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Mutual Additive-Induced Polymorphism in Aspirin / Aspirin **Anhydride Derivatives**

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Polymorphism is the ability of compounds to crystallise in different arrangements, and it is a common phenomenon in various classes of chemical materials. To be able to control polymorphism is extremely important because different crystal forms can have different physicochemical properties. Aspirin is a unique drug: it is effective against pain, it has anti-pyretic and anti-inflammatory properties, and it is widely used during heart attacks or strokes. The structural chemistry of aspirin has been found to be unusual because it has a tendency to crystallise as an "intergrown" form, which contains domains of two polymorphs within a single crystal [1-3]. We have recently reported that the second polymorph of aspirin can be obtained in the presence of a specific additive, aspirin anhydride [4]. Aspirin anhydride is a common impurity, which can be produced during "standard" aspirin synthesis or during heating of aspirin in various aprotic organic solvents. Our further research has been focussed on aspirin derivatives, since we were interested to find other systems similar to aspirin. The presented research examines several aspirin derivatives (5-X-aspirin, where X = Cl, Br, I, Me)and the corresponding anhydrides. We have found that the aspirin derivatives also have a tendency to be polymorphic and that the polymorphism is dependent on the presence of aspirin anhydride impurities. In addition, we have found that the aspirin anhydrides display polymorphism, and that the polymorphism is dependent on the presence of aspirin during crystallisation. The broader significance of this work lies in the illustration of polymorph control induced by specific impurities that can be generated as by-products during synthesis or even during a common crystallisation procedure such as heating in organic solvents.



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MAX IV MX: Macromolecular Crystallography at the New

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MAX IV is a new synchrotron radiation facility under construction in Lund, Sweden [1]. The new facility will include a linac working as a full energy injector, a 3 GeV storage ring with 528 m circumference, a 1.5 GeV storage ring with 96 m circumference and a short pulse facility using the linac for time-resolved experiments. Together these will provide optimal radiation sources for a wide spectrum and for a wide range of experimental techniques. The 3 GeV storage ring will have 20-fold symmetry and a horizontal emittance of well below 1 nmrad.

The funding of the beamlines are not yet secured but it is expected that the initial set of beamlines on the 3 GeV ring will include at least one macromolecular crystallography (MX) beamline.

The first MX beamline will be a multi-purpose high-throughput beamline that will be an ideal beamline for most MX experiments including e.g. challenging experiments with small crystals of large molecular complexes and membrane proteins. The beamline will be energy tunable with x-ray beam focus down to 10 µm, include a state-of-the-art experimental set-up with on-line UV/vis spectroscopy. The very small emittance of the MAX IV 3 GeV ring will give a very parallel beam suitable for the largest unit cells and for difficult crystals.

The MX microfocus beamline is suggested to focus down to 1 µm for the most challenging experiments with small and inhomogeneous crystals. The small focus size and small samples will put high demands on the experiment set-up and the beamline stability.

The MAX IV facility is also suggested to include other beamlines of interest for the life sciences e.g. x-ray absorption spectroscopy (XAS), small angle x-ray scattering (SAXS), infrared spectroscopy and imaging/tomography, as well as a nanofocusing beamline covering microscopy, spectroscopy, scattering, diffraction and imaging. Furthermore the short pulse facility will offer opportunities for time-resolved experiments. The number and types of beamlines in the first phase will depend on the available funding.

The construction of the MAX IV facility started on May 18th 2011 with beamline user operation starting in 2015/2016.

[1] http://www.maxlab.lu.se

Keywords: Synchrotron, Biocrystallography, Macromolecular

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Charge density study of phosphoglycolate monopotassium salt

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Phosphoglycolates are important compounds appearing in some metabolic pathways, such as photorespiration in plants, and DNA repair in bacteria [1]. Because of their importance we have performed charge density analysis of the title compound, and in this communication we report the preliminary analysis of its experimentally determined charge density.

The crystal structure of monopotassium phosphoglycolate was reported earlier by Lis [2] as part of a long study focused on elucidating the crystal chemistry and structure of organic phosphates. The aim of this paper is to push this work further by means of high resolution charge density study coupled with density functional theory (DFT) calculations.

First results indicate that both approaches produce comparable results. Testing different multipole models generally shows, that phosphorus has a higher positive Bader charge than in hydrogen methylphosphates of calcium and lithium (unpublished results) and in aminomethylphosphonic acid [3], that is approximately +3.9 e with regard ~+ 3.5 those to e in compounds.