signals of the snRNPs. As an import adaptor snurportin1 bridges the interaction between the m_3G-cap bearing snRNPs and the nuclear import receptor importin-β, which mediates the interaction with and translocation through the nuclear pore complex. Snurportin1 contains a N-terminal importin-β-binding (IBB) domain and a m_3G-cap-binding region, which shows no similarity to other known nuclear import factors. We have solved the crystal structure of the m_3G-cap binding domain of snurportin1 by means of MIRAS, and the structure was refined at 2.4 Å resolution. The crystal structure reveals an unexpected binding mode for the m_3G-cap, that significantly differs from other cap-binding proteins such as eIF4E and CBP20. The structural basis for the discrimination of m^7G-cap bearing RNAs by snurportin1 will be discussed.

Keywords: RNA-protein interactions, nuclear transport, MIRAS

MS44.27.5

Acta Cryst. (2005). A**61**, C60

Structural Basis for Antigene and Antisense Duplexes with Modified Nucleotides

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Oligonucleotides containing polyamines are currently being evaluated as potential antigene and antisense compounds. Those with 5-(*N*-aminohexyl)carbamoyl-2'-deoxyuridine (^{N}U) and its 2'-*O*-methyl derivative (^{N}U$_m$) exhibit improved nuclease resistance. Furthermore, these nucleotides stabilize duplex formation of the modified DNA and its target DNA or RNA strand. X-ray structures of these duplexes have shown good correlation between the conformational changes and the observed chemotherapeutic properties.

The amide groups of the modified uracil bases form six-membered rings through the intramolecular NH---O4 hydrogen bonds, so that the aminohexyl chains protrude into the major grooves. Some of the terminal ammonium groups are involved in intra-duplex interactions with phosphate oxygen anions, whereas the others interact with those of the adjacent duplex. Such interactions contribute to the stability of duplex formation. The 2'-*O*-methyl modification in ^{N}U$_m$ shifts the ribose ring toward the C3'-*endo* conformation and influences duplex stability. Observed changes in the dimensions of the minor grooves and in the hydration structures are well correlated to nuclease resistance.

Keywords: antigene, antisense, crystal structure

MS45 PACKING OF ORGANIC MOLECULAR COMPOUNDS

Chairpersons: Jonathan W. Steed, Carolyn Brock

MS45.27.1

Acta Cryst. (2005). A**61**, C60

Porosity in Molecular Crystals

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Crystals composed of purely organic compounds have largely been ignored as gas sorption substrates since such molecules usually pack with efficiencies in the narrow range of 60 to 67%. Consequently, void spaces larger than 25Å^3 are seldom encountered in organic solids. The host lattices of solvated inclusion compounds are often described as possessing zero-, one-, two- or three-dimensional solvent-accessible voids if the guest molecules are located in isolated cavities, channels, layers or networks of channels, respectively. It is therefore attractive to envision facile removal of the solvent molecules from these materials to yield highly porous host lattices analogous to those of zeolites. In reality, the process of desolvation is almost always accompanied by reassembly of the host molecules in the solid state to form one or more so-called apohost phases, where the pure compound is once again efficiently packed. However, a few exceptions to this phenomenon are known to exist.

We are interested in using the principles of crystal engineering to design and construct new solids for applications such as gas sorption. Although the availability of vacant lattice voids is essential, these solids are apparently not required to be "porous" in the classical sense when considering the van der Waals surfaces of the constituent host molecules. This contribution will focus very generally on the concept of porosity in molecular crystals, and on the phenomenon of guest transport within a solid host framework.

Keywords: porous materials, self assembly supramolecular chemistry, crystal engineering

MS45.27.2

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Exploring Structures and Structural Phenomena: The Derived Crystal Packing Model

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Improvements in the prediction and the design of molecular crystals have been dramatically enhanced the last decades. However, several problems during crystallization such as polymorphism or two-dimensional defects can lead to difficulties in interpreting the success of a theoretical study.

In this context, we developed the Derived Crystal Packing (DCP) model [1]. This two-step procedure allows to generate crystal structures (daughter phases) starting from periodic fragments retrieved from a known mother phase. The study of many examples has shown that concomitant polymorphism, twinning and epitaxies can be a direct consequence of the structural and energetical similarities between the mother and the daughter phases.

Theses issues will be illustrated by the case of (±) Modafinil, a pharmaceutical compound known to crystallize in several polymorphic forms and solvates [2].

[1] Gervais C., Coquerel G., *Acta Cryst. B*, 2002, **58**, 662. [2] Pauchet M., Gervais C., Courvoisier L., Coquerel G., *Cryst. Growth. Des.*, 2004, **4**, 1143-1151.

Keywords: crystal structure prediction, twinning, polymorphism

MS45.27.3

Acta Cryst. (2005). A**61**, C60-C61

Crystal Structure Analysis and Solid Form Selection in the Pharmaceutical Industry

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The selection of the solid form is an important milestone in the development of new drug product. The aim of the process is to select the solid form with the most desirable properties including aqueous solubility, chemical and physical stability and suitable drug product processing attributes for formulation e.g. mechanical properties. The selected form may be either the free base or acid of the active pharmaceutical ingredient (API) or a salt.

It is vital to ensure the most thermodynamically stable polymorphic form has been selected. Different polymorphs have unique physical properties resulting in different solubilities, chemical and physical stabilities and different bioavailabilities. Metastable polymorphs may convert to more stable forms on processing and examples of this have been reported [1]. The characterization of all solid forms is important and can provide many intellectual property opportunities [2].

Crystal structure analysis, taking a molecular perspective of the crystalline state, can be combined with both manual analytical techniques (e.g. PXRD, thermal analysis, microscopy) and automated high throughput solid form screening techniques to ensure the optimum solid form is selected.

