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Anion Binding versus Intramolecular Hydrogen Bonding in Neutral Macrocyclic Amides

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Abstract: Although amide groups are important hydrogen-bond donors in natural and synthetic anion receptors, studies on structure–affinity relationships of amide-based macrocyclic receptors are still very limited. Therefore, we synthesized a series of macrocyclic tetraamides **5**–**8** derived from 1,3-benzenedicarboxylic (isophthalic) acid and aliphatic α,ω-diamines of different lengths. ^{1}H NMR titrations in DMSO solution show that the anion affinity of these receptors decreases with increasing size of the macrocycle irrespective of the anion, and this suggests a minor role of geometric complementarity. Comparison with their previously studied pyridine congeners reveals that the isophthalic acid based macrocycles are less potent, in contrast to what was found for simple model diamides. Combined theoretical and experimental structural studies were carried out to determine the reasons behind this behaviour. The results show that the unexpectedly low anion binding ability of the isophthalic acid-based receptors is due to the self-complementary nature of the isophthalic bis-amide fragments: when two such moieties are present within a sufficiently flexible macrocycle, they adopt *syn–anti* conformations and bind each other by two strong intramolecular hydrogen bonds that close the macrocyclic cavity. Nevertheless, anion binding is able to break these hydrogen bonds and switch a macrocycle into a convergent all-*syn* conformation. Despite the ill-preorganized conformation, 20-membered receptor **6** is better than either its open-chain analogue (macrocyclic effect) and/or its isomer having differently placed carbonyl groups. The crystal structures of four anion complexes of the macrocyclic receptors are reported. X-ray studies and solution NMR data confirmed the inclusive nature of the complexes and pointed to strong involvement of aromatic CH hydrogen atoms in anion binding.

Keywords: amides · anion binding · hydrogen bonds · macrocyclic ligands · receptors

Introduction

Noncovalent interactions with negatively charged species play an important role in many essential chemical and biological processes.[1] Hydrogen-bonding interactions between anions and amide groups are an important example. Proteins can use multiple such interactions to achieve strong and selective binding of anions even in a highly competitive aqueous medium.[2,3] Accordingly, the development of amide-based anion receptors is of considerable interest.[4–7] Although, macrocyclic anion receptors generally perform better than their linear counterparts,[7] most efforts in this area were devoted to simple acyclic receptors. As a result, little is known about the relative influence of various factors such as the size, shape and rigidity of the macrocycle or the type and arrangement of building blocks on anion binding by macrocyclic, amide-based receptors. Therefore, we undertook systematic studies on anion recognition by this class of receptors.[8–10] Previously, we studied the influence of the size of a macrocycle on the stability of its anion complexes.[9] As model receptors, a series of macrocyclic tetraamides **1**–**4** derived from 2,6-pyridinedicarboxylic acid and flexible, aliphatic α,ω-diamines of various lengths was used.

To add another dimension to our study, we now also varied the structure of the diacid component. According to Crabtree et al.,[11] isophthalamides are much more potent anion receptors than 2,6-pyridine diamides,[12] in which the electron pair of the pyridine nitrogen atom competes with anions for hydrogen bonding with the amide NH groups. According to an alternative view, higher anion affinity of

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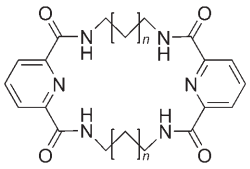
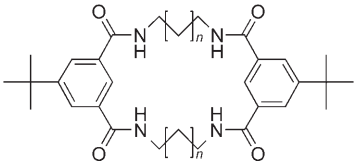


1 *n*=0
2 *n*=1
3 *n*=2
4 *n*=3

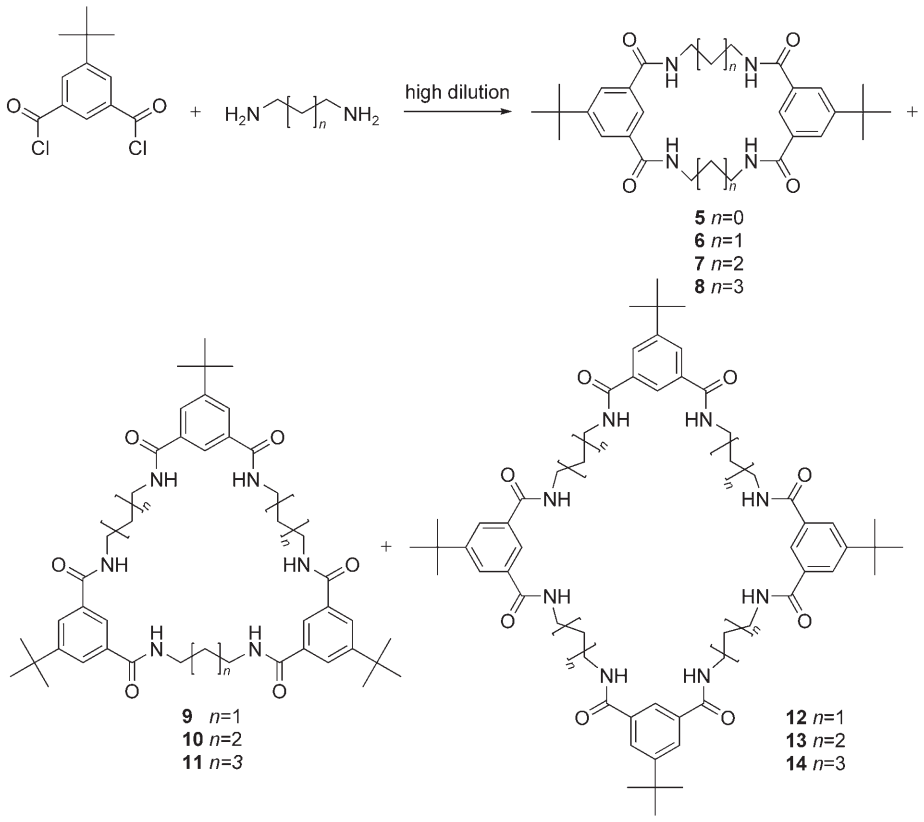


5 *n*=0
6 *n*=1
7 *n*=2
8 *n*=3

isophthalamides may be attributed to additional favorable interaction with aromatic CH protons at the 2-position. This second explanation was recently supported by a theoretical study of Bryantsev and Hay,[13] who convincingly demonstrated that even moderately acidic aromatic CH groups in the receptor structure could considerably enhance its anion-binding affinity. It was therefore natural to extend our studies to isophthalic acid based macrocycles. However, in contrast to pyridine diamides, the isophthalamides are not preorganized toward convergent binding. Thus, it was interesting to find out which effect would prevail and which family of macrocyclic receptors would show higher anion affinity. Here we describe the synthesis and anion-binding properties of macrocyclic isophthalamide receptors **5**–**8**. Particular attention was paid to conformational preferences of these receptors and their complexes and to anion-induced conformational changes they undergo. Furthermore, these new receptors proved be good models for studying competition between intramolecular hydrogen bonding and anion binding.

Synthesis

Low solubility notoriously hampers both the synthesis and study of macrocyclic amides. We already faced these problems during our previous work with pyridine derivatives. Thus, we decided to introduce *tert*-butyl groups into the structures to enhance their solubility in organic solvents, taking advantage of the commercial availability of 5-*tert*-butylisophthalic acid. All the desired macrocyclic tetraamides **5**–**8** were synthesized by one-step [2+2] condensation of 5-*tert*-butylisophthalic acid dichloride with an appropriate α,ω-diamine under high-dilution conditions (Scheme 1).[14]



Scheme 1. Synthesis of macrocyclic amides.

Despite the presence of the solubilising groups, the products derived from 1,2-diaminoethane turned out to be hardly soluble in most solvents, including DMSO, and therefore only a small sample of **5** could be obtained for analytical purposes. The solubility of the products of the remaining reactions, although still low, allowed for their separation, characterization and evaluation of their anion-binding properties. The yields of the macrocyclic tetraamides were moderate to low. In no case were we able to isolate the products of [1+1] condensation, the macrocyclic diamides, although analogous products were obtained earlier in similar reactions.[15–18] However, considerable amounts of larger macrocyclic products were formed: hexaamides, octaamides, and even traces of decaamides and dodecaamides. These large macrocycles are also potentially interesting as anion receptors; for example, a hexaamide simi-

lar to **9** having the same ring size is able to bind $CaCl_3^-$ ions in the solid state,[19] whereas octaamides have been shown by us[20] to bind two chloride ions simultaneously. For octaamides **12**, **13** and **14**, there is uncertainty concerning their structures: are they single macrocycles or catenanes built from two tetraamide rings? The macrocyclic structure of **12** was unambiguously confirmed by single-crystal X-ray analysis of its chloride complex, which also confirmed its ability to bind two Cl^- ions simultaneously. This extraordinary phenomenon will be described in detail elsewhere. The identity of octaamides **13** and **14** was confirmed on the basis of fragmentation patterns in their mass spectra.

In summary, the reaction is unselective and the product ratio resembles what might have been expected from the statistical mixture. This is in contrast to what was found in many condensations of isophthalic acid dichloride with longer and more rigid amines, where specific hydrogen-bonding interactions involving linear intermediates directed the course of the reaction and led to the preferential formation of, for example, catenanes or rotaxanes.[21,22,33,34] The above-described method of synthesis of the macrocyclic tetraamides suffers from low yields and problems with separation of the desired tetraamides from the larger macrocyclic products. However, these difficulties are compensated by the fact that this is a one-pot synthesis and that each such reaction affords at least three interesting macrocycles that are potential anion receptors, that is, tetraamides (**6**: 31.9%, **7**: 15.0%, **8**: 11.4%), hexaamides (**9**: 24.6%, **11**: 1.8%) and octaamides (**12**: 15.7%, **14**: 2.8%). It is therefore good enough for our exploratory studies.

