# Acyclic Cucurbit[n]uril-Type Receptors: Optimization of Electrostatic Interactions for Dicationic Guests

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**ABSTRACT:** The synthesis of acyclic CB[n]-type host (1) is reported. By optimizing the placement of the sulfate groups nearby the electrostatically negative ureidyl C=O portals, the binding affinity of this class of receptors toward hydrophobic (di)ammonium guest molecules (5 – 23) is maximized. The x-ray crystal structures of 1.6a and 1.6d are reported.

Molecular container compounds and their use in basic science and real world applications is a focal point of modern supramolecular chemistry.<sup>1-6</sup> For example, cyclodextrins are used as solubilizing excipients for hydrophobic drugs, as the active ingredient in Febreeze<sup>TM</sup>, and as a sequestration agent for neuromuscular blockers (NMBA, Sugammadex).7-9 Cucurbit[n]urils (CB[n]) have become increasingly popular due to their high affinity toward hydrophobic (di)cations (K<sub>a</sub> commonly >10<sup>6</sup> M<sup>-1</sup>) and their stimuli responsive host • guest binding properties. 10 CB[n] hosts are thereby well suited as components of functional systems (e.g. sensing ensembles, drug delivery systems, and supramolecular materials). 10-14 Recently, we and others, have been exploring the synthesis and molecular recognition properties of acyclic CB[n]-type receptors (e.g. M1, Scheme 1) which retain the essential binding properties of macrocyclic CB[n] but are more easily functionalized. 12,15-17 For example, M1 functions as a solubilizing excipient for insoluble drugs and a sequestration agent for NMBAs and drugs of abuse (e.g. methamphetamine and fentanyl). These applications require hosts with maximal binding affinities to outcompete the cognate biological receptors. 20-22 Herein, we report the synthesis of 1 whose anionic sulfate groups are positioned at the ureidyl C=O portals to complement cationic guests.

Previously, we studied the influence of the (CH<sub>2</sub>)<sub>n</sub> linker length between the aromatic walls and the SO<sub>3</sub> groups on their binding affinity toward guests but did not observe large differences for n = 2-4.<sup>23</sup> We reasoned that these alkylene linkers result in the anionic sulfonate groups being positioned away from the C=O portals of M1 and reduce the electrostatic driving force toward guest complexation. Accordingly, we hypothesized that complete removal of the linker would position the OSO<sub>3</sub> groups closer to the cation binding site at the C=O portals and thereby increase binding affinity toward cationic guests. Synthetically, we allowed tetramer (2)<sup>24</sup> to react with 3 in TFA at RT to deliver 4 in 99% yield. Reaction of 4 with pyridine SO<sub>3</sub> at 90 °C delivered 1 (60%, 0.5 gram scale) after purification by gel permeation chromatography. Host 1 was characterized spectroscopically and its structure was confirmed by x-ray crystallography of its host guest complexes (*vide infra*). For

example, the <sup>1</sup>H NMR spectrum of **1** shows six resonances for the diastereotopic CH<sub>2</sub>-groups of the glycoluril oligomer in the expected 4:4:4:4:2:2 ratio along with a singlet for the aromatic Hatoms, two Me resonances, and two glycoluril methine resonances which is consistent with the depicted  $C_{2\nu}$ -symmetric structure of **1**. In the <sup>13</sup>C NMR we observe all 14 resonances expected based on the depicted of the  $C_{2\nu}$ -symmetric structure of **1**. Finally, the electrospray ionization mass spectrum for **1** as its complex with **6d** exhibits a doubly charged ion ([M+**6d**-2Cl<sup>-</sup>]<sup>2-</sup>), calcd. for  $C_{54}H_{70}N_{18}O_{24}Na_4^{2-}787.1642$ , found 787.1679. Host **1** exhibits high water solubility (>40 mM). Next, we performed dilution experiments to ensure that self-association of **1** does not impinge upon the planned binding constant measurements.<sup>1</sup>

**Scheme 1**. Synthesis of **1**. Conditions: a) TFA, 25 °C, N<sub>2</sub>, 16 h; b) pyridine•SO<sub>3</sub>, 90 °C, 18 h.

