

MS32 Molecular recognition and crystal engineering

Chairs: Dr. Berta Gómez-Lor, Prof. Delia Haynes

MS32-O1

The many lives of resorcinarene cavitands: from molecular recognition to crystal engineering

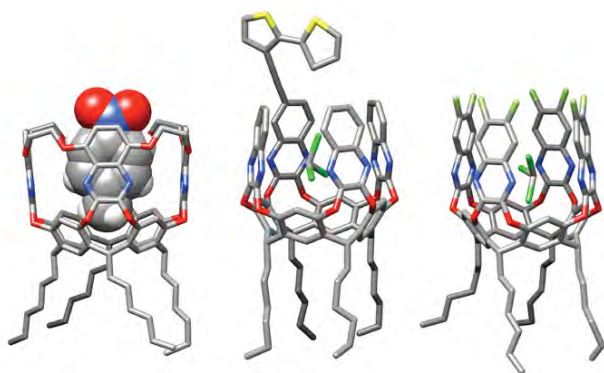
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Since their first appearance on the chemistry scene thirty years ago [1], resorcinarene-based cavitands have been exploited both as receptors for molecular recognition and as building blocks for crystal engineering [2]. Their versatility primarily stems from the possibility of choosing different bridging groups to connect the phenolic hydroxyls of the resorcinarene scaffold. This allows the tuning of the shape, dimension and complexation properties of the cavity, which can thus interact with neutral and charged molecules through H-bonding, $\pi \cdots \pi$ stacking and $\text{CH} \cdots \pi$ interactions, but also form coordinative bonds with metal centers to create discrete complexes, cages or extended networks.

We present our recent investigations on various functionalised quinoxaline-bridged cavitands for molecular recognition (see figure below) and phosphonate cavitands as ligands for the formation of coordination compounds



References:

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Keywords: cavitands, host-guest interactions, coordination compounds

MS32-O2

Close contacts involving carbon and antimony: Tetrel bonded and pnictogen bonded systems by design

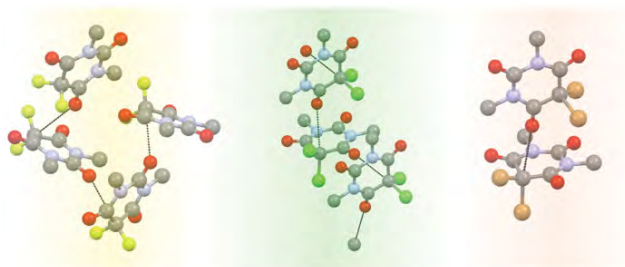
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In this communication we will describe the packing of some homomeric and heteromeric crystals wherein the composition and architecture is affected and/or determined by attractive interactions involving carbon and antimony atoms as electrophilic sites. Molecular modelling predicts that region(s) of depleted electron density are typically present on an atom opposite to the covalent bond(s) it is involved in. This is true for any element belonging to groups 14-18 of the periodic table [1] and the electrostatic potential at the depleted region(s) becomes positive when the atom is covalently bonded to strongly electron withdrawing residues [2]. We thus expected that the depleted regions on fluorinated carbon and antimony moieties might be positive enough to enable for the formation of attractive interactions with lone pair possessing atoms. We also expected that the resulting bonds might be strong enough to determine the crystal composition and architecture. Here we describe that various 5,5-difluorobarbituric derivatives form adducts were $\text{F}-\text{C} \cdots \text{O}=\text{C}$ intermolecular contacts can be as short as 90% of the sum of carbon and oxygen van der Waals radii. The $\text{C} \cdots \text{O}$ supramolecular synthon in these derivatives is robust enough to be observed also in 5,5-dichloro and 5,5-dibromo analogues, namely when halogens less electron withdrawing than fluorine are present (Fig. 1). As to fluorinated antimony derivatives, we report, for instance, that the tendency of antimony trifluoride to attractively interact with lone pair possessing atoms is so strong that in the tetrameric adducts formed on self-assembly with *p*-dipyridyl dioxide, two antimony atom gives two $\text{F}-\text{Sb} \cdots \text{O}$ close contacts with two different dioxide molecules. The described interactions are typically named tetrel bond and pnictogen bond [3], respectively. The reported results shown how their understanding is developed enough to enable for their successful use in the design of the intermolecular interactions of crystal lattices. The described structure may also suggest that tetrel bond and pnictogen bond are robust enough to become new, useful and general tools in crystal engineering.

Fig. 1 Adducts present in crystals of 5,5-difluoro- (left), 5,5-dichloro- (mid), and 5,5-dibromo-N,N'-dimethylbarbituric acid (right); F–C⋯O=C tetrel bonds are dashed black lines.



References:

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Keywords: Tetrel bond, Pnictogen bond, Crystal engineering

MS32-O3

Is it usual to be unusual? - An investigation into Molecular Conformations in Organic Crystals

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The molecular complexity and size of novel drug molecules is ever increasing, and so is their conformational flexibility. Complex flexible drug compounds may often be challenging to crystallise. Crystallisation is the final step in the manufacture of active pharmaceutical ingredients and with over 90% of pharmaceuticals being crystalline it is important to understand and control this process. The poor crystallisation behaviour of flexible molecules has been linked to the conformational diversity found in solution [1]. In solution, conformers are in equilibrium and their relative populations depend on their relative stabilities. If a crystal conformation is similar to that of a stable conformer in solution, no conformational change or adjustment would need to occur for the system to nucleate and grow [2]. However, if the crystal conformation corresponds to a highly distorted conformer or a higher-energy conformer, then significant conformational adjustment or change would need to occur during crystallisation [3]. Such conformational changes and adjustments may limit crystal growth and are the subject of the present research.

We have investigated the occurrence of unusual conformations in the Cambridge Structural Database (CSD) for various subsets of molecular crystals. Torsion angles in flexible molecules were classified as being “unusual” when they were observed in less populated areas of the CSD torsion distributions. We then investigate the conformational energy landscape of these molecules crystallising with unusual torsions. How usual is it to be unusual? Do these “unusual” torsions relate to high-energy conformations? How much conformational distortion is required for some molecule to crystallise? What causes these torsions to become unusual? Are certain torsions more prone to distortion and change? This contribution attempts to answer all of these questions by providing new insightful data on the effect of crystal structure on conformations.

References:

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Keywords: Molecular Conformation, Energy, Crystallisation