Anion binding in solution: The stability constants of receptors **6**, **7** and **8** with various anions were determined by ^{1}H NMR titration[23] in [D_6]DMSO (Table 1). The addition of anions in the form of tetrabutylammonium (TBA) salts to the solutions of each receptor caused significant downfield shifts of the amide NH and internal aromatic CH_{int} signals in the ^{1}H NMR spectra that indicated fast equilibrium between complexed and free ligands and also suggested anion encapsulation inside the macrocyclic cavity by N–H···A^- and C–H···A^- hydrogen-bonding interactions. Typical titration curves are shown in the Supporting Information.

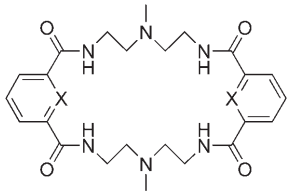
Table 1. Stability constants [M^{-1}] for the formation of 1:1 complexes of **6**, **7** and **8** with various anions in [D_6]DMSO at 298 K.[a] Values for receptors **2** and **4**[9] are listed for comparison.

Anion	**6**	**7**	**8**	**2**	**4**
Cl^-	378	296	48	1930	18
Br^-	20	20	6.5	150	<5
$PhCOO^-$	601	302	82	2283	30
AcO^-	3130	552	205	3240	310
$H_2PO_4^-$	–[b,c]	573	–[b]	7410	450
HSO_4^-	<5	–	–	75	<5

[a] Errors are estimated to be <10%. Tetrabutylammonium salts were used as the anion sources. [b] The data do not fit satisfactorily to a simple 1:1 binding model. [c] $K=1320$ was obtained in DMSO+5% H_2O.[10]

The stability constants collected in Table 1 are averaged values obtained from nonlinear fitting of a 1:1 binding model to the shifts of NH and CH_{int} protons. The low solubility of receptor **5** in DMSO precluded the determination of its stability constants.

Contrary to our initial assumptions, the isophthalamides turned out to be weaker anionophores than the pyridine diamides. Similar observations were made by Bowman-James et al.[24] on the 24-membered macrocyclic receptors **15** and **16** and were ascribed to worse preorganization of isophthalamide receptors. As will be shown below, there is also another and probably more serious reason: competition from intramolecular hydrogen bonds in the isophthalamide macrocycles.



15 X=CH
16 X=N

Previously, we found a peak affinity of the pyridine receptors as a function of ring size: the 20-membered receptor was better than either its smaller or larger homologues. In the present isophthalamide receptors, a similar maximum of affinity could not be demonstrated, due to the lack of data for the smallest, 18-membered macrocycle. However, the right-hand part of the size-affinity curve is now supplemented by the 22-membered receptor, which was unavailable in the pyridine series. Monotonic decrease of the binding affinity with increasing macrocycle size is clearly observed for all anions tested, irrespective of their size. Thus, the size match between an anion and the cavity of the receptor does not determine the observed selectivity. For instance, the cavities of the largest, 24-membered receptors **4** and **8** match the size of phosphate or carboxylate anions better than receptors **2** and **6**,[25] but their respective complexes are weaker. Apparently, anion binding abilities of our receptors result from intrinsic properties inherent to their structure. This is reminiscent of what is well-known for simple crown ethers and alkali metal cations: no matter what the cation diameter is, it is better complexed by [18]crown-6 than by either smaller or larger crowns.[26]

The selectivity trends displayed by all three receptors **6–8** are similar and common for hydrogen-bonding receptors: $AcO^- > Cl^- > Br^-$, $AcO^- > PhCOO^-$. Although it is tempting to link this order to the basicity of anions, such correlation may be valid only within the limited data set and may break when more basic anions such as *p*-nitrophenolate or cyanide are taken into account.[27] Remarkably, chloride anion forms more stable complexes than might be expected based on its

very weak basicity; for example, it binds to **7** as strongly as the much more basic benzoate anion.

Structural studies: To gain some insight into the structural determinants of the binding abilities observed above, we undertook systematic studies on the conformational preferences of isophthalamide receptors, starting with the simple building blocks.

Building blocks: 2,6-Pyridine diamides are well known for their strong preference for *syn–syn* conformation of both amide NH groups, stemming from hydrogen bonding with the pyridine nitrogen atom and lone-pair repulsion in the alternative conformations (Figure 1).[28,29] As a result of these interactions, the whole 2,6-bis(carbamoyl)pyridine fragment is rigid, planar, exhibits a well-defined U-shape, and displays two hydrogen-bond donating groups in a convergent manner.

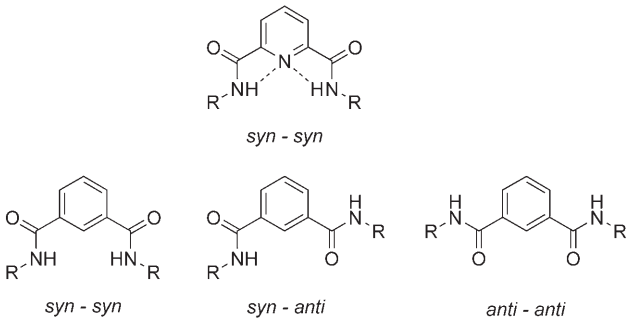


Figure 1. Conformations of isophthalamide amide groups.

On the contrary, the isophthalamide moiety, lacking such ordering interactions, is often perceived as having preference towards *syn–anti* conformation of its amide groups (Figure 1).[30] This conformation does not allow two convergent hydrogen bonds to be formed and is therefore unsuitable for anion binding. Such a view was gained from numerous crystal structures of *syn–anti* isophthalamides and reinforced by calculations of Hunter and Purvis.[28] However, these calculations explored the rather special case of 2,6-dimethylaniline derivatives in which each aromatic substituent on nitrogen is perpendicular to the plane of amide group. In contrast to these results, Malone et al.[29] have shown that simple *N,N′*-diphenylisophthalamide crystallizes in a *syn–syn* conformation. This is also the most stable conformation according to AM1 calculations, although it is only 3 kJ mol^{-1} more stable than the *syn–anti* conformation. In the context of the present studies, we were interested in the conformational preferences of aliphatic isophthalamides, and therefore we performed ab initio calculations on the simple model compound *N,N′*-dimethylisophthalamide.

In crystal structures, the amide groups are usually tilted with respect to the adjacent benzene rings. Therefore, two starting geometries were set for each of the three basic conformations depicted on Figure 1: one with both amide hydrogen atoms on the same side of the central ring, denoted as (+,+), and the other with amide hydrogen atoms on opposite sides, labelled (+,−). The resulting six starting geometries were optimized at both B3LYP/6-31G+(d,p) and HF/6-31G+(d,p) levels of theory. For comparison, much simpler semiempirical AM1 calculations were also performed. The results are collected in Table 2. On optimisation, the *syn–anti*(+,+) conformer twisted into the *syn–anti*-(+,−) one, so there are only five entries in the table.

The results obtained by both ab initio methods are similar. As anticipated, the amide groups are not coplanar with the benzene ring and the respective torsion angles vary between 20 and 30°, depending on the particular conformation and the method applied.[31] This twist is a compromise between the tendency of the molecule to maximize amide–phenyl conjugation and to minimize steric repulsion between the NH hydrogen atom and the *ortho* CH group of the aromatic ring. The mutual arrangement of both amide groups in the molecule is apparently governed by the interaction of their local dipole moments: in all cases, the (+,−) conformation is more stable than the (+,+) one, and, more generally, the energy of each conformation rises monotonically with increasing overall dipole moment of the molecule (Figure 2a). As a result, the *syn–anti*(+,−) conformation is the most stable according to both ab initio methods. Such a preference is disadvantageous with respect to anion binding, but, fortunately, it is not very strong: only 3–4 kJ mol^{-1} relative to the *syn–syn*(+,−) and about 6 kJ mol^{-1} relative to the *syn–syn*(+,+) conformation. Note that only this less stable *syn–syn*(+,+) conformation is truly convergent. In fact, the amide groups of *syn–syn*(+,−) isophthalamide may bind two

Table 2. Relative energies [kJ mol^{-1}], dipole moments [D] and torsion angles between the amide groups and phenyl ring [°] of five different conformations of dimethyl isophthalamide as calculated at the B3LYP, HF and AM1 levels of theory.[a]

	B3LYP/6-31G+(d,p)//6–311G++(3df,3pd)			HF/6-31G+(d,p)//6–311G++(3df,3pd)			AM1		
	Relative energy [kJ mol^{-1}]	Torsion angles [°]	Dipole moment [Debye]	Relative energy [kJ mol^{-1}]	Torsion angles [°]	Dipole moment [Debye]	Relative energy [kJ mol^{-1}]	Torsion angles [°]	Dipole moment [D]
syn–anti(+,−)	0	158.7, 20.2	3.32	0	155.5, 24.6	3.34	0	143.5, 37.4	2.70
syn–syn(+,−)	3.77	27.6, 27.6	3.77	3.16	29.1, 29.1	3.44	1.34	41.4, 41.4	2.04
syn–syn(+,+)	6.30	24.2, −24.2	5.21	6.09	27.0, −27.0	5.28	3.79	38.4, −38.5	4.77
anti–anti(+,−)	7.07	152.4, 152.4	5.89	6.70	150.2, 150.2	6.06	3.52	137.2, 137.2	4.80
anti–anti(+,+)	8.39	155.5, −155.5	7.00	8.32	153.4, −153.3	7.37	5.89	140.9, −140.9	6.72

[a] Zero-point energy and thermal corrections have not been applied.