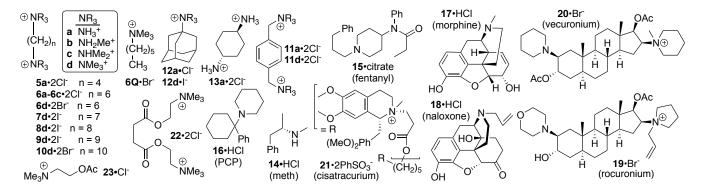


Figure 1. Structures of guests 5 - 23.

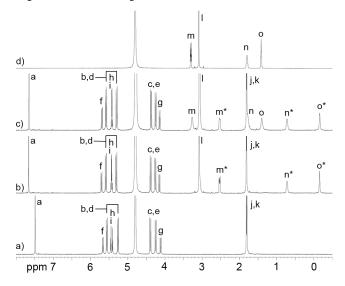
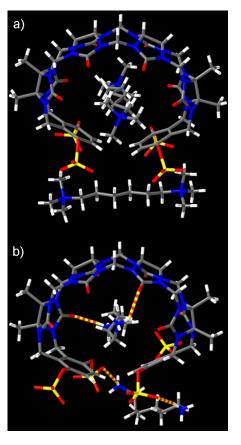


Figure 2.  $^{1}$ H NMR spectra (D<sub>2</sub>O, 600 MHz) recorded for: a) 1 (1 mM), b) 1 (1 mM) and 6d (1 mM), c) 1 (1 mM) and 6d (2 mM), and d) 6d (1 mM). \*Resonances for 1-6d.

Accordingly, we measured the  $^1H$  NMR spectrum of 1 upon dilution from 40 to 1 mM. We did not observe significant changes in chemical shifts ( $\Delta\delta$  <0.02 ppm) over this concentration range and therefore conclude that 1 is monomeric in water (Supporting Information).

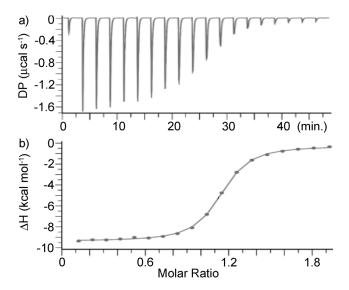
Next, we performed qualitative host • guest binding studies of 1 with guests 5-13 (Figure 1, Supporting Information) as monitored by <sup>1</sup>H NMR. Figure 2 shows the <sup>1</sup>H NMR spectra recorded for 1, 6d, and 1:1 and 1:2 mixtures of 1:6d. As expected the methylene resonances for guest **6d** (H<sub>m</sub>, H<sub>n</sub>, H<sub>o</sub>) within the **1.6d** complex (Figure 2b) experience a sizable upfield shift upon complexation due to the anisotropic shielding effects of the aromatic walls and the glycoluril concavity. 15,25-26 At a 1:2 1:6d ratio, resonances are observed for both free 6d and 1.6d which indicates slow exchange on the <sup>1</sup>H NMR time scale which is usually observed only for tight host guest complexes. Similar <sup>1</sup>H NMR measurements were made for the remainder of the guests (Supporting Information). We find that the narrow guests (e.g. 11a,d and 6a-d) display slow exchange kinetics whereas the bulkier guests 12a,d display intermediate to fast exchange on the chemical shift timescale. We attribute this to their lower binding constants (vide infra) as a result of the expansion of the cavity of 1 required to accommodate the larger adamantane framework.



**Figure 3**. Renderings of the crystal structures of: a) **1.6d**, and b) **1.6a**. Color code: C, gray; H, white; N, blue; O, red; H-bonds red-yellow striped.

