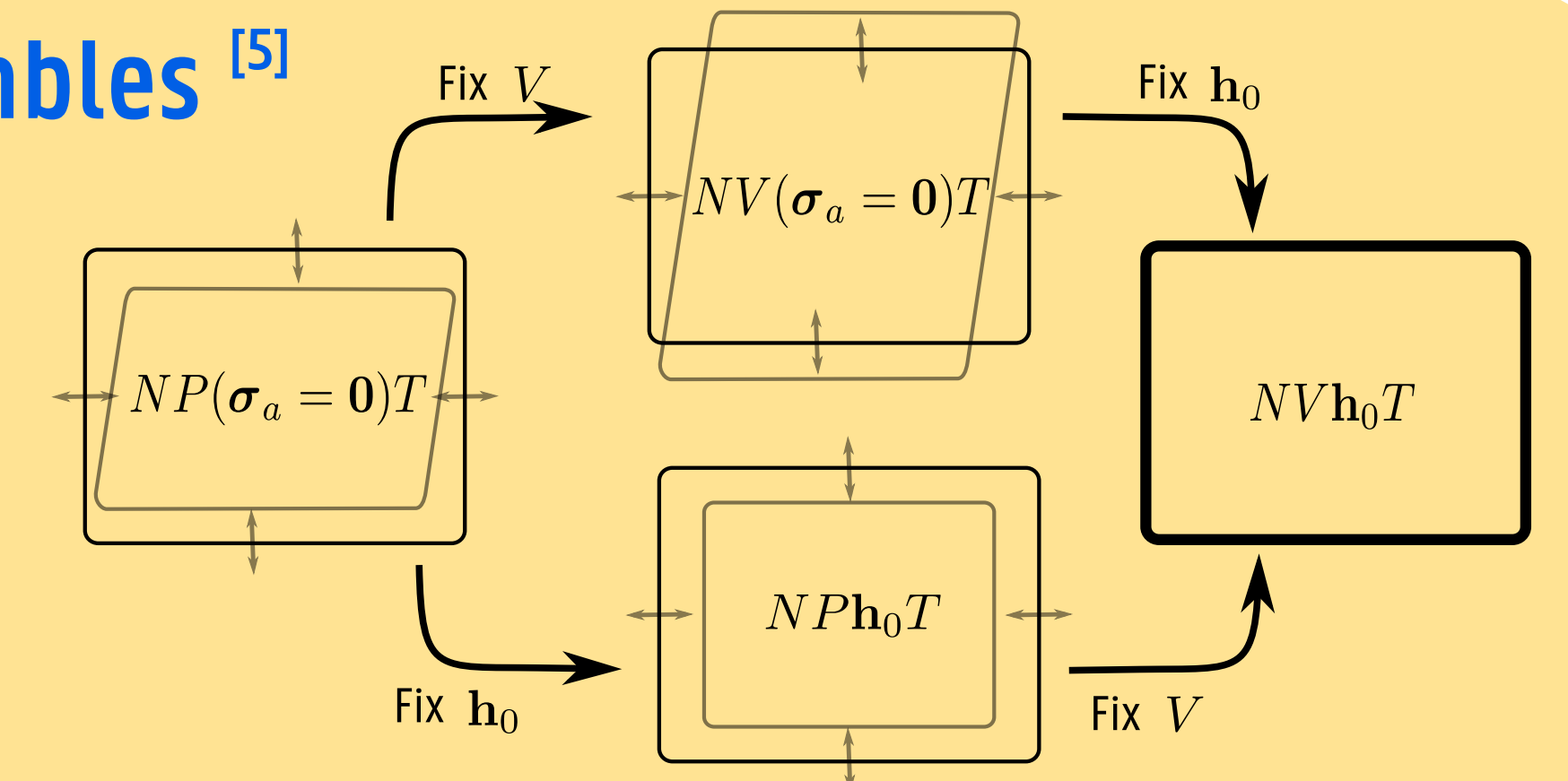
## The unit cell at 300K



## Notation

Periodicity  $\vec{a}, \vec{b}, \vec{c}$   
 Unit cell matrix  $\mathbf{h} = \begin{pmatrix} a_x & a_y & a_z \\ b_x & b_y & b_z \\ c_x & c_y & c_z \end{pmatrix}$   
 Cell volume  $V = \det(\mathbf{h})$   
 Cell shape  $\mathbf{h}_0 = \mathbf{h}/V^{1/3}$

