KrF laser (60 μJ in a 0.25-mm spot) was used for desorption, and ionization was accomplished with an ArF laser (200 μJ in a 1.5-mm spot). The mass spectrum obtained is displayed in Figure 1. The observed C_{60}^+/C_{70}^+ peak ratio is 3.3.

^{13}C NMR spectra were obtained without ^{1}H decoupling, and Figure 2 shows the downfield portion of C_{60}/C_{70} in CCl_4. An extremely sharp single resonance is observed at 142.5 ppm. The line shape of this resonance is independent of magnetic field strength, and a similar resonance at 142.6 ppm is obtained with some of the same C_{60}/C_{70} material dissolved in benzene. The line width of the resonance is limited by magnetic field inhomogeneity, and we note the absence of any appreciable [1]H J coupling in the resonance line shape. The line intensity is consistent with the amount of C_{60} estimated to be present in the sample (∼200 μg). The observed chemical shift is in the range reported for non-protonated, aromatic carbons, ca. 155-130 ppm.[12] These results lead us to conclude that the observed resonance is due to C_{60}. The sensitivity of ^{13}C NMR chemical shifts to chemical structure is well-known, and from the appearance of a single resonance for C_{60} we conclude that all 60 carbon atoms are chemically equivalent, implying that the structure must necessarily have icosahedral symmetry.

Several weak resonances can be seen downfield from the C_{60} resonance. The strength of these resonances is consistent with estimates of C_{70} NMR line intensities based on the composition of the sample as reflected in Figure 1 and the reduced symmetry expected for this molecule.

In conclusion, the NMR spectrum of a purified C_{60}/C_{70} solution has been obtained, and a single line is found for C_{60}. This is conclusive evidence for its icosahedral symmetry.

Note Added in Proof. Independent measurements of the NMR spectra of C_{60} and C_{70} will be published by Taylor, R.; Hare, J. P.; Abdul-Sade, A. K.; Kroto, H. W. *Chem. Commun.* In press.

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A Host for the Water Dimer

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The water dimer has intrigued chemists for the past century. Early workers saw it as a model for water aggregates and the hydrogen bond.[1] More recently it has become a benchmark for computational and spectroscopic techniques.[2] We have discovered a macrocyclic host for the water dimer and report the crystal structures of the host–guest complex, and of a related host hydrate, which cannot recognize the water dimer.

In the course of our work to construct ion channels,[3] we have

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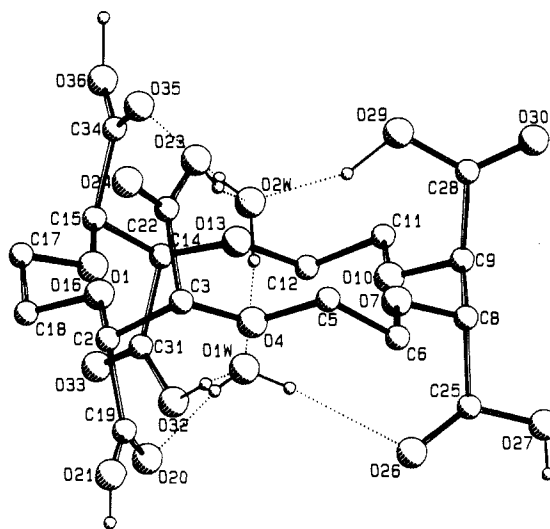

Figure 1. Structure of the water dimer inclusion complex of 18C6A₆ showing atom numbering. Two water molecules in the lattice and hydrogen atoms bonded to carbon are omitted for clarity. One water bridges between O36 and an O30′ on an adjacent molecule, the other bridges between O21 and an O33 on an adjacent molecule.
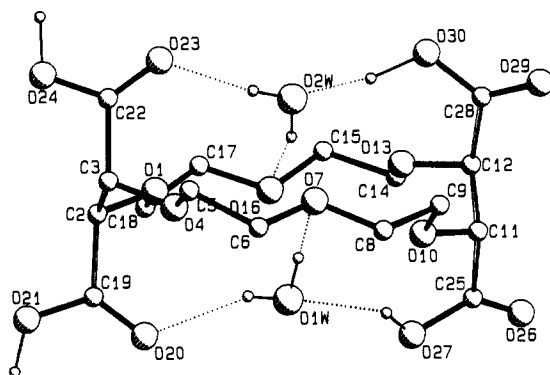

Figure 2. Structure of the hydrate of 18C6A₄ showing atom numbering. Hydrogen atoms bonded to carbon are omitted for clarity.

Table 1. Comparison of Selected Parameters of Water Dimers[a]

structure	O···O, Å	H–O···O, deg	tilt,[b] deg
18C6A₆ complex[6]	2.805 (5)	4.8	71.8
Ice XI (neutron)[9]			
dimer 1	2.750 (3)	8.3	31.0
dimer 2	2.763 (3)	9.8	45.5
dimer 3	2.793 (3)	3.5	69.8
$(H_2O)_2$ (microwave)[12]	2.976 (3)	6	57
$(H_2O)_2$ (computational)[13]	3.01	6	56
α-cyclodextrin inclusion hydrate[10]	2.931		

[a] O···O distances for other structures (Å): Ice Ih (X-ray),[14] 2.751 (3); amorphous solid water (X-ray), 2.76 (1); liquid water (X-ray and neutron), 2.85. [b] Angle between the O···O axis and the H–O–H angle bisector of the hydrogen bond acceptor molecule.

prepared crown ethers with six (18C6A₆)[4] and four (18C6A₄)[5] carboxylic acid groups attached to the macrocycle. When deprotonated, these macrocycles strongly bind metal ions in water.[4] Crystal structures of the fully protonated acids encapsulate two water molecules.[6] In 18C6A₆, a water dimer fills the cavity

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(Figure 1), while in 18C6A₄, a water bridges each pair of coaxial carboxylic acids (Figure 2).

