

FA4-MS11-O1**Predicting Solvent Inclusion in Molecular Crystal Structures.** Graeme Day^a, Aurora Cruz-Cabeza^a.^a*University of Cambridge, Department of Chemistry, United Kingdom.*E-mail: gmd27@cam.ac.uk

Developments in molecular modelling methods in the past few years mean that it is now possible to predict the most likely crystal structures of a given molecule by computational methods alone. The set of computer-generated low energy crystal structures of a molecule, and their associated energies (the crystal energy landscape), is a powerful tool for understanding the crystallisation behaviour of organic molecules. As well as using such method to predict the crystal structures available to the pure molecule, we have recently been exploring whether computational crystal structure prediction methods can be applied to understanding and predicting solvent incorporation in molecular crystals. Examples from recent studies will be presented and discussed, exploring the following questions: when will a solvate form in preference to the neat crystal structure [1]; what will be the resulting stoichiometry of the crystal if a solvate does form [2]; what will be the crystal structure of the solvate [3].

[1] Cruz Cabeza, A. J., Day, G. M., Motherwell, W. D. S., Jones, W., *Chem. Commun.*, **2007**, 1600-1602. [2] Cruz-Cabeza, A. J., Day, G. M., Jones, W., *Chemistry – A European Journal*, **2008**, 14, 8830-8836. [3] Cruz Cabeza, A. J., Day, G. M., Motherwell, W. D. S., Jones, W., *J. Amer. Chem. Soc.*, **2006**, 128, 14455-14467.

Keywords: simulation; solvates; prediction**FA4-MS11-O2****Using Energy Landscapes to Determine Crystal Structures from Low-Quality Experimental Data.** Jacco van de Streek^a, Marcus A. Neumann^a.^a*Avant-garde Materials Simulation, Freiburg, Germany.*E-mail: vandestreek@avmatsim.de

As algorithms and computers become more and more powerful, crystal structures can be solved based on less and less experimental data. This is especially useful when growing single crystals of suitable quality is not possible, for example when trying to determine all crystal structures of all polymorphs of a compound. Methods have therefore been developed to determine crystal structures from diffraction data with a reduced information content. This includes solving crystal structures from X-ray powder diffraction data, but also includes solving crystal structures from high-pressure data or from data from twinned crystals.

As the amount of experimental data decreases, it becomes more and more justified to ask how we can be certain whether a crystal structure determined from e.g. laboratory powder diffraction data is correct. Rietveld refinement and its associated figures of merit can only provide partial reassurance (see e.g. [1]), especially if a preferred orientation correction was necessary or if only experimental data of limited quality is available.

In this contribution, we will demonstrate the use of dispersion-corrected Density Functional Theory (DFT) to reproduce small-molecule crystal structures in silico with

unparalleled accuracy and speed [2]. The method can be used to validate crystal structures, and when augmented with a structure-generation algorithm can even be used to solve crystal structures from limited experimental data or even in the absence of any experimental data at all [3].

[1] Buchsbaum, C. & Schmidt, M. U. (2007), *Acta Cryst.* **B63**, pp. 926-932. [2] Neumann, M. A. & Perrin, M.-A. (2005) *J. Chem. Phys. B* **109**, pp. 15531-15541. [3] Neumann, M. A., Leusen, F. J. J. & Kendrick, J. (2008) *Angew. Chem. Int. Ed.* **47**, pp. 2427-2430.

Keywords: ab-initio calculations; crystal structure determination X-ray powder data; crystal structure prediction**FA4-MS11-O3****The Computational Prediction Of Spontaneous Resolution.** Emiliana D'Oria^a, Panagiotis G. Karamertzanis^b.^a*Department of Chemistry, University College London, 20 Gordon Street, London WC1H 0AJ, UK.* ^b*Centre for Process Systems Engineering, Imperial College London, South Kensington Campus, London SW7 2AZ, UK.*E-mail: e.doria@ucl.ac.uk

In spontaneous resolution the two enantiomers in melt or solution crystallize separately into a mixture of optically pure crystals. Crystal structure prediction methods are used to study the thermodynamic favourability of crystallizing as a racemate or chirally pure structure to test whether they can predict spontaneous resolution. This rare phenomenon may be implicated in the origin of life[1]. It is generally assumed that spontaneous resolution requires the observed enantiopure crystal to be more thermodynamically stable than all possible racemic crystals[2]. A computational method to generate low-energy crystal structures can reveal whether a stable crystal structure in chiral (Shonke) space groups can be more stable than those in centrosymmetric ones for thermodynamically driven spontaneous resolution. Such crystal structure searches have been performed on five diverse compounds which are known to spontaneously resolve[2], namely naproxen, 5-hydroxymethyl-2-oxazolidinone, 3,4-dehydroproline anhydride, benzo(c) phenanthrene, glycouril. Crystal structure searches were successful in locating all known crystals and in generating several energetically competitive crystal structures. The results suggest that there is not a large thermodynamic driving force for spontaneous resolution. When the conformation of these structures is allowed to adjust to the crystal packing forces, the observed enantiopure structure is often the most stable, but the difference is comparable with the accuracy of the lattice energy, evaluated by quite sophisticated methods.

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