## Ensembles [5]



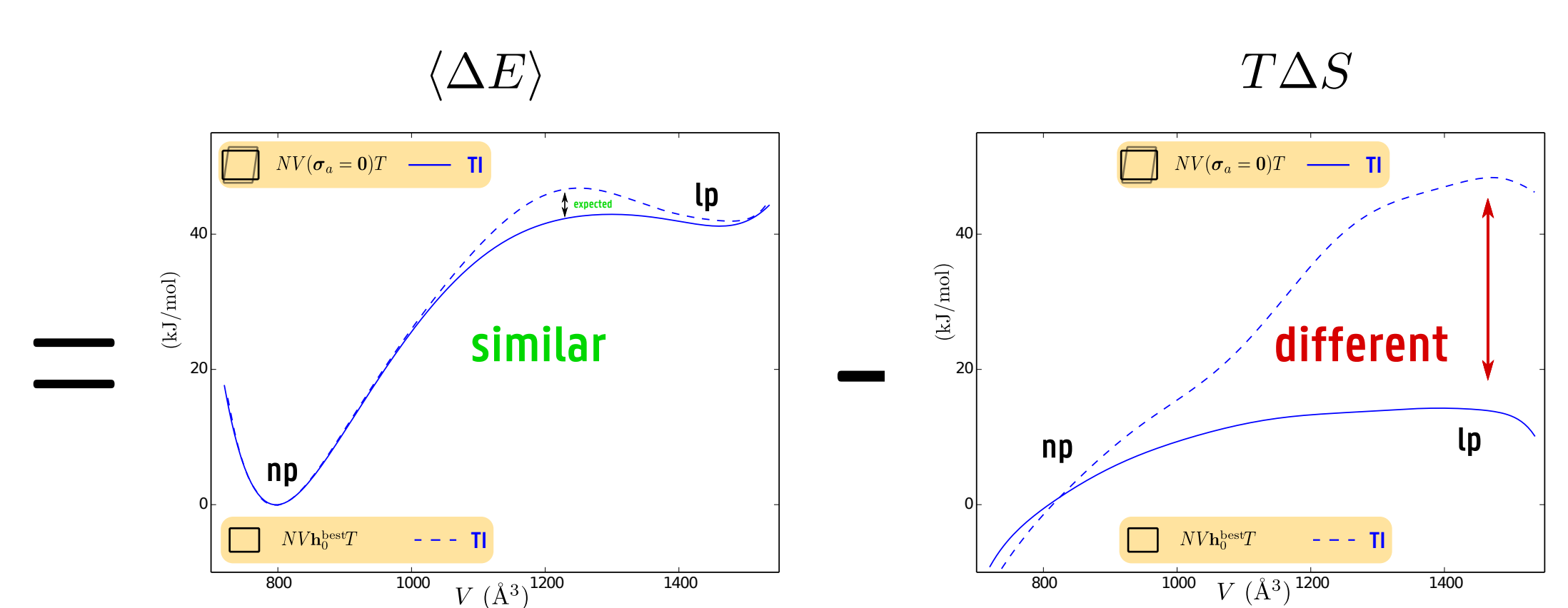
