X-Ray structure of the 1:1 complex of a tripodal receptor and *cis*-cyclohexane-1,3,5-tricarboxylic acid

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The X-ray crystal structure of the 1:1 complex of a tripodal abiotic receptor and *cis*-cyclohexane-1,3,5-tricarboxylic acid is reported; the 1:1 complex is devoid of C_3-symmetry and packs into a multi-columnar self-assembly.

Two years ago, some of us reported[1] the synthesis and binding properties of the tripodal receptor **1**, designed to bind tricarboxylic acids.[2] The receptor **1** shows high selectivity[3] for binding *cis*-cyclohexane-1,3,5-tricarboxylic acid **2** (Fig. 1) and forms a very stable complex with it in chloroform solution. Molecular modeling studies[4] suggested that two different C_3-symmetric geometries, **3a** and **3b**, were possible for the binding of triacid **2** by receptor **1**. In both cases, six intermolecular hydrogen bonds could form between the three carboxylic acids of the guest and the three amidopyridine ‘arms’ of the receptor.

ROESY[5] ^{1}H NMR studies of the complex in $CHCl_3$ revealed intermolecular contacts that agreed with a predominance in solution of the ‘*endo*’† supramolecular complex **3a**. Slow diffusion of cyclohexane into a 1:1 solution of **1** and **2** in CH_2Cl_2 produced colourless plates that were relatively unstable when removed from the mother liquor. After numerous attempts to obtain a suitable dataset, the X-ray crystal structure was solved,‡ revealing that **2** is docked into the receptor *via* six intermolecular hydrogen bonds (Fig. 2). This structure shows a complex geometry which is in general agreement with the solution structure **3a** proposed previously based on NMR data. However, the triacid complex does not possess the anticipated C_3-symmetry axis. The O···N distances for all six hydrogen-bonded interactions are different, ranging from 2.612 (0.010) to 2.739 (0.010) Å (N···HO) and from 2.854 (0.010) to 2.910 (0.010) Å (O···HN). The dihedral angles about the carboxy–cyclohexyl single bonds vary by as much as 94°. The asymmetry is also evident in the three propyl chains, where two are in different *anti* conformations while the third chain is *gauche*. Deviation from C_3-symmetry undoubtedly arises from the presence of disordered cyclohexane, which was found to be present at an occupancy less than 1 in the difference map.

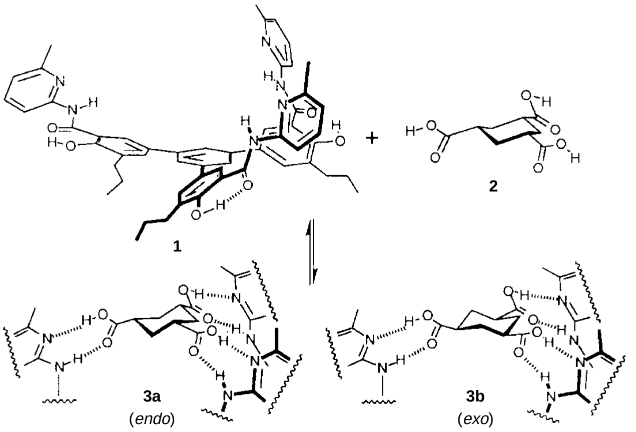

Fig. 1 Possible binding geometries for the 1:1 complex of **1** and **2**

Further inspection of the crystal packing reveals a columnar motif. The 1:1 complexes stack on top of each other in an alternating top-to-top and bottom-to-bottom fashion and form columnar supramolecular arrangements (Fig. 3). The bottom-to-bottom interaction involves π–π interaction[6] between the two central benzene rings of the receptor in a perfect face-to-face geometry separated by *ca.* 3.9 Å. The absolute stereochemistry of the complexes alternates within a single column. Thus, any two adjacent complexes within a column (whether top-to-top or bottom-to-bottom) form a perfectly centrosymmetric dimer, a direct consequence of the $C2/c$ space group in which the complex crystallizes.

The columnar structures pack in parallel fashion to form palisade-like sheets, which are stabilized by antiparallel π–π

