

MS31-P3 Accurate and efficient representation of intramolecular energy in *ab initio* generation of crystal structures.

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The CrystalPredictor I^{1,2} and II³ codes have been used to explore the space of crystal structures have been used successfully in several crystal structure prediction (CSP) investigations in recent years⁴, including in the series of blind tests organised by the Cambridge Crystallographic Data Centre^{5,6} and in the prediction of the crystal structures of pharmaceutically-relevant molecules^{7,8}. We present a summary of CrystalPredictor, focussing on improvements to the lattice energy evaluation that the most recent blind test⁹, as well as our own investigations into a variety of flexible polymorphic molecules, has prompted. These improvements aim to achieve greater accuracy in the initial ranking of potential crystal structures, while managing computational cost so that a thorough exploration of the search space is possible. Firstly we discuss non-uniform LAMs; an innovation in CrystalPredictor II that allows the most efficient use of computational effort to cover a flexible molecule's conformational space. We use blind test molecule 26 as an example. Secondly, we discuss the smoothing of the intramolecular potential, which improves accuracy in CrystalPredictor II by collating data from *ab initio* calculations. The impact of this approach is investigated based on a CSP study for flufenamic acid¹⁰.

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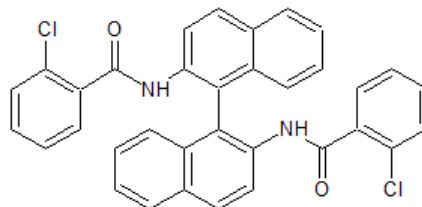


Figure 1. The flexible molecule 26

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