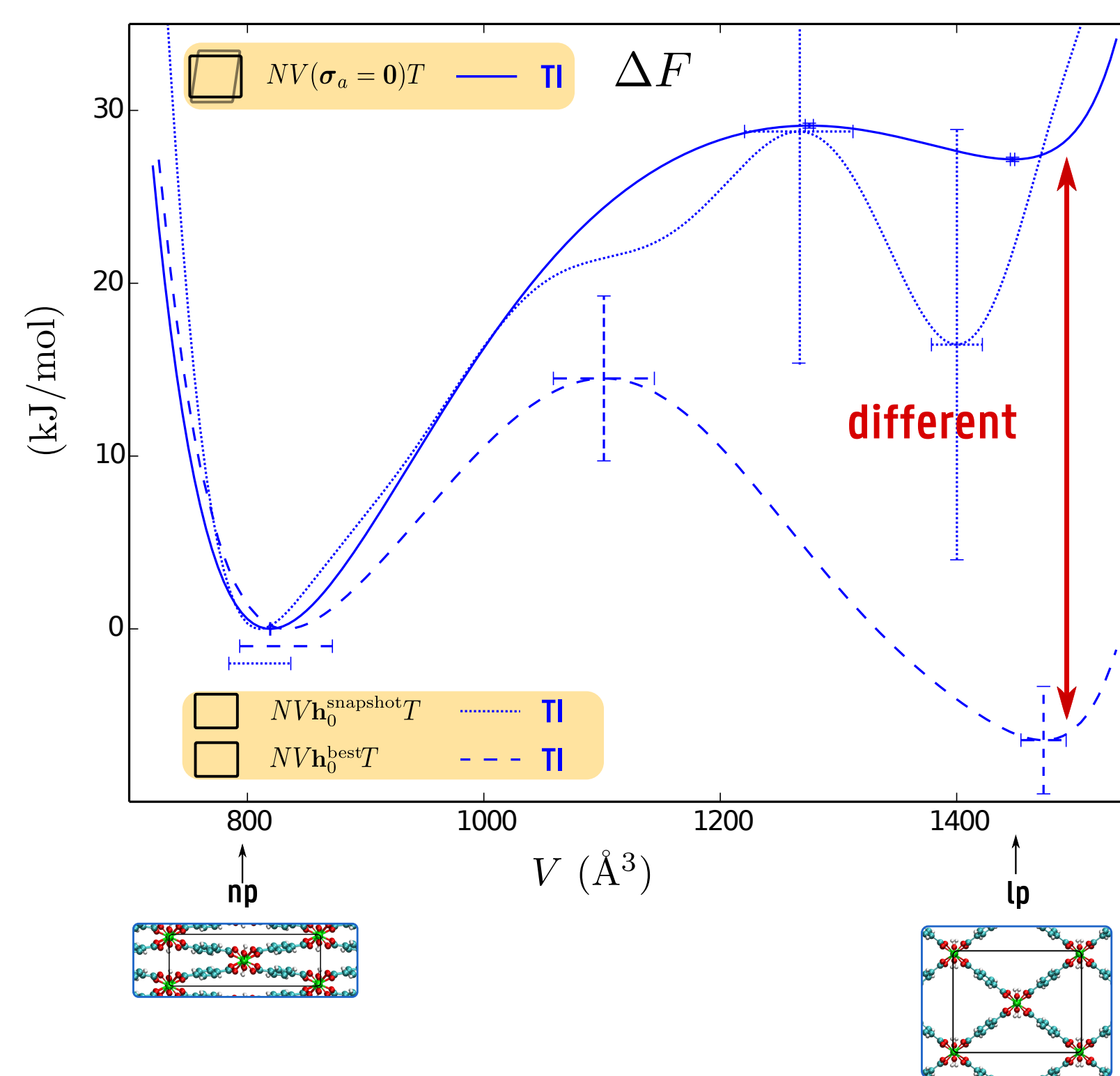
## Results