We obtained x-ray crystal structures of the 1.6d (CCDC 2003520) and 1.6a (CCDC 2003521) complexes (Figure 3; See Figure S54 for enlarged stereoviews). Figure 3a shows that 1.6d adopts a geometry that optimizes Me<sub>3</sub>N<sup>+</sup>•••O=C electrostatic interactions at both portals and displays only small out-of-plane skewing of the terminal aromatic rings. The geometry of 1.6d is reminiscent of CB[n]•guest complexes where the  $Me_3N^+$ •••O=C distances cluster in the 3.810-4.690 Å range to spread the positive charge to the carbonyl portals.<sup>14</sup> Interestingly, a second molecule of **6d** fits into a cleft created by the sidewalls and the outward pointing OSO<sub>3</sub> groups to balance the overall 4- charge of 1. These OSO<sub>3</sub> groups also engage in electrostatic interactions with 6d (Me<sub>3</sub>N<sup>+</sup>···O-S distances: 3.808-4.722 Å). The crystal structure of 1.6a (Figure 3b) also shows intracavity and extracavity molecules of 6a but displays significant out-of-plane twisting of the aromatic termini. Interestingly, one of the four OSO<sub>3</sub>- groups turns inward toward the ammonium ion guest which establishes that this group can directly participate in the guest recognition process.

Given the high binding constants typically observed for host guest complexes (acyclic) CB[n]-type receptors, 10,15 we elected to use isothermal titration calorimetry (ITC) to measure the Ka values between host 1 and guests 5–23. For the weaker binding complexes  $(K_a \le 10^7 \,\mathrm{M}^{-1})$ , we performed the direct titration of host 1 in the ITC cell with a solution of guest in the syringe and fitted the data to a 1:1 binding model implemented by the PEAQ ITC software to obtain K<sub>a</sub> and ΔH values (kcal mol<sup>-1</sup>). Table 1 reports the thermodynamic data for 1.5, 1.6Q, 1.12a, 1.13a, 1.14-1.18, and 1.21-1.23 obtained by direct ITC titrations (Supporting Information). Complexes with K<sub>a</sub> values that exceed 10<sup>7</sup> M<sup>-1</sup> cannot be measured accurately by direct titrations, so we turned to ITC competitive titrations.<sup>27-28</sup> In competitive titrations, a solution of host and an excess of a weak guest of known ΔH and Ka is titrated with a solution of a tighter binding guest. Fitting of the heat released during the displacement process is analyzed by a competitive binding model in the PEAQ ITC data analysis software which delivers  $\Delta H$ and Ka for the tighter complex. Figure 4a shows the thermogram recorded when a mixture of 1 and 13 was titrated with 6d; Figure 4b shows the fitting of the integrated heats to a competitive binding model to determine  $K_a = 6.79 \times 10^9 \text{ M}^{-1}$  and  $\Delta H = -12.1 \text{ kcal mol}^{-1}$ . Table 1 reports K₁ and ∆H values for the remaining 1•guest complexes obtained in an analogous manner (Supporting Information).



**Figure 4.** a) ITC titration of **1** (100  $\mu$ M) and **13** (2 mM) in the cell with a solution of **6d** (1.0 mM) in the syringe, and b) data fitting to a competition binding model to extract  $K_a = 6.79 \times 10^9 \, M^{-1}$  and  $\Delta H = -12.1 \, kcal \, mol^{-1}$ .

Table 1. Binding constants measured by ITC for 1-guest complexes and comparative literature values for M1. Conditions: 20 mM sodium phosphate buffered  $\text{H}_2\text{O}$ , pH 7.4,  $25\,^{\circ}\text{C}$ .

	$K_{\rm a}$ [M <sup>-1</sup> ]; $\Delta$ H (kcal mol <sup>-1</sup> )		
Guest	Host 1	Host M1 <sup>e)</sup>	
5	$1.68 \times 10^6$ ; $-6.76 \pm 0.020^a$	_	
6a	$3.70 \times 10^8$ ; $-8.60 \pm 0.021$ <sup>b)</sup>	$5.05 \times 10^7$ ; -6.23±0.014	
6b	5.26×108; -9.82±0.038c)	9.43×10 <sup>7</sup> ; -7.15±0.025	
6c	5.74×108; -10.5±0.028c)	4.81×10 <sup>7</sup> ; -7.66±0.073	
6d	6.71×10°; -12.1±0.042°)	8.93×10 <sup>7</sup> ; -9.35±0.021	