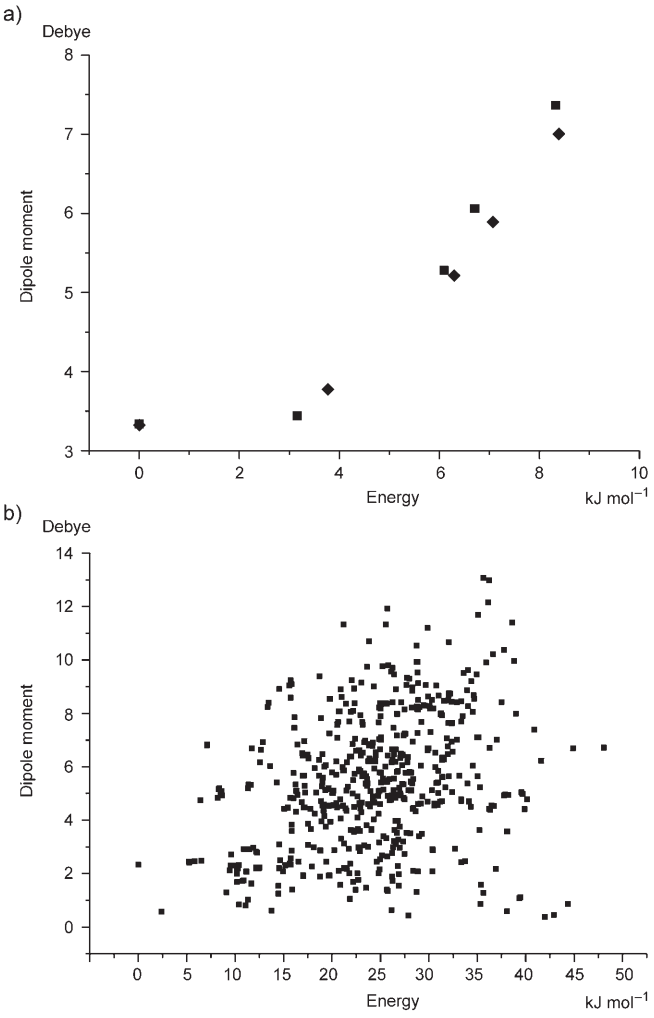


Figure 2. Correlation between dipole moment and energy of a) the five conformers of dimethyl isophthalamide (squares: calculated using HF method, diamonds: calculated using B3LYP method) and b) conformers of **5** calculated using the AM1 method.

different acceptors, as exemplified by the 2:2 complex with fluoride anions observed in the solid state.[32] However, even this larger energy difference is still rather small compared to the intermolecular hydrogen-bonding interactions. Thus, the isophthalamide moiety may be depicted as rigid but readily adaptable. This paradoxical characteristic is the reason for many fascinating phenomena, such as high-yield one-pot syntheses of rotaxanes, catenanes and knotanes. The isophthalamide fragments play different roles at various stages of these syntheses by switching between their three basic conformations to satisfy the needs of interacting partners.[33,34]

Qualitatively, the semiempirical AM1 method gave results similar to the previous higher level ab initio methods. The method is very fast and gives a qualitatively acceptable description of hydrogen bonding. Thus, it can be applied to modelling large systems dominated by strong hydrogen-bonding interactions.[35] Hence, we employed the AM1 method to study the conformational preferences of receptors **5**–**8**, in order to investigate whether the macrocyclic topology is able to preorganize the isophthalamide moieties towards anion binding.

Macrocycles: An extensive conformational search shows a huge variety of structures available for macrocyclic tetraamides **5**–**8** within an energy span of 50 kJ mol^{-1}. Here we discuss only selected conformations which are relevant to experimental results. Further data are tabulated in the Supporting Information.

Even the smallest, 18-membered macrocycle **5** is flexible enough that its isophthalamide moieties can be either *syn–syn*, *syn–anti*, or *anti–anti*. In the largest, 24-membered macrocycle **8**, both isophthalamide units can adopt all possible arrangements almost independently of each other. Many of the calculated conformations are stabilized by one or two intramolecular hydrogen bonds.

However, the most stable conformations of each macrocycle are very similar: both isophthalamide units adopt *syn–anti*(+,−) conformation and are connected by two NH···O$_{amide}$ hydrogen bonds (Figure 3a and b). These two intramolecular hydrogen bonds close the macrocyclic cavity so that the receptor in such a conformation can form only weak, external complexes with anions through single hydrogen bonds. This is why the macrocyclic isophthalamide receptors form weaker anion complexes than their pyridine analogues: the energy gain from the formation of four strong intermolecular hydrogen bonds is partially lost for breaking of two strong intramolecular hydrogen bonds.

There are two major variants of these doubly *syn–anti* (or SASA for short) conformations: U-shaped and roughly planar (Figure 3a and b). Depending on the macrocycle, either the former or the latter is preferred. Interestingly, both possibilities were found in the crystal structure of free ligand **6** (vide infra).

The SASA conformation is not the only one that allows for the simultaneous formation of two intramolecular hydrogen bonds. The all-*anti* AA(+,+)AA(+,+) conformation **6.3** is an example, and is only 9.9 kJ mol^{-1} less stable than **6.1**. Astonishingly, even the smallest, 18-membered macrocycle **5** can exist as an all-*anti*, doubly hydrogen bonded conformer (AA(+,+)AA(+,+), 12.0 kJ mol^{-1} above the energetic minimum, see Supporting Information).

In the context of anion binding, the all-*syn* conformations are most interesting. As they are not stabilized by intramolecular hydrogen bonds,[36] they are ranked significantly higher in energy than the most stable conformers: 21 kJ mol^{-1} for **5**, 27 kJ mol^{-1} for **6**, 13 kJ mol^{-1} for **7** and 19 kJ mol^{-1} for **8**. The relatively low energy of the SSSS conformation of receptor **7** is noteworthy. As will be shown below, this is the preferred conformation of this ligand both in solution and in the solid state. Importantly, although the above-mentioned structures must be formally described as SSSS, they are not truly convergent: their NH bonds are not oriented in the same direction (e.g., compare Figure 4a and b).

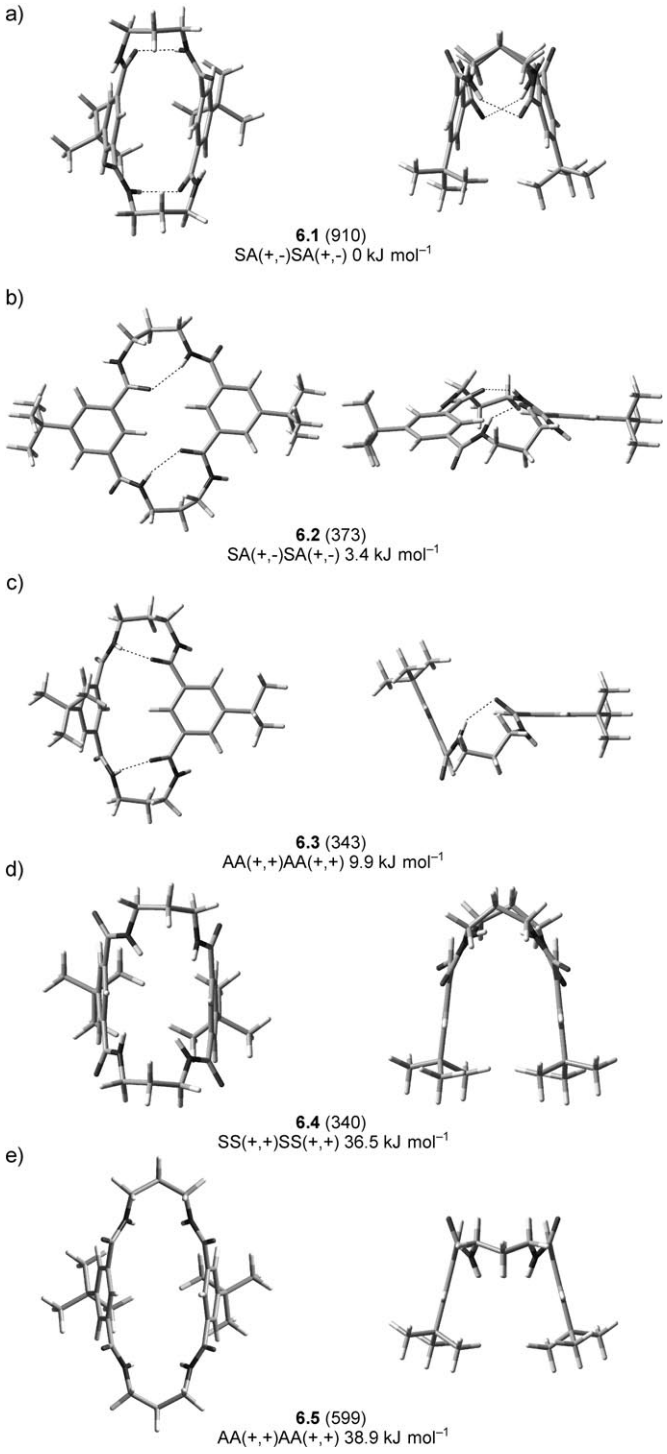


Figure 3. Geometries and relative energies of five selected conformers of 20-membered macrocycle **6** calculated using the AM1 method. Numbers in parentheses refer to conformation numbers from Supporting Information.

Truly convergent conformations lie even higher on the energetic scale: 31 kJ mol^{-1} for **5**, 34 kJ mol^{-1} for **6**, 21 kJ mol^{-1} for **7** and 29 kJ mol^{-1} for **8**. This second set of values estimates the energetic cost of the conformational change that each ligand must undergo to form four hydrogen bonds with the same acceptor in the gas phase. The respective values are probably lower in DMSO solution, because the two intramolecular hydrogen bonds to be broken are weakened by this highly polar solvent with pronounced hydrogen-bond accepting ability.

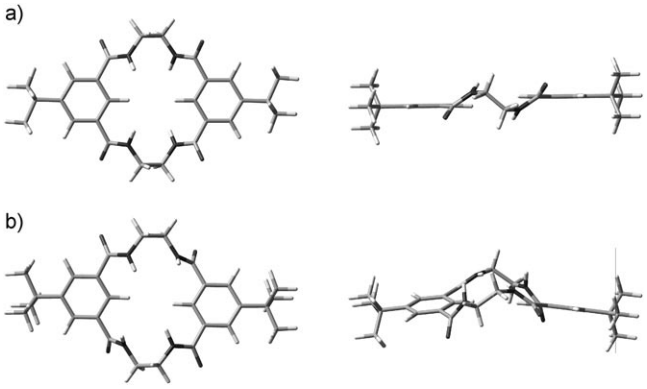


Figure 4. Two SS(+,+)SS(+,+) conformations of 18-membered macrocycle **5**: a) partially convergent, b) fully convergent.