### 1. Thermodynamic integration (TI) [6]

$$\left(\frac{\partial F}{\partial V}\right)_T = -P$$

$$\Delta F = F(V) - F(V_{np}) = -\int_{V_{np}}^V \langle P \rangle_{V'} dV'$$

- We tested two ensembles:
- The  $NV(\sigma_a = 0)T$  ensemble
  - The  $NV\mathbf{h}_0T$  ensemble, so choose  $\mathbf{h}_0$ :
    - Snapshots,  $\mathbf{h}_0^{\text{snapshot}}$ , from  $NP(\sigma_a = 0)T$
    - Best guess,  $\mathbf{h}_0^{\text{best}}$ , average of  $NV(\sigma_a = 0)T$



#### Observation:

Good estimation of mean total energy difference  $\langle \Delta E \rangle$   
 Difference in entropy  $\Delta S$

#### Conclusion:

Fixing the shape  $\mathbf{h}_0$  gives an incorrect free energy profile  
 For thermodynamic integration, use the  $NV(\sigma_a = 0)T$  ensemble

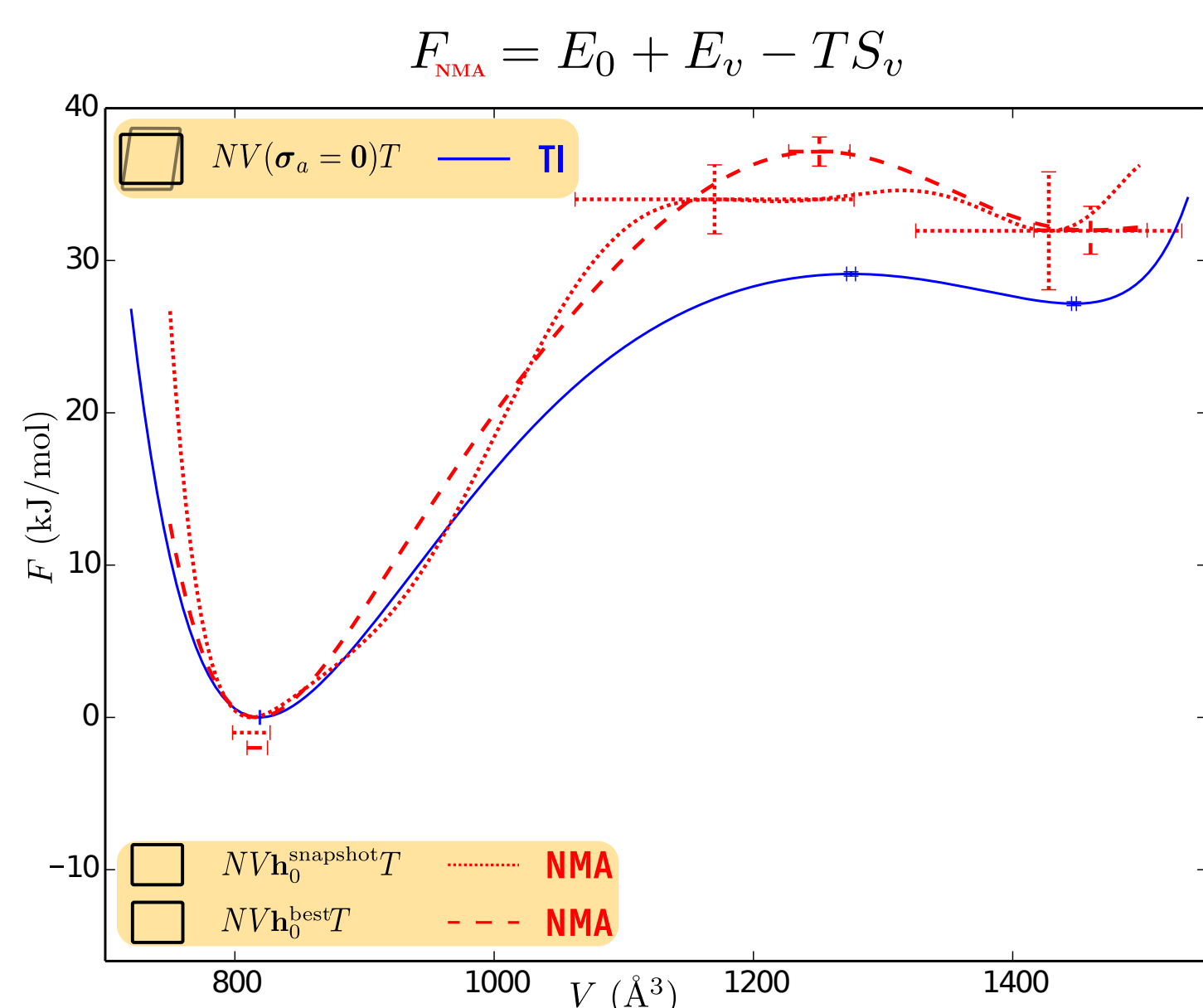
### 2. Normal mode analysis (NMA) [7] and principal component analysis (PCA) [8]

Compute the frequencies  $\nu_i$  in the system, using the classical approximation

**NMA:** by optimising at constant  $\mathbf{h}_0$  ( $\rightarrow$  energy  $E_0$ ) and by diagonalising the hessian (harmonic approximation)

