

for all types of guest molecules which are ordered in the middle of the channel, whereas inflexible  $[V(O)(bdc)]_n$  can adsorb only a little amount of the guest (5-10 mol. %). In the first case, the stoichiometry of inclusion compound is  $Guest_{0.5}@[Al(OH)(bdc)]_n$  or  $Guest_{0.25}@[Al(OH)(bdc)]_n$ . In the case of  $[V(O)(bdc)]_n$ , only cobaltocene forms inclusion phase composition cobaltocene $_{0.5}@[V(O)(bdc)]_n$  due to the formation of charge-transfer complex [4]. Hydrogen bonds, host-guest and guest-guest interactions as well as structural effects of the substitute group inside the guest molecule have been studied in details for all inclusion compounds.

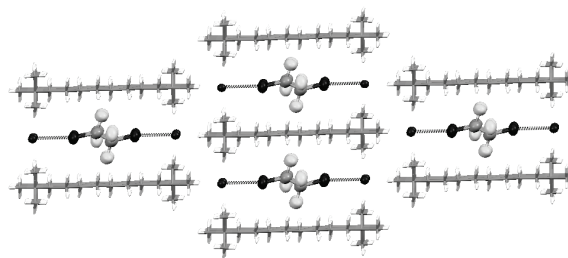
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**Keywords:** coordination polymers, host-guest complexes, powder structure determination

#### FA4-MS29-T04

**Dimensional Encapsulation of Halogen-Bonded Supramolecular Anions.** Pierangelo Metrangolo<sup>a,b</sup>, Gabriella Cavallo<sup>a</sup>, Manu Lahtinen<sup>c</sup>, Tullio Pilati<sup>d</sup>, Kari Rissanen<sup>e</sup>, Giuseppe Resnati<sup>a,b,d</sup>, Giancarlo Terraneo<sup>a,b</sup>. <sup>a</sup>NFMLab - D.C.M.I.C. "Giulio Natta", Politecnico di Milano, Via L. Mancinelli 7, 20131 Milan, Italy. <sup>b</sup>CNST - IIT@POLIMI, Politecnico di Milano, Via G. Pascoli 70/3, 20133 Milan, Italy. <sup>c</sup>Department of Chemistry, University of Jyväskylä, Post Office Box 35, Jyväskylä FI-40014, Finland. <sup>d</sup>C.N.R. - I.S.T.M., University of Milan, Via C. Golgi 19, 20133 Milan, Italy. <sup>e</sup>Department of Chemistry, Nanoscience Center, University of Jyväskylä, Post Office Box 35, Jyväskylä FI-40014, Finland.  
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Halogen bonding [1] has increasingly facilitated the assembly of diverse host-guest solids. In this contribution, we show that a well-known class of organic salts, bis(trimethylammonium) alkane diiodides, can reversibly encapsulate  $I_2$  [2] and a series of  $\alpha,\omega$ -diiodoperfluoroalkanes (DIPFAs) through intermolecular interactions between the host's  $\Gamma$  anions and the guest's terminal iodine substituents [3]. In particular, bis(trimethylammonium)hexane diiodide encapsulates  $I_2$  yielding in a predictable and controllable manner the selective formation of the rare polyiodide species  $\Gamma \cdots I-I \cdots \Gamma$ . Similarly, the process is highly selective for the DIPFA that forms an  $\Gamma \cdots I(CF_2)_m I \cdots \Gamma$  superanion, which matches in length to the chosen dication. DIPFAs that are 2 to 12 carbons in length can thereby be isolated from mixtures by means of crystallization from solution upon addition of the dissolved size-matched ionic salt. The solid-state salts can also selectively capture  $I_2$  and the DIPFAs from the vapour phase, yielding the same product formed from solution despite a lack of porosity of the starting lattice structure.



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**Keywords:** Halogen Bonding, Dynamic Porous Materials, Anions

#### FA4-MS29-T05

**Towards docking-based prediction of host-guest framework systems** Peter A. Wood, Oliver Korb. Cambridge Crystallographic Data Centre, Cambridge, UK.  
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The design and prediction of multi-component organic crystal structures is of interest to many areas of the chemical industry. Host-guest framework structures can, for example, be used to tune the physicochemical properties of a solid form, to achieve selective separation and even as catalysts. Current design and prediction methods have limitations though; crystal structure prediction (CSP) can be very computationally expensive for each individual multi-component system and there is also a limit to the number of experimental screens that can be carried out.

These multi-component structures do, however, essentially represent a form of host-guest binding related to that seen when a ligand interacts with a protein binding site. In this study we investigate whether established techniques for predicting protein-ligand binding can be applied to the challenge of modelling small molecule host-guest crystalline frameworks.

In order to examine the general applicability of this technique, an off-the-shelf docking package (GOLD [1]) is used with a standard scoring function (CHEMPLP [2]) that has been trained for interactions in protein-ligand binding sites. A range of experimentally-determined channel-based test structures are used to evaluate the effectiveness of the docking package. The test structures include API frameworks, well-known organic inclusion compounds and metal-organic frameworks. This work shows that the principles of docking can be successfully applied to the crystal engineering problem of predicting host-guest systems.

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**Keywords:** crystal engineering, docking, guest-host structures