The stabilizing hydrogen-bonding interactions together with the destabilizing steric repulsions seem to be the most important factors influencing the relative energies of the conformers. The effect of remote dipole–dipole interactions, observed in a model diamide, is completely masked here (Figure 2b).

The number of unique structures grows very quickly with increasing size of the macrocyclic ring (see Supporting Information), due to rapid increase in flexibility of the aliphatic linkers. Thus, although even tight macrocyclic confinement is not able to force our tetraamide receptors into the convergent, all-*syn* conformation, the smaller macrocycles **5** and **6** have a significantly reduced conformational space in comparison to the larger macrocycles **7** and **8**, and therefore presumably pay a smaller entropic penalty due to anion binding. That is probably why the stability constants decrease monotonically with increasing size of the macrocycle irrespective of the anion tested.

X-ray studies on free ligands: The X-ray crystal structures of receptors **6**, **7**, and **8** were determined. Two different solvates **6**·0.5 H_2O and **6**·CH_3OH were obtained by slow diffusion of pentane or diethyl ether, respectively, into a solution of **6** in a CH_2Cl_2/CH_3OH (1/1).

The quality of the first structure is poor due to severe disorder. Nevertheless, it is apparent that the isophthalic moieties are in a *syn–anti* conformation, similar to the lowest energy structure **6.1** (Figure 5). However, there are no intramolecular hydrogen bonds in the crystal structure. Instead, four intermolecular N–H···O=C hydrogen bonds link two neighbouring, symmetrically equivalent molecules to form a dimer. Due to the flexibility of the aliphatic linkers, the macrocycle adopts a highly bent, U-shaped conformation, characterized by a very acute angle between its two phenyl rings (ca. 30°).

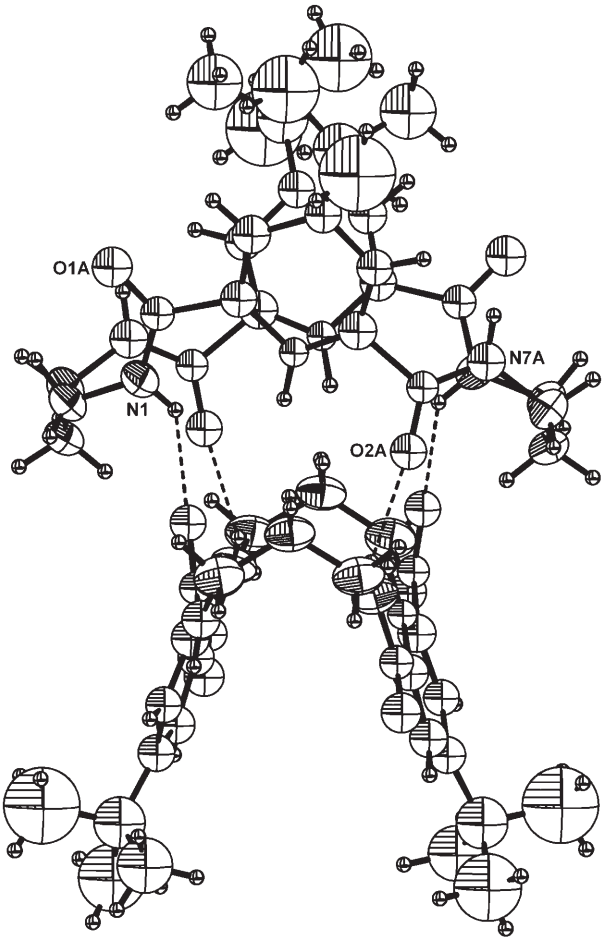


Figure 5. ORTEP view of the X-ray crystal structure of **6**·0.5 H_2O. Part of the disorder has been removed for clarity. Displacement ellipsoids are scaled to the 50% probability level. Dashed lines indicate hydrogen-bonding interactions.

In the second structure, the free ligand **6** adopts a roughly planar, but highly twisted conformation similar to **6.2** (Figure 6). Both symmetrically equivalent isophthalic moieties are in a *syn–anti*(+,+) conformation and bind each other in a complementary fashion by two NH···O_{amide} hydrogen bonds. The externally directed N−H and C=O groups form four intermolecular hydrogen bonds with the neighbouring macrocycles from the crystal lattice.

The *syn–anti* isophthalamide moieties in the above two crystal structures are self-complementary and bind each other by strong hydrogen bonds. It might therefore be expected that such a dimeric motif will also be found in the crystal structures of other macrocyclic isophthalamides, as it exists in their most stable conformations. However, 22-membered receptor **7** prefers an open conformation in the solid state, with both isophthalamide halves in a convergent, *syn–syn*(+,+) conformation (Figure 7). Although such a conformation is energetically unfavorable, as revealed by calculations, it allows both amide groups of the same isophthalamide moiety to bind to the same acceptor, that is, the carbonyl oxygen atom of the neighbouring molecule. This leads

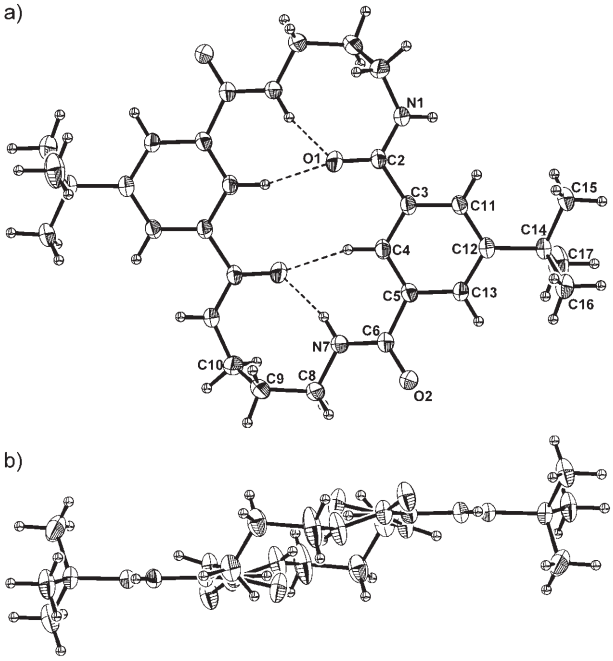


Figure 6. ORTEP view of the molecular structure of **6**·CH_3OH. a) Top view, atom numbering is limited to symmetrically independent part. b) Side view. (Displacement ellipsoids are scaled to the 30% probability level. Dashed lines indicate hydrogen-bonding interactions.)

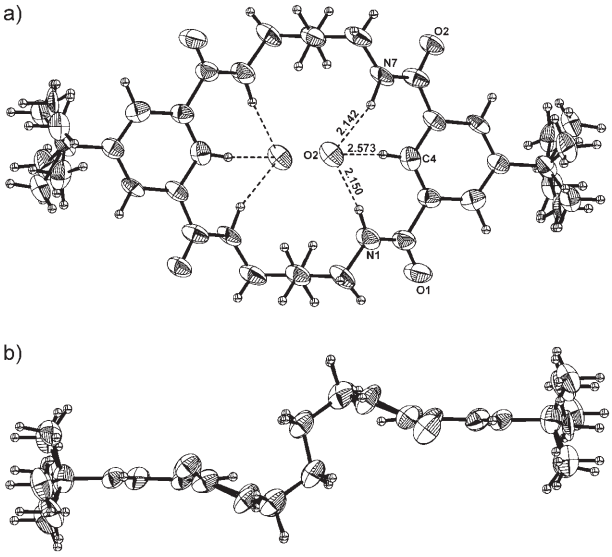


Figure 7. ORTEP view of the X-ray crystal structure of **7**. a Top view; carbonyl oxygen atoms of neighbouring macrocycles are shown inside the cavity. b) Side view. (Displacement ellipsoids are scaled to the 50% probability level. Dashed lines indicate hydrogen-bonding interactions. Distances are given in angstrom.)

to the crystal packing very similar to that previously observed in the crystal structure of its pyridine congener.[37]

X-ray-quality single crystals of 24-membered tetraamide **8** were grown by slow diffusion of diethyl ether into a solution of the ligand in CH_2Cl_2/CH_3OH (1/1). The structure of **8**·$(C_2H_5)_2O$ closely resembles that of **6**·0.5 H_2O. The isophthal-

amide moieties are again in the *syn–anti* conformation (Figure 8). Two U-shaped macrocycles dimerize by means of four intermolecular N−H···O=C hydrogen bonds. However, both the angle (43°) and the distance between the opposite phenyl rings in **8**·$(C_2H_5)_2O$ are larger than in **6**, and the resulting empty space is filled with a solvent molecule (diethyl ether).