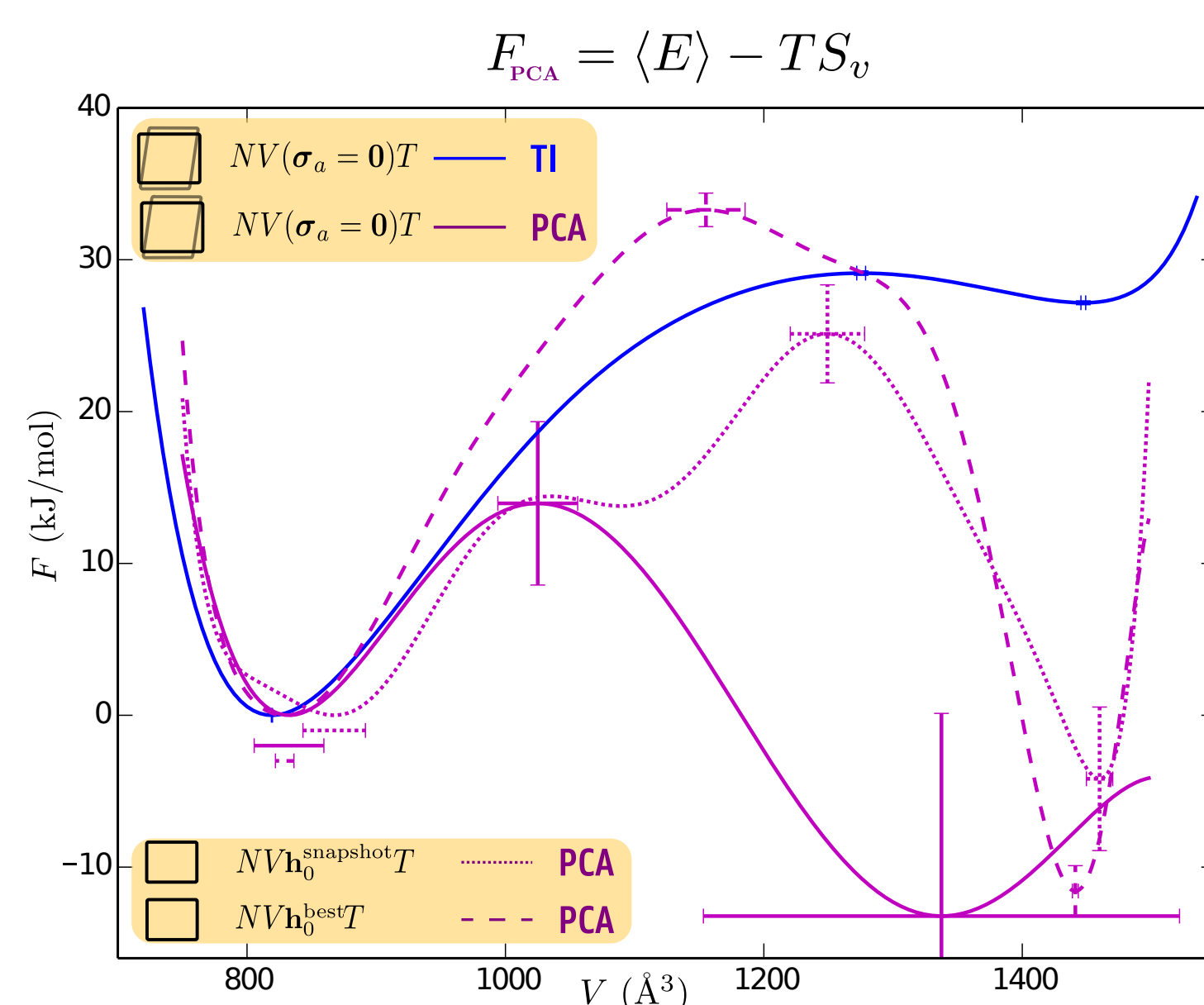
**PCA:** by diagonalising the massweighted covariance matrix at 300 K

With these frequencies, calculate the vibrational energy  $E_v = 3NRT$  and the vibrational entropy  $S_v = R \sum_i (1 - \ln \frac{h\nu_i}{k_B T})$



