Supporting Information for

Simulation of solid-state phase transition in DL-methionine

Saba Ghasemlou, Bernd Ensing and Herma M. Cuppen

Herma M. Cuppen.
E-mail: h.cuppen@science.ru.nl

This PDF file includes:

Supporting Information Text

1. Construction of collective variables

This Supporting Information describes the technical details of the construction of the collective variables. In constructing the torsional CVs, t_α and t_β, the torsional angles' periodicity has been considered. For the α configuration, the dihedral angles range from $50°$ to $100°$ for the L-enantiomer and from $-100°$ to $-50°$ for the D-enantiomer. In the β configuration, these ranges are from $150°$ to $200°$ and from $-200°$ to $-150°$, respectively. The fractions of D- and L- enantiomers that fall in either of the two ranges ($t_{\alpha-D}$ and $t_{\beta-D}$ for D and $t_{\alpha-L}$, $t_{\alpha-L}$ for L) is determined using the TORSIONS keyword in plumed (1–5) and are subsequently combined to obtain t_α and t_β via

$$t_\alpha = 0.5 t_{\alpha-D} + 0.5 t_{\alpha-L} \qquad [1]$$

and

$$t_\beta = 0.5 t_{\beta-D} + 0.5 t_{\beta-L}. \qquad [2]$$

For the $\alpha \rightarrow \beta$ transition, the t_α varies from 0.52 to 0.09 while t_β varies from 0.09 to 0.52.

The CVs d_b^i and d_c^i measure the relative positioning of the bilayers during the phase transition with the minimum shifting along the "b" and "c" vectors. The d_b^i and d_c^i use the projected distances between sulfur atoms of opposing bilayers on the lattice vectors b and c, respectively. To write this in a mathematical notation, we label the different sulfur atoms of the D-molecules to indicate their order in the simulation cell along the three axes: $S_{i,j,k}$. This label remains throughout the simulation, regardless of their movement through the periodic boundary. Either the D or L-molecules should be included and thus labeled in Fig. S1. This is because including both enantiomers, causes the α and β states to appear at the same values of d_b^i and d_b. In Fig. S1 sulfur atoms $S_{i,j,k}$, and $S_{i+1,j,k}$ are in bilayers facing each other. An extra superscript label indicates that the position of the sulfur atoms is expressed in fractional coordinates with respect to the three lattice vectors of the simulation cell and only the component indicated by the label is considered. A variable d_b^i determines the shift between layers i and $i+1$:

$$d_b^i = \frac{1}{n_c} \sum_{k=1}^{n_c} \sum_{j=1}^{n_b/2} (S_{i,j,k}^b - S_{i+1,j,k}^b) \qquad [3]$$

with n_i the number of D-molecules in the direction i. Periodic boundary conditions are considered such that j' becomes $|n_b - j'|$ for any $j' > n_b$. The equilibrium value for the α form is around 0.5. Because of the periodic nature of the system, the transition towards β can either occur by increasing or decreasing this value. To account for this, we combine the values for the different layers in the following fashion:

$$d_b = \sum_{i=1}^{n_a/2} |d_b^i + 0.5|. \qquad [4]$$

Using d_b we account for the shifts along b and between all adjacent bilayers. Its equilibrium value is near 0 for α and near 1 or -1 for β. A similar collective variable is constructed for shifts along c. Here the equilibrium value for d_c^i is 0 in α and -0.5 or 0.5 in β.

Since a full six-dimensional space is too large to explore, we have further combined these six CVs into two CVs. One that mostly concerns the changes in the (a, b) projection: d_b which is a combination of d_b^1 and d_b^2. During the initialization of the system, we force two bilayers to change simultaneously, since this leads to the least distorted final cells with the lowest final (free) energies and the two CVs can easily be combined into one average shift. The changes in the (a, c)-plane mostly concern shifts d_c^1 and d_c^2 and torsions t_α and t_β. The latter two are highly correlated. Initial exploratory simulations in which the system was pushed along on CV in the direction of its β-value showed that *(i)* both bilayers need to shift simultaneously for the system not to get very slanted and distorted unit cells and *(ii)* the changes in d_c and torsions are highly correlated and that changes in one CV lead to changes in the other as well. We hence combine all four CVs in a path collective variable (PCV)(2, 4). This PCV has two properties: s which is the progress along the path from the fully-ordered α form ($s = 0$) to the β form ($s = 1$). The property z is the deviation of the system from the path. The property s is the only CV that describes the changes in (a, c) projection. The z is not a CV but we explain in Section 3.3 of the main paper how restraining it is essential to obtain the free energy surface for a not disrupted simulation cell.