[1] Bauer J.F., Spanton S., Henry R., Quick J., Dziki W., Porter W., Morris J.,

Pharm. Res.,2001, **18(6)**, 859. [2] Bernstein J.,*Polymorphism in Molecular Crystals*, OUP, New York, 2002.
Keywords: pharmaceutical crystallography, polymorphs, structural databases

MS45.27.4
Acta Cryst. (2005). A**61**, C61
Different Reasons for Packing with Z'=2: 4-nitroimidazole Derivatives
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The packing of the molecules in crystals is a result of the compromise between different intermolecular interactions, tendency towards close packing, symmetry requirements etc. All these factors, hierarchically organized and influencing one another, determine the unique three-dimensional structure, the molecular crystal.

The compromise between different requirements sometimes requires the presence of more than one molecule in the asymmetric unit. That means that there are molecules in the crystal which are not related by any symmetry operation while still being chemically identical. A study of the connections between this phenomenon and packing conflicts is essential for predicting organic crystal structures. A further goal could be to try to correlate the occurrence of multiple molecules in the asymmetric unit with the presence of certain functional groups in the molecules, space group symmetries etc.

The analysis of the frequency of different Z' values in the crystal structures shows that above-average percentage of the structures with Z'>1 is observed for imidazole derivatives.

The different reasons for packing with Z'=2 will be presented for 4-nitroimidazole derivatives. For example, in two closely-related 1-R-2-methyl-4-nitroimidazoles the creation of bilayers of molecules, the primary building blocks of the crystal structures, is possible because there are two symmetry-independent molecules that have either different conformations or take part in different intermolecular interactions.

Keywords: crystal packing, weak interactions, imidazole derivatives

MS45.27.5
Acta Cryst. (2005). A**61**, C61
Directed Assembly and Covalent Capture of Supramolecular Architectures in the Solid State
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In this presentation, we demonstrate how principles of supramolecular chemistry involving molecules that function as linear templates can be used to direct the formation of finite molecular assemblies with components that react to form covalent bonds. We demonstrate how forces such as hydrogen bonds and coordination bonds can be used to direct the construction of molecules. The targets include linear and bent cyclophanes, as well as molecular ladders. The ability to construct complex molecules in the solid state relies on an ability of the templates to insulate reactants from vexatious structural effects of molecular close packing, effects which have made directing the formation the covalent bonds in organic solids difficult to control. Thus, the templates are able to adapt to changes to size and shape of the reactants and thereby provide a mean to control the size and shape of the resulting products. In that way, the covalent-bonding-forming process provides a means to covalently capture the geometry of reactants within supramolecular architectures with structures largely independent of long-range packing. The molecular targets form in the organized, solvent-free environment of the solid state in 100% yield and gram quantities.

Keywords: supramolecular chemistry, covalent capture, hydrogen bonds

MS46 In-situ Observation of Crystal Growth Processes

Chairpersons: Tadashi Ohachi, Vladimir Kaganer

MS46.27.1
Acta Cryst. (2005). A**61**, C61
Time-Resolved X-ray Topography Study on Growth of 180° Ferroelectric Domains
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Understanding the mechanism of nucleation and growth of 180° ferroelectric domains is an on-going subject of numerous theoretical and experimental investigations. The ferroelectric transition and the domain structure are intimately coupled to dielectric, ferroelectric, piezoelectric, pyroelectric, and nonlinear optical properties in a wide range of materials. In the past, the x-ray topography technique has been applied to investigate the ferroelectric domains in single crystals. However, the lack of sufficient diffraction contrast between the adjacent antiparallel ferroelectric domains made it difficult for investigation of domain dynamics.

Using the coherent x-rays from a third generation synchrotron source, we have greatly enhanced the diffraction contrast from the neighboring antiparallel ferroelectric domains. With this phase-contrast topography technique, we carried out a time-resolved diffraction imaging study of the nucleation and growth of 180° ferroelectric domains in barium titinate single crystals during the polarization switching. The diffraction images were collected with 1-micron spatial resolution and down to 10-ms acquisition time. We have observed drastically different domain growth mechanisms due to the surface treatment at the electrode-sample interfaces, suggesting the nucleation and growth is dominated by the defects at the electrode interface. We present the morphology of 180° domains and describe growth kinetics as a function of temperature and applied potentials.

Keywords: X-ray topography, ferroic domain structure, growth kinetics

MS46.27.2
Acta Cryst. (2005). A**61**, C61
***In-situ* Observation of Surface Kinetics during MBE Growth using Synchrotron X-ray Diffraction**
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The weak interaction of x-rays with matter offers the advantage of not disturbing the system under investigation and in most cases allows us to analyze the results using kinematical scattering theory. Both properties make x-ray diffraction an almost ideal tool to study crystal growth in situ and in real time.

To obtain the necessary sensitivity to study surfaces and interfaces that consist of a very limited number of scatterers, high primary beam intensities usually available at synchrotrons are required. Using a dedicated beamline at BESSY in Berlin, we study the surface kinetics of various III-V materials during deposition and the subsequent recovery under standard molecular-beam epitaxy conditions.

Following the diffraction oscillations during layer-by-layer homoepitaxy on GaAs(001) and the closely related InAs and GaSb surfaces, we can analyze the coverage of the different levels that constitute the growth front. After deposition, the system reduces to a two-level system. This initial, fast recovery is followed by a slower recovery phase in which the two-level structure laterally coarsens until the big terraces of the pre-growth state are recovered.

Despite their similarity in crystal structure, the three materials systems exhibit strong differences in their deposition and recovery kinetics, which are obviously related to the detailed atomistic processes taking place at the reconstructed surface during deposition.

Keywords: molecular-beam epitaxy, coarsening, III-V compounds