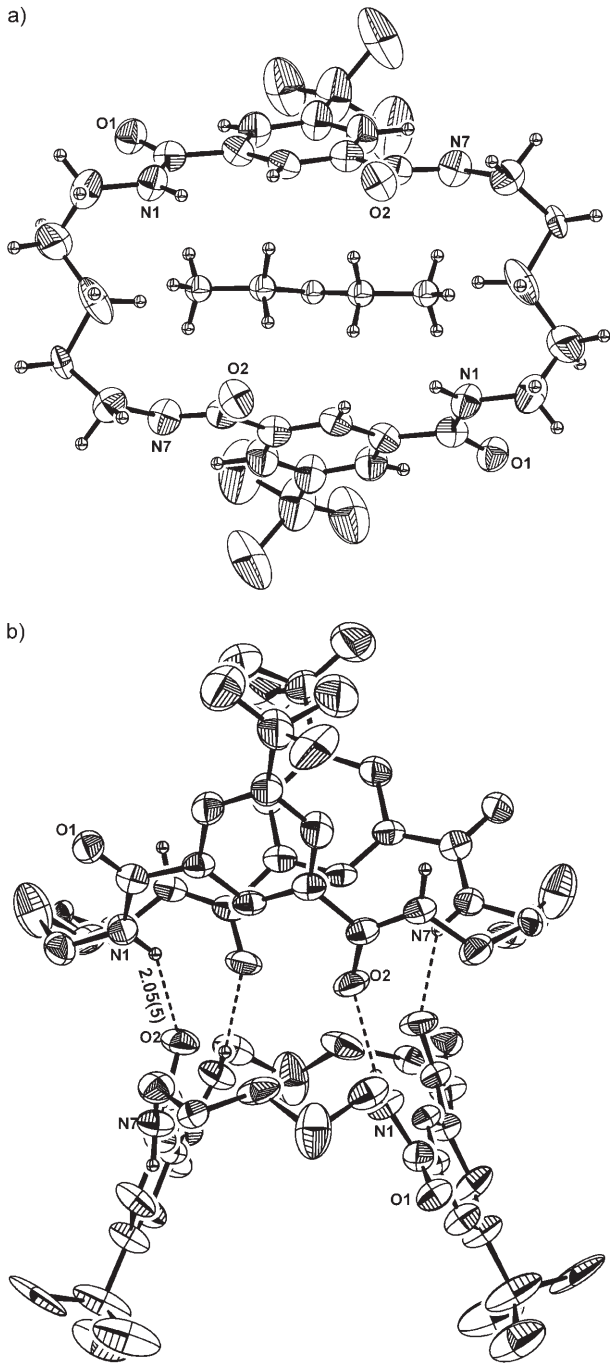
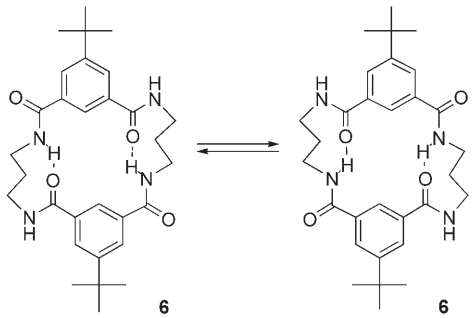


Figure 8. ORTEP view of the X-ray crystal structure of **8**·$(C_2H_5)_2O$. a) Top view. b) Side view. (Part of the disorder has been removed for clarity. Displacement ellipsoids are scaled to the 50% probability level. Dashed lines indicate hydrogen-bonding interactions. The distance is given in angstroms.)

Owing to the many strong intermolecular interactions present in the above crystal structures, the conformations described above may be unrepresentative for the solution structures. Nevertheless, the solution conformations of receptors **6** and **7** in DMSO are similar to those observed in the solid state, as revealed by 2D NOESY experiments. A nuclear Overhauser effect between the amide NH protons and both internal and external CH protons of the benzene ring (see Supporting Information) observed for solutions of **6** both in DMSO and DMF indicates considerable fractions of both *syn*- and *anti*-oriented amide hydrogen atoms in an averaged conformation.

The apparent symmetry observed in the 1D NMR spectra must therefore be due to rapid interconversion between the equivalent *syn–anti* conformations (Scheme 2). This dynamic process is fast on the NMR timescale even at −70 °C (in $[D_7]$DMF).



Scheme 2. Fast conformational equilibrium between two equivalent structures of **6** leading to the high symmetry in the ^{1}H NMR spectra of the receptor.

In contrast to **6**, cross-peaks between amide NH protons and only internal CH benzene protons are visible for receptor **7** (see Supporting Information). This suggests that the all-*syn* conformation of **7**, similar to that in the crystal structure, also predominates in solution. According to AM1 calculations, the all-*syn* conformation of **7** is the second most stable and lies only about 13 kJ mol^{-1} above the SASA structure. Apparently, stabilization due to intramolecular hydrogen bonds is less effective in this compound, possibly due to an uncomfortable arrangement of the aliphatic linkers.

We were unable to obtain good quality NOESY spectra of **8** in $[D_6]$DMSO, but the similarity of the spectrum recorded in $[D_7]$DMF to that of **6** indicates the *syn–anti* conformation, in agreement with the crystal structure.

X-ray studies on anion complexes: To gain insight into the binding modes and coordination geometries, X-ray analysis of crystals of several anion complexes of **6** and **8** was performed.

*Complexes of 20-membered ligand **6***: Crystals of the chloride complex **6**-PPh_4Cl suitable for X-ray analysis were

grown by vapour diffusion of pentane into a solution of **6** and PPh_4Cl in 1,2-dichloroethane.

In the crystal structure, the chloride anion resides inside the macrocyclic cavity of the receptor **6**, docked by six hydrogen bonds, four of which are donated by amide NH groups and two by internal aromatic CH protons (Figure 9). Thus, the receptor sacrifices its intramolecular hydrogen bonds to adopt an SSSS conformation and to maximize the interactions with the anion. In contrast to both structures of the free ligand **6**, and also to most known structures of benzamides and isophthalamides, the amide groups are almost coplanar with the adjacent benzene rings. A side view (Figure 9b) reveals that the chloride ion is only shallowly inserted into the cavity of the V-shaped receptor (ca. 1.3 Å above the mean plane of the amide hydrogen atoms). The fact that even the small chloride ion is not truly surrounded by the macrocycle is probably responsible for a rather secondary

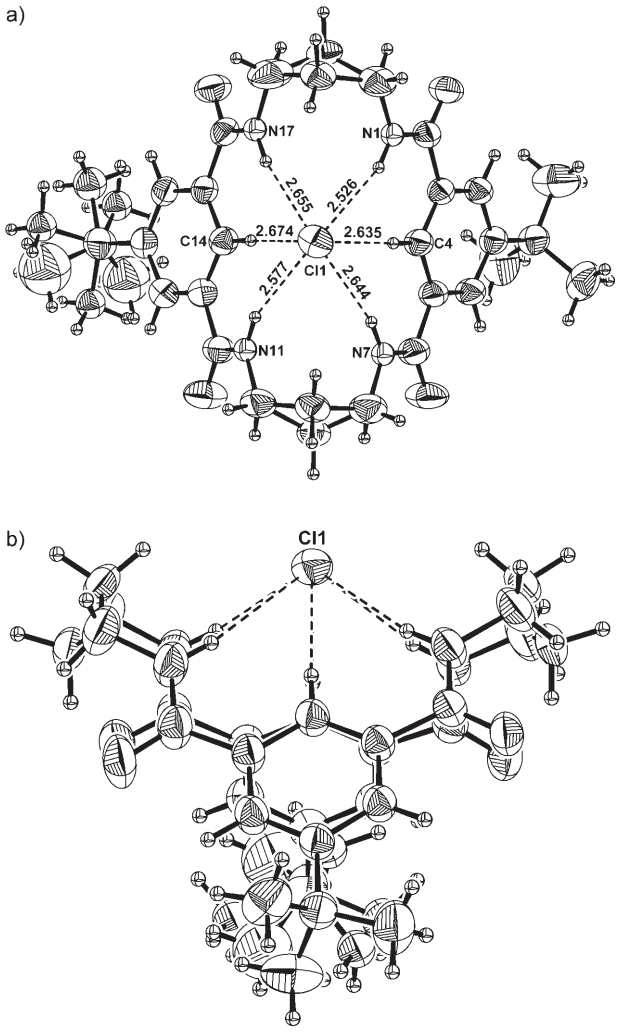


Figure 9. ORTEP view of the molecular structure of **6**-Ph_4PCl. a) Top view. b) Side view. (Part of disorder in b) has been removed for clarity. Displacement ellipsoids are scaled to the 50% probability level. Dashed lines indicate hydrogen-bonding interactions. The distances are given in angstroms.)

significance of the geometric complementarity in selectivity displayed by the receptor. The whole structure is very similar to that of the chloride complex of receptor **2**, a pyridine analogue of **6**.

Vapor diffusion of diethyl ether into a solution of **6** and tetrabutylammonium fluoride (TBAF) trihydrate in 1,2-dichloroethane resulted in a crystalline complex of unexpected stoichiometry $\mathbf{6}\cdot TBAPF_6\cdot TBAF\cdot C_2H_4Cl_2\cdot 1.8\,H_2O$, instead of the fluoride complex of **6** (Figure 10). The hexafluorophosphate ions were not added deliberately, but were probably present as an impurity in the commercial fluoride.[38] Both PF_6^- and F^- ions are present in the crystal structure. Whereas the fluoride ion, due to its high charge density, is well known for its ability to form very strong hydrogen bonds, PF_6^- is an archetypal example of weakly interacting anion. Surprisingly, however, it is the PF_6^- ion that is complexed by the receptor. What is even more astonishing is that the water molecules present in the structure also prefer the PF_6^- ion. In fact, F^- forms only C–H···F^- contacts, of which the shortest is that with the N^+CH_2 methylene group of the TBA^+ ion (2.31 Å). It is therefore worthwhile to look closer at the geometry of binding between the PF_6^- ion and **6**. The shape of the receptor molecule is very similar to that in the chloride complex discussed above. The place of the chloride ion is taken by axial fluoride F1, which is docked inside the cavity by hydrogen bonds with all six donors. Unlike the chloride complex, the F1 atom does not occupy the central position; it is considerably shifted towards N7 and N11: H7–F1 2.06, H11–F1 2.14, H1–F1 2.76, H17–F1 2.93 Å. This shift enables two vertical fluoride atoms F4 and F5 to approach closer to N1 and N17 on the opposite side of the macrocycle (H1–F4 2.06, H17–F5 2.09 Å). As a result, the vertical axis of symmetry of the PF_6^- ion is tilted with respect to the mean plane of the amide nitrogen atoms. In total, the anion forms 12 hydrogen-bonding contacts with the receptor. Furthermore, it is additionally coordinated by two water molecules and two tetrabutylammonium cations, increasing the number of hydrogen bonds to 23. In contrast, the fluoride anion forms only five C–H···F^- hydrogen bonds: three from the TBA^+ ion (H48B–F7 2.31, H41A–F7 2.93, H68B–F7 2.73 Å), one from the dichloroethane molecule (H70B–F7 2.55 Å) and one from the aliphatic linker of the receptor (H9A–F7 2.76 Å). Multipoint binding of the hexafluorophosphate ion does not translate into high stability of the complex in solution: the stability constant in DMSO is too small to be determined by ^1H NMR titration (ca. $1\,M^{-1}$).