6Q	7.57×10 <sup>6</sup> ; -9.68±0.063 <sup>a)</sup>	1.24×10 <sup>6</sup> ; -5.67±0.033
7 <b>d</b>	6.06×10 <sup>9</sup> ; -12.2±0.041 <sup>c)</sup>	-
8d	1.75×10 <sup>9</sup> ; -10.5±0.032 <sup>c)</sup>	_
9d	7.57×108; -10.2±0.030c)	-
10d	5.43×108; -10.3±0.088c)	-
11a	9.71×10 <sup>8</sup> ; -9.69±0.014 <sup>b)</sup>	1.67×10 <sup>8</sup> ; -8.09±0.018
11d	1.05×10 <sup>9</sup> ; -12.0±0.030 <sup>b)</sup>	1.78×10 <sup>8</sup> ; -11.4±0.022
12a	9.90×10 <sup>5</sup> ; -4.45±0.021 <sup>a)</sup>	9.62×10 <sup>5</sup> ; -6.55±0.029
12d	6.66×10 <sup>6</sup> ; -7.36±0.030 <sup>d)</sup>	1.70×10 <sup>7</sup> ; -9.09±0.027
13a	$3.41\times10^6$ ; $-2.92\pm0.019^a$ )	1.95×10 <sup>6</sup> ; -5.70±0.027
14	3.02×10 <sup>6</sup> ; -9.28±0.058 <sup>a)</sup>	7.5×10 <sup>6</sup>
15	3.64×10 <sup>6</sup> ; -12.2±0.076 <sup>a)</sup>	1.1×10 <sup>7</sup>
16	1.89×10 <sup>5</sup> ; -6.18±0.069 <sup>a)</sup>	4.7×10 <sup>4</sup>
17	7.69×10 <sup>5</sup> ; -8.03±0.07 <sup>a)</sup>	5.3×10 <sup>5</sup>
18	$4.85 \times 10^6$ ; $-5.90 \pm 0.205^a$ )	_
19	6.29×10 <sup>8</sup> ; -12.9±0.056 <sup>b)</sup>	8.4×10 <sup>6</sup>
20	1.00×10°; -9.62±0.036°)	5.8×10 <sup>6</sup>
21	5.32×10 <sup>5</sup> ; -15.4±0.174 <sup>a)</sup>	9.7×10 <sup>5</sup>
22	2.41×10 <sup>4</sup> ; -5.26±0.372 <sup>a)</sup>	-
23	2.31×10 <sup>5</sup> ; -8.54±0.063 <sup>a)</sup>	2.4×10 <sup>4</sup>

not reported. a) Direct titration. Competive ITC using: b) 5 as competitor, c) 13a as competitor, d) 6d as competitor, e) Literature values.<sup>18,29-31</sup>

The binding constant data reported in Table 1 allows us to draw some conclusions about the molecular recognition preferences of host 1 in comparison to M1. As expected, we find that the 1•guest complexes are uniformly driven by favorable enthalpic ( $\Delta H$ ) contributions. In the CB[n] series of hosts these favorable enthalpy values are attributed to the presence of high energy host intracavity water molecules that are released upon guest binding.<sup>32-33</sup> Host 1 displays high affinity toward hexanediammonium ion guests 6a -6d with K<sub>d</sub> values in the single digit nM to sub-nM range. Host 1 prefers the quaternary ammonium ion guest 6d by ≈10-fold over the primary - tertiary ammonium ions 6a - 6c. In selected contexts, related preferences have been seen for CB[7]34 where they are attributed to the more efficient spreading of positive charge to the entire ureidyl C=O portal. Host 1 binds quaternary monoammonium ion guest 6Q 890-fold weaker than the corresponding quaternary diammonium 6d; this ≈10<sup>3</sup> M<sup>-1</sup> difference in affinity is also noted for CB[n]-type receptors. 10 Importantly, we find that 1 binds to guests **6a** – **6c** 5.6 – 11.9-fold stronger than **M1**, but 75fold stronger than M1 toward bis(quaternary) guest 6d. Similar preferences are observed for dicationic guests 11a and 11d but not for monocationic guests 12a and 12d which suggests that the defined separation between OSO3 groups in 1 makes it especially complementary to diammonium ion guests. Host 1 also binds with high affinity (single digit nM to sub nM K<sub>d</sub> values) toward the longer alkanediammonium ions 7d - 10d although 6d is the tightest binder in this series which reflects the ability of acyclic CB[n] to flex their cavity to accommodate larger guests and optimize binding affinity. Related preferences have previously been seen for M1 and related receptors toward primary alkane diammonium ion guests.<sup>24</sup>