#### Observation:

NMA renders a slightly inaccurate estimate  
 PCA does not work

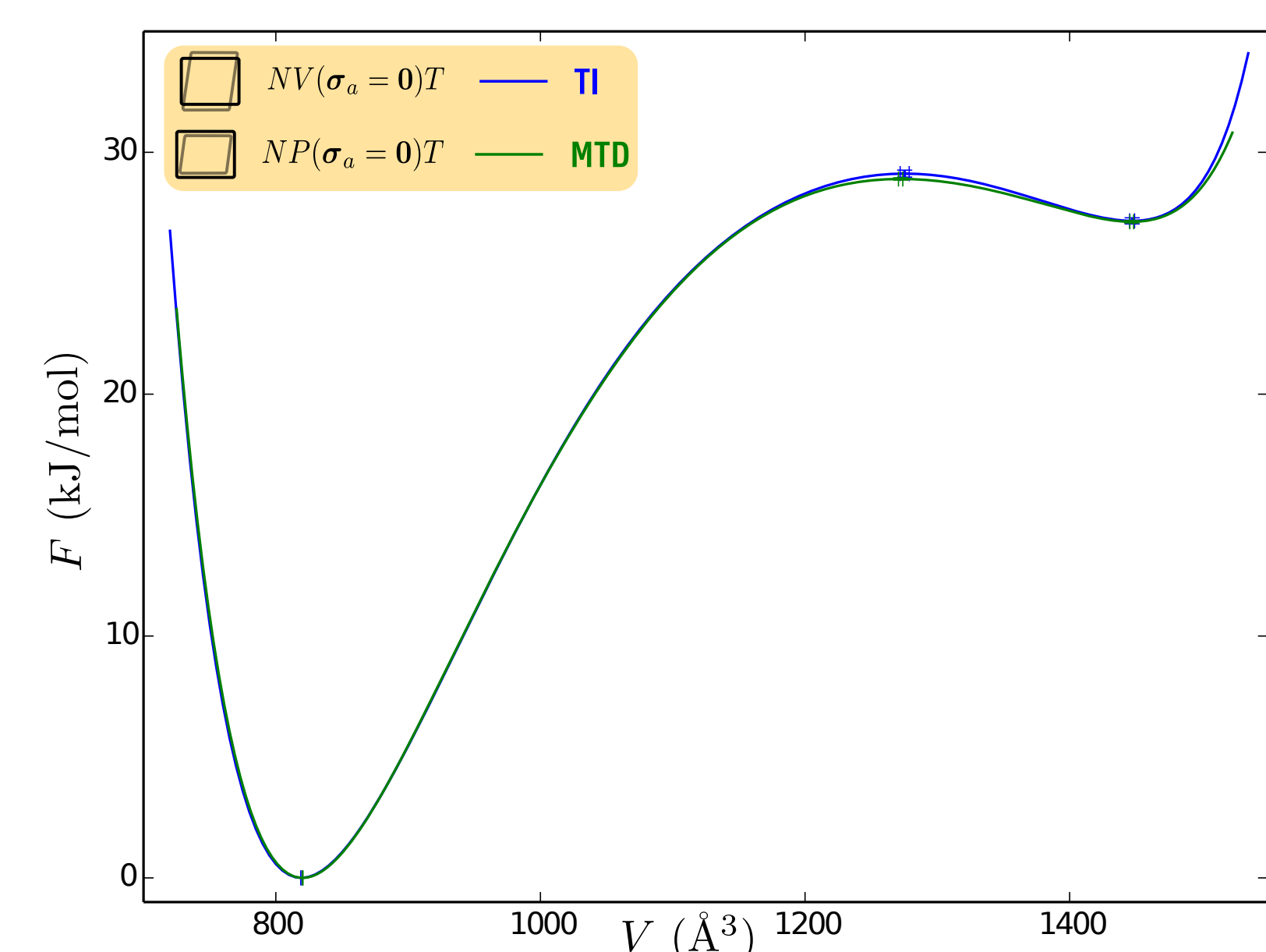


### 3. Metadynamics (MTD) [9]

Add bias potential to the system

Update bias throughout the simulation until convergence

Bias potential gives the free energy profile



#### Observation:

Metadynamics and thermodynamic integration are equivalent  
 Here, metadynamics is twice more precise for one fourth of the simulation

## Conclusions

For MIL-53(AI), the narrow-pore structure is the most stable at room temperature. The unit cell shape fluctuations during a molecular dynamics simulation are important for estimating a correct free energy profile.

In thermodynamic integration, fixing the unit cell shape during simulations has a large, incorrect effect on the results. One should always use the correct ensemble. With these simulation parameters, metadynamics renders an equally accurate but more precise free energy profile with an increased computational efficiency.

Normal mode analysis gives a precise but inaccurate estimate of the free energy. Finally, principal component analysis is very inaccurate and inefficient at calculating the free energy.

## Prospects

Is the effect of unit cell shape fluctuations equally large for bigger unit cells containing more nuclei?  
 What happens in other materials?

## References

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