*Complexes of 24-membered ligand **8***: The 24-membered macrocycle of **8** is large enough to encapsulate two oxygen atoms of carboxylate, phosphate or sulfate anions.[25,39] Unfortunately, all attempts to obtain X-ray quality crystals of these complexes have been unsuccessful so far. However, the structures of two different chloride complexes of receptor **8** were solved. Although the 24-membered receptor **8** is clearly too large for a single chloride ion, the study of such geometrically mismatched systems may give interesting in-

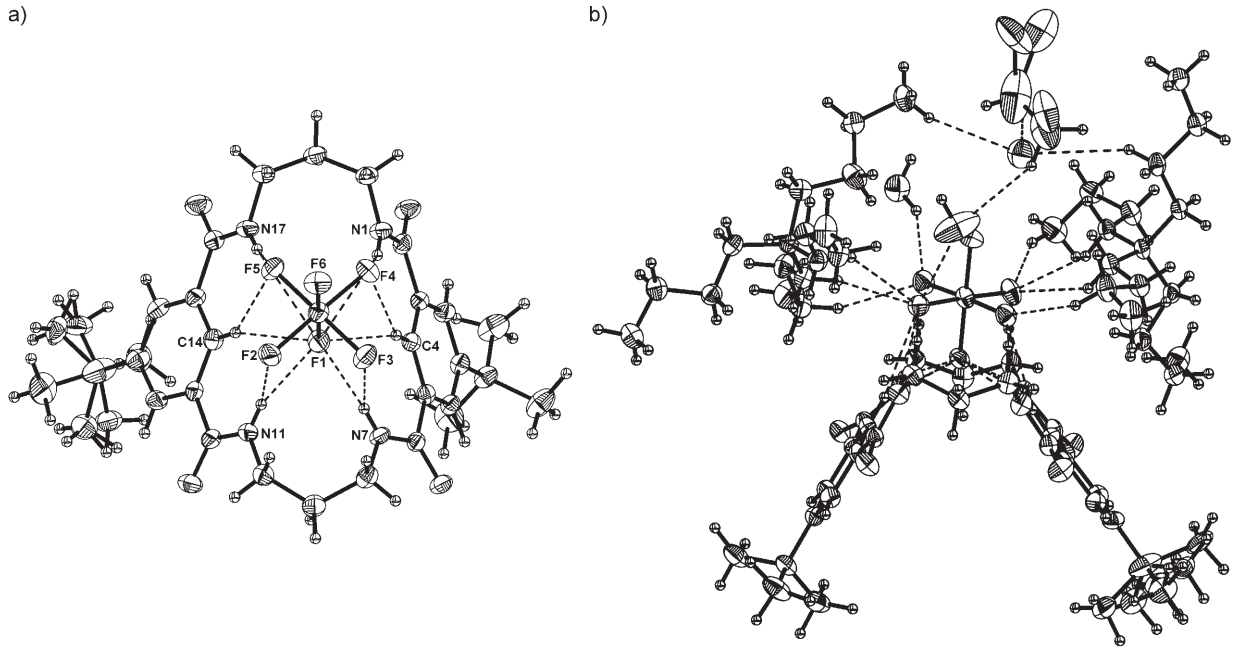


Figure 10. ORTEP view of the X-ray crystal structure of **6**·TBAPF_6·TBAF·$C_2H_4Cl_2$·1.8H_2O. a) Top view. Binding mode of the PF_6^- ion in the cavity of **6**. b) Side view. An array of hydrogen bonds. (Displacement ellipsoids are scaled to the 50% probability level. Dashed lines indicate hydrogen-bonding interactions.)

sight into means by which they adapt to maximize the number of noncovalent interactions.[40]

The first complex was obtained by slow diffusion of hexanes into a solution of **8** and TBACl in 1,2-dichloroethane (Figure 11). Unlike in the structure of the free ligand, both isophthalamide moieties are in the *syn–syn* conformation. To form reasonably short hydrogen bonds with the central anion, these two diamide units approach and twist with respect to each other. As a result, the amide protons form a distorted tetrahedron around the guest. The chloride ion forms two further hydrogen bonds with internal aromatic CH_{int} protons and additional contacts with methylene groups of aliphatic linkers.

The second chloride complex was obtained during our efforts to isolate the benzoate complex of **8** by diffusion of diethyl ether vapour into a dichloromethane solution containing **8** and tetrabutylammonium benzoate. The chloride anions in the solution arose from the reaction of benzoate anions with the solvent. X-ray structural analysis revealed the presence of two guests inside the macrocyclic cavity: a chloride anion and a water molecule (Figure 12). Each guest is chelated by one isophthalamide moiety. These two guests are connected by an almost linear O–H···Cl^- hydrogen bond (O–H···Cl^- angle 164°, H···Cl^- distance 2.41 Å). The coordination sphere of the chloride anion is completed from the

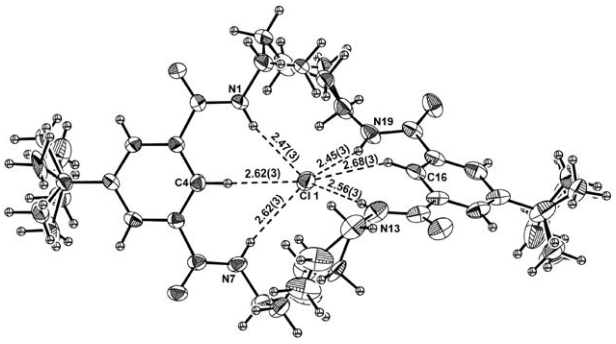


Figure 11. ORTEP view of the X-ray crystal structure of **8**·TBA^+Cl^-. (Displacement ellipsoids are scaled to the 50% probability level. Dashed lines indicate hydrogen-bonding interactions. The distances are given in angstroms.)

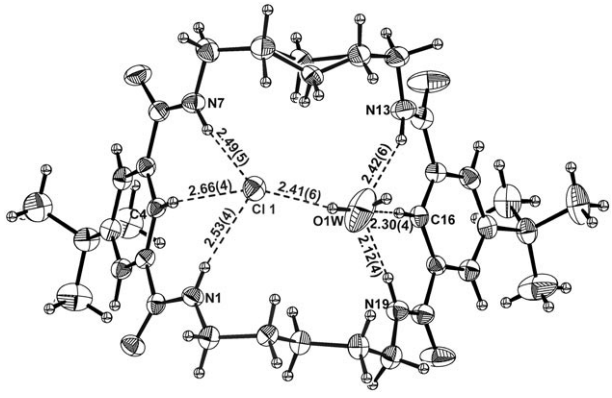


Figure 12. ORTEP view of the X-ray crystal structure of **8**·TBA^+Cl^-·2H_2O; top view. (Displacement ellipsoids are scaled to the 50% probability level. Dashed lines indicate hydrogen-bonding interactions. The distances are is given in angstroms.)

top by two hydrogen bonds to a tetrabutylammonium cation: H52B–Cl^- = 2.82 Å, H41A–Cl^- = 2.81 Å.

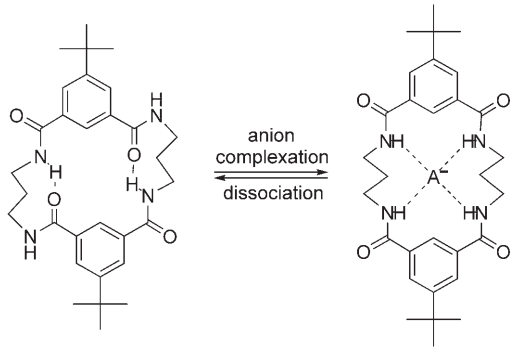
Previously we reported a very similar structure of the chloride complex of pyridine-based macrocyclic tetraamide **4**, which has the same size as **8**.[9] These two structures, together with the other known from the literature,[41,42] serve to highlight the role of the water molecules that fill the gaps between anionic guests and excessively large hosts. Considering the strong interaction of water with anions, it seems reasonable to deliberately construct hosts that can accommodate the target anion along with a fraction of its hydration sphere. Such receptors may be useful in applications such as the transport of anions through lipophilic channels or membranes, where stripping off the solvation shell gives rise to a high energy barrier.[43] Recently, a strong impulse to such studies was given by Burns et al.,[44] who found that anion complexation in a competitive solvent was enhanced when a solvent molecule was incorporated into the binding motif. This strategy is also widely used in Nature, where enzymes bind water for use as a part of their substrate-recognition domains.[44] Receptors **4** and **8** may serve as prototype anion receptors of this class.

Structure of the anion complexes in solution: Complexation-induced shifts in the ^{1}H NMR spectra give valuable hints about the structure of complexes in solution and the nature of interactions between host and guest. The most striking anion-induced changes in the spectra of **6–8**, apart from the expected downfield shifts of amide signals, are the large downfield shifts of internal aromatic protons CH_{int}, indicative of $C–H_{int}\cdots A^-$ hydrogen-bonding interactions. Noticeably, in many cases these shifts are larger than those of the amide NH protons. In the extreme case of **6** and the bromide anion, the NH signals even move slightly upfield on anion binding. This upfield shift can be explained by assuming that the amide protons are already engaged in hydrogen bonding (either intramolecular or with a solvent) before anion binding.