We have previously studied the use of M1 and a naphthalene walled analogue known as M2 as *in vivo* sequestration agents for drugs of abuse (e.g. methamphetamine (14)).<sup>18</sup> Accordingly, we decided to measure the binding affinities of some compounds (14)

- 18) relevant to counteracting the effects of drugs of abuse. We find that host 1 binds less tightly than M1 toward 14 and 15. In contrast, host 1 binds somewhat tighter to PCP (16) and morphine (17) than M1 does, but the single digit  $\mu$ M dissociation constants are unlikely to render 1 an efficient *in vivo* sequestration agent for 16 and 17. Accordingly, 1 is not an improved lead compound for the sequestration of drugs of abuse (14 – 17). This is perhaps not surprising given that 1 has a distinct preference for bis(quaternary) diammonium ions whereas 14 – 17 are secondary and tertiary ammonium ions.

In a separate line of inquiry, we have shown that M1 and M2 act as *in vivo* reversal agents for NMBAs 19-21.<sup>29,35-37</sup> Accordingly, we measured the binding constants of 1 toward a panel of compounds relevant to its potential use as an *in vivo* reversal agent. Table 1 shows that 1 possesses higher binding affinity toward 19 (75-fold) and 20 (172-fold) than M1. Importantly, 1 binds >2700-fold tighter to 19 or 20 than to 23. Acetylcholine is also present in the neuromuscular junction and must not be sequestered. The affinity of 1-19 (6.29×10<sup>8</sup> M<sup>-1</sup>) and 1-20 (1.00×10<sup>9</sup> M<sup>-1</sup>) are comparable to those of M2-19 (3.4×10<sup>9</sup> M<sup>-1</sup>) and M2-20 (1.6×10<sup>9</sup> M<sup>-1</sup>) which function very well *in vivo*.<sup>29</sup> Host 1, however, possesses superior solubility (>40 mM) compared to M2 (18 mM) which might prove advantageous for formulation purposes.

In summary, we have presented the synthesis of host 1 with OSO<sub>3</sub> groups directly connected to the aromatic walls. Host 1 has excellent solubility (40 mM), does not self-associate, and binds to quaternary diammonium ions tighter than M1 which features propylene linkers. The x-ray crystal structures of 1.6a and 1.6d show cavity inclusion of the diammonium guest and an external diammonium ion that balances the overall charge of tetraanionic 1. In conclusion, we find that the OSO<sub>3</sub> groups do not merely function as solubilizing groups, but rather their close proximity to the C=O portals of 1 delivers enhanced binding affinity toward quaternary diammonium ions including important NMBAs 19 and 20. Host 1 should be considered alongside M1 and M2 as *in vivo* reversal agents for neuromuscular blockers.

#### **ASSOCIATED CONTENT**

## **Supporting Information**

The Supporting Information is available free of charge on ACS publication website at DOI: xxxxxxx.

Experimental procedures, characterization data, <sup>1</sup>H and <sup>13</sup>C NMR spectra for new compounds, <sup>1</sup>H NMR spectra for **1**•guest complexes, and data from ITC experiments (PDF); crystallographic information files for **1**•**6a** and **1**•**6d** (CIF).

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## **Author Contributions**

<sup>†</sup>X.L. and S.Z.N. contributed equally. X.L. and S.Z.N. performed experiments and analyzed data. P.Y.Z. collected x-ray diffraction data and solved the crystal structures. L.I., X.L., and S.Z.N. wrote the paper. All authors have given approval to the final version of the manuscript. L.I. supervised the entire project.

#### **Notes**

L.I. is an inventor on patents held by the University of Maryland on the use of acyclic CB[n]-type receptors in biomedical applications.

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