The crystal structure of 18C6A₆ contains four water molecules.[6] In addition to the encapsulated water dimer, two waters solvate carboxyls in the syn direction. The host has 3-fold symmetry with the required six-point recognition to satisfy all of the hydrogen-bonding sites on the water dimer. Three carboxyl oxygens accept hydrogen bonds in the preferred anti direction.[7] The other three host carboxylic acids donate hydrogen bonds with the hydroxyl hydrogen in the less preferred, more acidic, anti conformation.[8] Distances of the macrocyclic oxygens to the hydrogen that connects the dimer range from 2.75 to 2.78 Å. These distances give a mean cavity radius of 1.37 Å, somewhat larger than the van der Waals radius of hydrogen. The length of these contacts excludes significant interactions with the macrocyclic oxygens.

The crystal structure of 18C6A₄ contains two waters that are similarly hydrogen bonded to the host with three-point recognition.[6] One carboxyl oxygen accepts a hydrogen bond from water, one carboxylic acid donates the hydroxyl hydrogen in an anti conformation, and a macrocyclic oxygen accepts the remaining hydrogen from water. The two waters are close to each other, O2W···O1W, 3.77 Å, but outside the sum of the van der Waals radii, and the orientations of the hydrogen atoms are not indicative of dipolar interactions.

Table 1 summarizes the parameters of the water dimer in the crystal structure and from recent experiments and calculations. The dimer in the 18C6A₆ crystal structure is virtually identical with one of the three unique dimers that define the ice IX structure.[9] A comparison of the solid-state structures of the tetra- and hexaacids suggests that the antiprismatic six-point recognition provided by 18C6A₆ (or ice IX) is required for binding the water dimer. Four-point recognition is insufficient. Cavity size is also important. Compare the water dimer complex of 18C6A₆ with the inclusion hydrate of α-cyclodextrin.[10] The included water molecules in the latter have a significantly longer O···O separation and contact the host with only two hydrogen bonds, suggestive of an adventitious hydrate rather than a defined complex.[11]

Employment of the less preferred anti conformation of the carboxylic acid for donation of hydrogen bonds begs the question of whether this conformation is as unfavored in solution or the solid state as it is in the gas phase. The host carboxylic acids can only bind guests in the cavity in the anti direction. If the carboxyls did not donate the hydrogen but adopted a syn conformation, a

repulsion would be created by the close proximity of the lone pairs on water and on hydroxyl or carbonyl. The interatomic distances preclude additional intramolecular hydrogen bonding to stabilize the anti configuration, e.g., O29-H to O7 or O10 in the 18C6A₆ structure. We don't know how much of the stability of the crystal structure comes from the complex and how much from the crystal-packing forces. We do know that a 100-mg sample crystallized to a 100-mg single crystal. The crystal structure reveals a chain of syn-oriented carboxyls hydrogen bonded to other carboxyls and the other two waters. Even so, there are only two of these lattice hydrogen bonds per water molecule, compared to four per water molecule in the 18C6A₆-water dimer complex.

These macrocycles provide an expanded architecture for binding guests by hydrogen bonding together with the usual toroidal array of macrocyclic oxygens. In 18C6A₆, the macrocycle serves as collar to anchor six carboxyls in 3-fold symmetry to form a cylindrical cavity with potentially 12 points for recognition of guests. The structures of 18C6A₆ complexes with the water dimer and monohydrated cations suggest a reason for the success of this ligand as complexing agent in water: cationic guests do not have to be completely dehydrated, as the host can recognize the water too. This solid-state structure of the water dimer joins structures in other phases to provide a clear picture of this most fundamental example of molecular recognition—the water-water hydrogen bond.

Supplementary Material Available: Tables of atomic positional coordinates, bond distances, bond angles, torsional angles, and anisotropic thermal parameters (27 pages); listing of observed and calculated structure factors for 18C6A₄·2H₂O and 18C6A₆·4H₂O (68 pages). Ordering information is given on any current masthead page.

(6) The hexaacid 18C6A₆ crystallizes from water as the tetrahydrate (C₁₈H₃₂O₂₂) in orthorhombic space group P2₁2₁2₁: a = 11.214 (2), b = 11.7829 (11), c = 19.920 (2) Å; V = 2632.0 (10) Å³; R = 0.0284 for 5124 observed of 5312 unique data. All hydrogen atoms were refined except for two on uncomplexed water molecules. The absolute configuration was assigned from starting materials; the enantiomorphous structure has R = 0.0286. The tetraacid 18C6A₄ crystallizes from water as the dihydrate (C₁₆H₂₈O₁₆) in monoclinic space group P2₁: a = 11.2002 (9), b = 8.0803 (4), c = 12.0390 (5) Å; β = 102.225 (5)°; V = 1064.8 (1) Å³; R = 0.0277 for 4235 observed of 4374 unique data. The absolute configuration was assigned from starting materials; the enantiomorphous structure has R = 0.0281. Tables of atomic positional coordinates, bond lengths, bond angles, torsion angles, and structure factor amplitudes are available as supplementary material.

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Total Synthesis of (+)-Verrucosidin

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A potent mycotoxin, verrucosidin (1) was isolated from the fungus *Penicillium verrucosum* var. *cyclopium* in 1983.[1] Verrucosidin has a close structural relationship to citreoviridin (2)[2] and related polyene α-pyrone mycotoxins,[3] most of which are known to be potent inhibitors of mitochondrial ATPase and oxidative phosphorylation.[4] Herein we report a total synthesis of (+)-verrucosidin (1) which highlights an efficient, stereocontrolled

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