Signals of external aromatic CH protons also moved downfield in several titrations, albeit to a much lesser extent. This is opposite to what might have been expected, since anion binding increases the electron density of phenyl rings, and this should result in upfield shifts of phenyl protons. This effect is probably due to the interaction of these protons with oxygen atoms of the amide groups. Anion binding forces isophthalamide moieties into *syn–syn* conformations, in which both external aromatic protons are in close proximity to the amide oxygen atoms. Furthermore, the angle between the phenyl ring and amide groups decreases significantly on anion binding, as revealed by X-ray analyses, and consequently the carbonyl oxygen atoms approach CH groups even more closely.

In most cases, slight deshielding of methylene hydrogen atoms of aliphatic linkers was observed, which suggests their close proximity to the anion and points to additional participation of these groups in anion binding. The only case in which upfield shift of central methylene protons was recorded was the chloride complex of **6**. These observations can be interpreted by bearing in mind the above-discussed X-ray structure of this complex, in which the central methylene group is disordered over two positions: one close to the anion, and the other bent to the opposite side. Apparently, most complexes in solution prefer the first possibility, whereas **6**-Cl chooses the second. Unfortunately, in most cases, these signals overlap with signals of tetrabutylammonium ion.

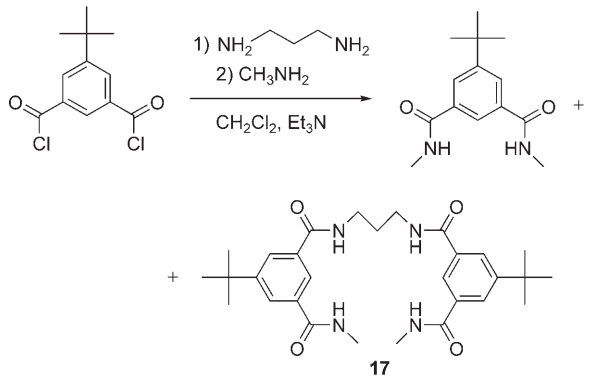
All the above observations point to a conclusion that, also in solution, the anionic guests are bound inside the macrocyclic cavities of the receptors **6–8**. Further evidence concerning the conformation of ligands in complexes comes from the 2D NOESY spectra. In the ^{1}H NMR spectra of fluoride and acetate complexes of **6**, all aromatic and amide signals are clearly distinguishable, and therefore NOE could be observed between amide NH protons and internal aromatic CH protons (see Supporting Information). At the same time, no effect was detected between the amide protons and the external aromatic protons. These spectra indicate that the *syn–syn* conformation of the isophthalic moieties in **6** largely predominates in the presence of anions. It is thus evident that anion-induced conformational change of receptor **6** takes place and, as a result, all amide NH protons point towards the cavity (Scheme 3).



Scheme 3. Anion-induced conformational change taking place in the DMSO solution of **6**.

This observation is interesting in view of the fact that, in Nature, conformational changes on substrate binding, amplified and propagated through space, are one of the most common pathways of transduction of biological signals. Artificial systems based on this principle utilize mostly cation coordination to trigger molecular shape changes.[45–49] An analogous and complementary approach based on anion binding has only recently been pioneered, so there is still a very limited number of well-defined anion-triggered shape-switching systems.[50–56] Some of them have already been applied for construction of fluorescent and chromogenic sensors[51–55] or for controlled translocation of a macrocyclic ring in a rotaxane.[56] Amides derived from 2,6-pyridinedicarboxylic acid have been used for the construction of switching systems because they exist as a single *syn–syn* conforma-

tion and can be forced to adopt an *anti–anti* conformation through cation binding[57,58] or protonation.[59,60] The second method was used to reversibly switch oligoamides of this type between linear and helical forms.[59,60] In contrast, simple isophthalamides may exist as mixtures of the possible conformers: *syn–syn*, *syn–anti* and *anti–anti*. Small energy differences between these forms make it relatively easy to amplify one of them by using an external factor. Such a system, however, does not constitute a molecular switch, due to undefined starting point. If two such units are incorporated within one molecule, the number of possibilities rises dramatically. However, within an appropriate macrocyclic structure, like that of tetraamide **6**, the self-complementary character of the *syn–anti* conformation stabilizes one particular structure to such an extent that it dominates even in a highly competitive solvent such as DMSO. We have demonstrated here that anion binding provides sufficient energy to break the two intramolecular hydrogen bonds and switch both isophthalic moieties into a *syn–syn* conformation. It may be speculated that other effectors (cations or neutral molecules) should be able to amplify some other conformations from the plethora of structures uncovered by conformational search.



Scheme 4. Synthesis of the open-chain tetraamide **17**.

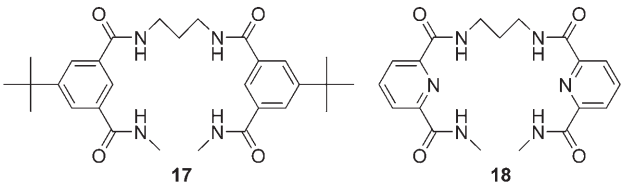
Table 3. Binding constants [M^{-1}] for the formation of 1:1 complexes of **6** and **17** with various anions in [D_6]DMSO at 298 K.[a]

Anion	Protons used for determination of *K*	**6**		**17**	
		K [M^{-1}]	$\Delta\delta_{max}$ [ppm]	*K* [M^{-1}]	$\Delta\delta_{max}$ [ppm]
Cl^-	amide (triplet)	371 ± 13	0.18 ± 0.001	14.0 ± 0.3	0.63 ± 0.006
	"internal" arom.	385 ± 8	0.55 ± 0.002	13.1 ± 0.2	0.42 ± 0.004
	amide (quartet)	–	–	8.4 ± 0.3	0.59 ± 0.02
Br^-	amide (triplet)	22 ± 2.1	−0.03 ± 0.001	2.3 ± 0.2	0.39 ± 0.03
	"internal" arom.	19 ± 0.2	0.38 ± 0.002	2.8 ± 0.2	0.29 ± 0.02
	amide (quartet)	–	–	1.8 ± 0.2	0.38 ± 0.02
AcO^-	amide (triplet)	3202 ± 179	0.55 ± 0.003	126 ± 4	1.31 ± 0.007
	"internal" arom.	3066 ± 132	0.43 ± 0.002	71 ± 4	0.40 ± 0.005
	amide (quartet)	–	–	29 ± 2	1.28 ± 0.04
$H_2PO_4^-$	amide (triplet)	222 ± 17	1.04 ± 0.01	63 ± 5	1.51 ± 0.04
	"internal" arom.	473 ± 32	0.69 ± 0.004	59 ± 5	0.57 ± 0.02
	amide (quartet)	-	-	[b]	[b]

[a] Tetrabutylammonium salts were used as anion sources. [b] Value could not be determined due to severe broadening of the signal.

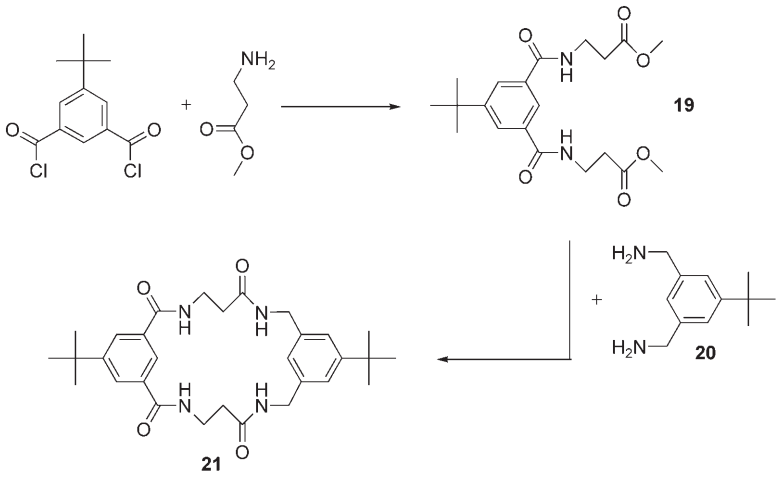
Macrocyclic effect: Macrocyclic topology clearly fails to preorganize isophthalamide receptors towards anion binding. Moreover, it can actually stabilize an array of intramolecular hydrogen bonds that hamper anion binding. To probe the macrocyclic effect in anion recognition by receptor **6**, analogous acyclic tetraamide **17** was prepared and titrated with selected anions. Its one-pot synthesis consisted of the reaction of 5-*tert*-butylisophthalic acid dichloride with half an equivalent of 1,3-diaminopropane and subsequent quenching of the reaction mixture with an excess of anhydrous methylamine (Scheme 4).

It is difficult to ascribe specific values to the stability constants of receptor **17**, because of considerable discrepancies between the values obtained from different signals: the stability constants derived from amide groups joined by aliphatic linkers (triplet) are higher than those from internal aromatic CH protons, which are in turn higher than the values resulting from terminal amide protons (quartet; Table 3). A similar phenomenon was observed by Gale et al. for another acyclic tetraamide and interpreted as reflecting the differences in the strength of interaction with the anion.[61] However, discrepancies among the dissociation constants determined by following the shift of different protons indicate that the observed titration curves may not be the result of a simple 1:1 binding process.[62] For example, in the previously studied acyclic tetraamide **18**, in which both aromatic halves are locked in a convergent *syn–syn* conformation, we have found an excellent agreement between the association constants determined from both amide groups in the case of chloride and acetate, whereas large differences were observed for dihydrogenphosphate, an anion which very often gives complicated stoichiometries.



Thus, despite a very good fit of a 1:1 binding model to the titration data for **17**, the values obtained should be interpreted with caution. Nevertheless, it is apparent that macrocyclic receptor **6** is much more effective than **17**: even the highest values obtained for **17** are still several times lower than the respective values obtained for **6** (Table 3).

