MS38-P14 Combination of solid state NMR, DFT and XRPD for determination of a theophylline : 4-aminobenzoic acid cocrystal phase

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Theophylline and 4-aminobenzoic acid in 1:1 ratio selectively, and quantitatively, generate, by Liquid Assisted Grinding (LAG), a new cocrystal phase (**1**). Its structure was retrieved by conventional laboratory X-ray powder diffraction methods, using the programme TOPAS academic for solving and refining the structure. The unusual absence of hydrogen-bond interactions involving the amino groups required further validation, performed by solid state NMR and IR characterization.

The use of 1D/2D ^{1}H high-resolution solid-state NMR techniques provided structural insight on local length scales revealing internuclear proximities and relative orientations between the building blocks of the title compound **,** thus providing information on the type of hydrogen bond synthons formed. DFT calculations were also employed to generate meaningful structures and calculate NMR ^{1}H and ^{13}C chemical shifts to further validate the XRPD model.

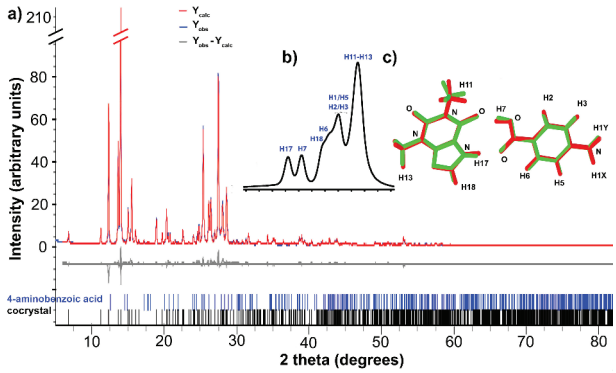

Figure 1. a) Final Rietveld refinement plot. Blue and black bars refer to the angular positions of Bragg reflections for 1 and the minor 4-aminobenzoic acid (<5%) contaminant, respectively; b) ^{1}H MAS NMR spectrum of 1 (B_0=16.4 T; 30 kHz MAS); c) Overlap of the structures obtained by XRPD and DFT.

Keywords: powder diffraction, solid state nuclear magnetic resonance, DFT, TOPAS, CASTEP

MS38-P15 ADPs simulations as an additional source of fine structural information

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The effect of the atomic thermal motion about their equilibrium positions, **u**, enters in the calculation of the structure-factor, which is a function of the Miller indexes defined by the vector h, as the Debye-Waller factor, T(**h**). The calculation of the ADPs from the MD simulation ($\mathbf{U}_{MD\_cif}$) was carried out as follows: the first step involved the calculation of the symmetric tensor U* from the MD trajectory by converting, in each of the N snapshots, the atomic Cartesian coordinates (*r*) into fractional coordinates (*r**), and applying to the fractional coordinates the usual definitions of mean coordinates and variance-covariance matrix; thereafter, the calculation of the average values of the cell parameters and the determination of the averaged reciprocal lattice parameters lengths were carried out. These values, as calculated from the MD trajectory, were used to finally obtain $\mathbf{U}_{MD\_cif}$. Apart from the possible comparison between X-ray and neutron inferred ADP data – the latter being more trustable for several physical reasons – valuable information could be obtained from their detailed analysis with a particular emphasis not only on their size but on their shape and spatial distribution. In this contribution we provide several examples – spanning, among others, from the study of polymorphism and pseudosymmetry to the energy ranking and stability of crystalline arrangements (1-4) – on extremely different chemical species thus confirming the wide pertinence of the proposed approach.

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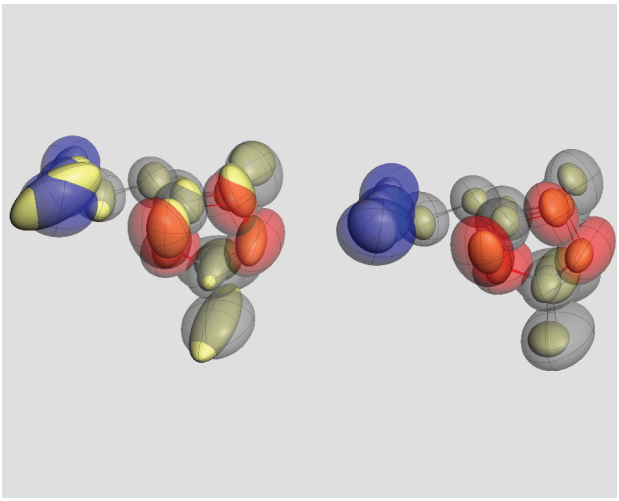

Figure 1. An example of adp qualitative comparison between computed, on the left (single cell, yellowish and supercell, coloured), and between computed and experimental, on the right (experimental, yellowish and supercell, coloured).

Keywords: adp, Molecular Dynamics, polymorphism, symmetry, pseudosymmetry, Shannon entropy

MS38-P16 Combining X-ray crystallography and ultrafast infrared spectroscopy – monitoring photo-induced guanine oxidation by $[Ru(TAP)_2(dppz)]^{2+}$

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Time resolved spectroscopy can be used to study reaction processes on a short timescale (as low as fs). Time-Resolved Infra-Red (TRIR) is a particularly powerful technique as it can be used to monitor the formation and breakage of individual chemical bonds, and therefore can be used to study fundamental chemical processes in biological[1] and chemical systems. However, whilst this technique is very powerful, interpretation of the results can be hampered by a lack of information about the local chemical environment of the group of interest as the sample is usually in solution. This means that, when studying biomolecules and in particular nucleic acids, there may be multiple conformations or binding sites present[2] which can be very difficult to assign.

In contrast, X-ray crystallography allows us to determine the position of every ordered atom or group within a crystal, providing unparalleled structural information about the environment within the sample. However, whilst facilities are available for time resolved experiments, it is difficult to reach into the sub-ns time domain without the use of specialised Laue or FEL sources.

Here we present the adaptation of pump-probe TRIR to measure data, in the ns and ps time domain, from samples consisting of 5μm crystal fragments. This technique was used to monitor the one electron photooxidation of guanine by a Ruthenium polypyridyl bound to a DNA duplex, the crystal structure of which we have previously reported[3] (Figure 1). By assigning the spectroscopic result to a known structure, we are able to propose an individual base as the site of oxidation. Additionally, the spectroscopic fingerprint (reaction rate, relative yield, peak position) obtained from a crystal sample allows us to compare with that found in solution.

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