2. Schematic comparison between DL-Methionine and DL-aminoheptanoic acid in CV space

DL-aminoheptanoic acid polymorphs (forms I to IV) are compared to the α-DL-MET and β-DL-MET in CV space. The packing and conformation of forms I and III are similar to the α and β states respectively. Form V is not present in this figure since it is highly disordered and can not be directly compared to DL-MET.

Saba Ghasemlou, Bernd Ensing and Herma M. Cuppen

α -DL-MET

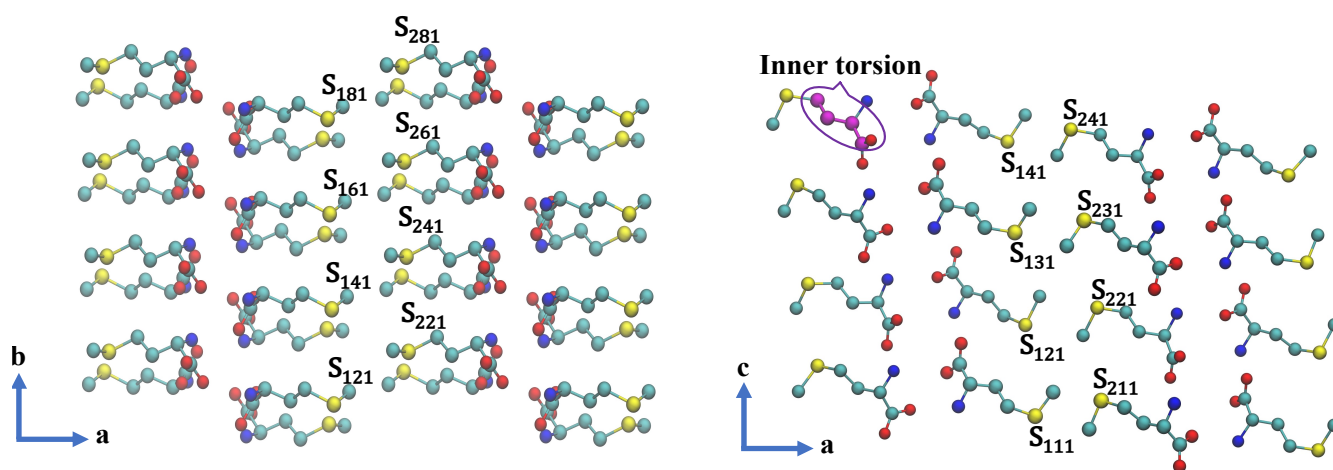**Fig. S1.** The α polymorph with labeled sulfur atoms ($S_{i,j,k}$) generates the CV representing the shifts. All torsions like the one indicated in purple are restrained to avoid highly slanted structures.
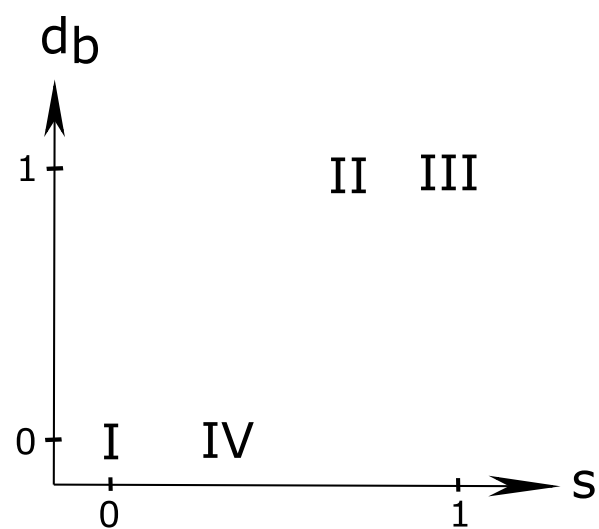
Fig. S2. The location of the DL-aminoheptanoic acid polymorphs in CV space in comparison with DL-MET α and β polymorphs.

Saba Ghasemlou, Bernd Ensing and Herma M. Cuppen

References

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