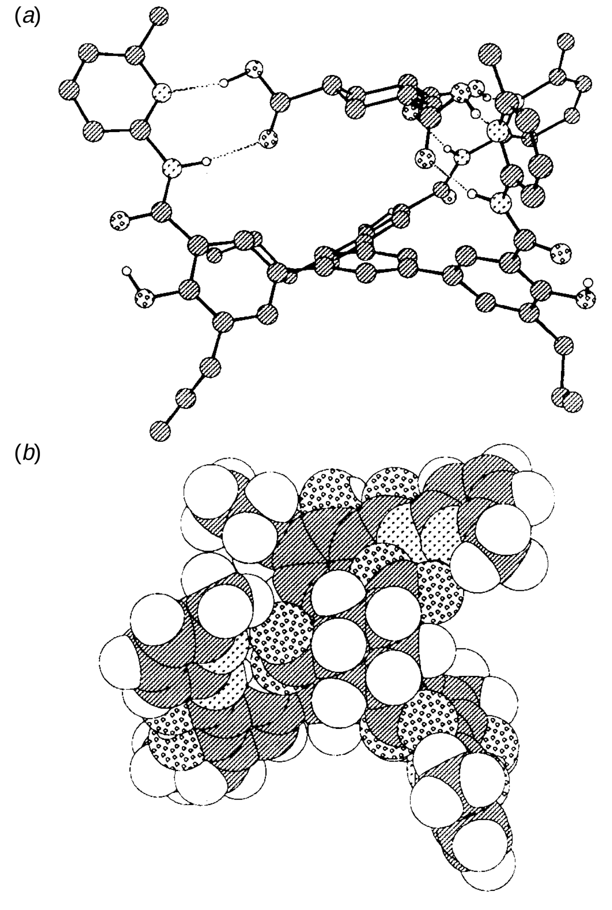

Fig. 2 X-Ray structure of 1:1 complex between **1** and **2**: (*a*) side view (only polar hydrogens in calculated positions are shown, dotted lines indicate intermolecular hydrogen bonds) and (*b*) top view of a CPK representation

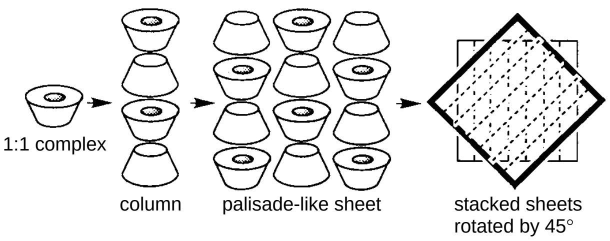

Fig. 3 Schematic crystal packing of the 1 : 1 complex

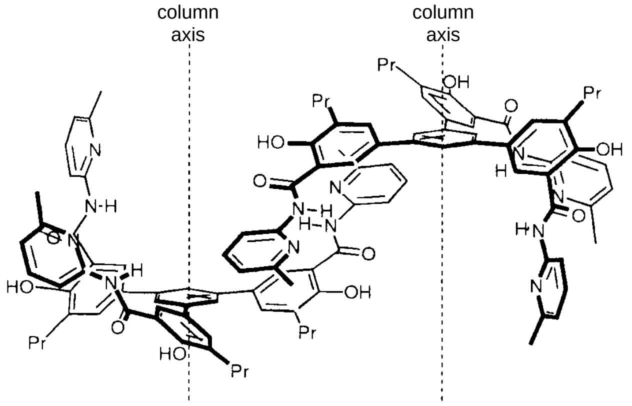

Fig. 4 Antiparallel π-stacking between arylamidopyridine arms

stacking between arylamidopyridine 'arms' from adjacent columns (Fig. 4). The sheets stack on top of each other to complete the packing and are rotated with respect to each other by about 45°. Attempts at the X-ray characterization of other supramolecular complexes of triacids are under way, including *trans*-cyclohexane-1,3,5-tricarboxylic acid, and we will report on these findings in due course.

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Footnotes

† The terms '*endo*' and '*exo*' refer to the orientation of the three equatorial carboxy groups of **2** with respect to the receptor cavity.

‡ *Crystal data* for $C_{54}N_6O_6H_{54}\cdot C_9O_6H_{12}\cdot 0.5\ C_6H_{12}$: $M = 1141.30$, crystallizes from dichloromethane–cyclohexane as colourless plates; crystal dimensions 0.25 × 0.25 × 0.08 mm, monoclinic, $a = 32.562(6)$, $b = 14.825(8)$, $c = 27.201(4)$ Å, $\beta = 105.93(1)°$, $U = 12626(8)$ Å^3, $Z = 8$, $D_c = 1.201$ g cm^{-3}, space group $C2/c$, $F(000) = 4848$. Three-dimensional, room-temperature X-ray data were collected in the range 33 to 60° in 2θ on a Rigaku AR5F diffractometer by the θ–2θ scan method using Cu-Kα radiation; 9388 independent reflections ($R_{\text{int}} = 0.054$ on F^2) were collected. The structure was solved by direct methods and refined by full-matrix least-squares methods on F^2. Hydrogen atoms were included in calculated positions and refined using a riding model. Refinement converged at a final $R1 = 0.0741$ ($wR2 = 0.2098$ for all 9326 data, 747 parameters, mean and maximum δ/σ 0.003, 0.043), with allowance for the thermal anisotropy of all non-hydrogen atoms. Minimum and maximum final electron density −0.307 and 0.549 e Å^{-3}. A weighting scheme $w = 1/[\sigma^2(F_0{}^2) + (0.030P)^2 + (0.00P)]$ where $P = [\max(F_0{}^2, 0) + 2F_c{}^2]/3$ was used in the latter stages of the refinement. Complex scattering factors were taken from the software package.[7]

Atomic coordinates, bond lengths and angles, and thermal parameters have been deposited at the Cambridge Crystallographic Data Centre (CCDC). See Information for Authors, Issue No. 1. Any request to the CCDC for this material should quote the full literature citation and the reference number 182/344.

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