The influence of the position of carbonyl groups: Thus, the macrocyclic topology is crucial for the high anion affinity of our receptors, and the optimal macrocycle size was estimated at about 20. However, there are still many possibilities for further variation of the structure. One of them consists of changing the positions of carbonyl groups in the macrocycle. To explore the potential of this approach, we studied receptor **21**, an isomer of **6**. This compound, derived from β-alanine, is an especially interesting model, because it would be relatively easy to obtain its chiral analogues by using enantiomerically pure β-amino acids.



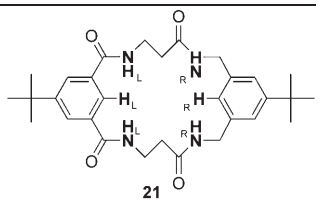
Scheme 5. Synthesis of **21**.

Receptor **21** was obtained according to Scheme 5. Reaction of 5-*tert*-butylisophthalic acid dichloride with β-alanine gave ester **19**, which was subjected to double amidation with amine **20**. Owing to the low reactivity of diester **19**, sodium methoxide was used as basic catalyst in this macrocyclization reaction.

This relatively small structural change resulted in a significant deterioration of the anion-binding ability (Table 4). As in **17**, there are also two distinct kinds of amide groups in this receptor. In this case, however, the association constants determined from each pair are in reasonable agreement (again with the exception of hydrogenphosphate), whereas the asymptotic values of chemical shifts $\Delta\delta_{max}$ differ significantly. This is in agreement with common intuition: the macrocyclic structure imposes severe constraints on the conformational space and, once a complex is formed, the anion interacts with all hydrogen-bond donors inside the macrocyclic cavity. But these interactions are not equally strong: aromatic amides are known to form stronger hydrogen bonds than aliphatic amides,[63] and this is reflected by the δ_{max} values.

These observations suggest that the "right" (R) fragment of macrocycle **21** is not a good building block for the construction of strong anion receptors. However, the catalytic activity does not always parallel strong substrate binding and, on the other hand, the strength of interaction depends strongly on the solvent. Thus, the applicability of such receptors as organocatalysts in enantioselective synthesis is still to be explored.

Table 4. Binding constants [M^{-1}] for the formation of 1:1 complexes of **21** with various anions in [D_6]DMSO at 298 K.[a]

Anion	Protons used for determination of *K*		
		K [M^{-1}]	δ_{max} [ppm]
Cl^-	amide "L"	29 ± 1	0.54 ± 0.005
	amide "R"	27 ± 2	0.18 ± 0.007
	aromat. "internal L"	27 ± 1	1.24 ± 0.007
	aromat. "internal R"	28 ± 2	0.25 ± 0.006
AcO^-	amide "L"	160 ± 7	1.28 ± 0.02
	amide "R"	147 ± 6	0.82 ± 0.01
	aromat. "internal L"	155 ± 9	1.10 ± 0.02
	aromat. "internal R"	181 ± 10	0.17 ± 0.003
$H_2PO_4^-$	amide "L"	231 ± 10	1.42 ± 0.02
	amide "R"	327 ± 10	1.25 ± 0.006
	aromat. "internal L"	306 ± 15	1.20 ± 0.01
	aromat. "internal R"	163 ± 8	0.65 ± 0.007

[a] Tetrabutylammonium salts were used as anion sources.

Conclusion

The isophthalamide moiety has only minor conformational preferences and thus easily conforms to the needs of the interacting partners. When two such moieties are incorporated within a sufficiently flexible macrocyclic structure, they can adopt numerous mutual arrangements and bind to each other via one or two hydrogen bonds. In the case of tetraamides **5**–**8**, the most stable conformations are those in which both isophthalamide moieties adopt a self-complementary *syn–anti* conformation, form two strong intramolecular hydrogen bonds and thus close the macrocyclic cavity. Some of these structures are stable enough that they can be observed in condensed phases: in the crystal structures of **6** and **8**, and for **6** even in DMSO solution. On the other hand, 20-membered macrocycle **7**, for which the SASA conformation results in particularly little energy gain, sacrifices it to maximize intermolecular contacts in the solid state and in DMSO solution (with the solvent molecules). Anions are sufficiently strong hydrogen-bond acceptors to force even 20-membered receptor **6** to switch to a convergent, all-*syn* conformation. However, the energy required for such dra-

matic conformational change lowers the anion-binding affinity of isophthalamide receptors. That is why, although simple isophthalamides are better anion receptors than pyridinediamides, the contrary is true for the macrocyclic tetraamides. On the basis of these results, two further directions of research may be suggested. First, the construction of stronger anion receptors would lead to better conformational control of isophthalamide building blocks and prevent them from forming intramolecular hydrogen bonds. This can be achieved in a number of ways, and the first, promising step in this direction was reported by us recently.[10] The second direction would focus on the anion-induced conformational change and try to couple it to some signal-generation mechanism in order to construct supramolecular switching devices.

As in our previous studies on pyridine-based macrocyclic tetraamides, the best anion affinities were obtained for the 20-membered macrocycle **6**, irrespective of anion size. This confirms a minor role of geometric complementarity in recognition by these receptors. One reason for this finding is apparent from the crystal structures of anion complexes of receptor **6**: anions are not truly encapsulated by the receptor; instead, they perch on the top of the A-shaped ligand.

The macrocyclic topology and the position of carbonyl groups in the macrocycle are crucial for the effectiveness of receptor **6**, as revealed by the comparison of **6** with model compounds **17** and **21**. These structural elements should remain unchanged in future modifications.

Experimental Section

Instruments and methods: NMR spectra were measured on a Varian Gemini 200 (^{1}H: 200 MHz, ^{13}C: 50 MHz) or a Bruker AM-500 (^{1}H: 500 MHz, ^{13}C: 125 MHz) spectrometer. The chemical shifts are given in ppm relative to solvent signals as internal standards; the coupling constants are in hertz. The ESI mass spectra were obtained on Mariner (ESI TOF) and API 365 (ESI 3Q) mass spectrometers with methanol as a spray solvent. The melting points are uncorrected.

Syntheses: All precursors for syntheses were obtained from Aldrich or Fluka and were used as received. 5-*tert*-Butyl-isophthalic acid chloride was obtained from 5-*tert*-butyl-isophthalic acid according to the literature procedure.[64] TLC was carried out on Merck silica gel 60 F_{254} plates; for column chromatography, Merck silica gel 60 (63–100 μm mesh size) was used. The studied macrocycles gave unsatisfactory elemental analyses due to solvent molecules encapsulated in the crystals. This phenomenon is well known and, even after prolonged heating in high vacuum, the solvents can still be detected by NMR spectroscopy. The isotope patterns obtained by ESI-MS spectra are, however, consistent with those calculated on the basis of natural isotope abundances and thus confirm the elemental composition.

Macrocyclic tetraamide 5: M.p. >350 °C. ^{1}H NMR (500 MHz, [D$_6$]DMSO): δ = 8.33 (br, 4H), 8.29 (br, 2H), 7.90 (d, J = 1.5 Hz, 4H), 3.47 (br, 8H), 1.32 (s, 18H); HRMS (ESI): m/z calcd for $C_{28}H_{36}N_4O_4Na$ $[M+Na]^+$: 515.6133, found 515.6131.

Reaction of 5-*tert*-butylisophthalic acid chloride with 1,3-diaminopropane: A solution of 5-*tert*-butylisophthalic acid chloride (324 mg, 1.25 mmol) in dry CH_2Cl_2 (1.5 mL) was added dropwise to a mixture of 1,3-diaminopropane (92 mg, 1.24 mmol), triethylamine (0.5 mL) and dry CH_2Cl_2 (250 mL) over 5 min. The next day, the mixture was filtered and the filtrate evaporated. The dry residue was boiled with water (ca. 150 mL) and than left for 24 h at room temperature. The solution was then decanted and the precipitate was again washed with water in a similar manner and dried. The residue was purified by chromatography on 30 g of silica gel using 1 dm^3 of 2% CH_3OH in CH_2Cl_2, and then 2.5% CH_3OH in CH_2Cl_2 until macrocylic tetraamide **6** was completely eluted. Further elution with 3% methanol gave hexaamide **9** and octaamide **12**. Tetraamide **6**: Yield: 104 mg, 31.9%. M.p. 302–304 °C. ^{1}H NMR (500 MHz, [D$_6$]DMSO): δ = 8.58 (t, J = 5.6 Hz, 4H), 8.27 (t, J = 1.4 Hz, 2H), 7.89 (d, J = 1.5 Hz, 4H), 3.47 (q, J = 5.4 Hz, 8H), 1.89 (br, 4H), 1.26 ppm (s, 18H); ^{13}C NMR (125 MHz, [D$_6$]DMSO): δ = 165.81 (4°), 150.63 (4°), 133.88 (4°), 126.6 (3°), 123.16 (3°), 39.15 (2°), 34.592 (4°), 30.924 (1°), 28.21 ppm (2°); HRMS (ESI): m/z calcd for $C_{30}H_{40}N_4O_4Na$ $[M+Na]^+$: 543.2942, found: 543.2947. Hexaamide **9**: Yield: 64 mg, 24.6%. M.p. 308–310 °C. ^{1}H NMR (200 MHz, [D$_6$]DMSO): δ = 8.60 (t, J = 5.3 Hz, 6H), 8.09 (br, 3H), 7.97 (d, J = 1.2 Hz, 6H), 3.42–3.22 (br, 12H), 1.81 (br, 6H), 1.34 Hz (s, 27H); ^{13}C NMR (50 MHz, [D$_6$]DMSO): δ = 166.24 (4°), 151.16 (4°), 134.67 (4°), 126.54 (3°), 123.22 (3°), 36.89 (2°), 34.76 (4°), 31.01 (1°), 29.30 Hz (2°). HRMS (ESI): m/z calcd for $C_{45}H_{60}N_6O_6Na$ $[M+Na]^+$: 803.4467; found: 803.4493. Octaamide **12**: Yield: 51 mg, 15.7%. M.p. 198–210 °C (decomp). ^{1}H NMR (200 MHz, [D$_6$]DMSO): δ = 8.60 (t, J = 5.3 Hz, 6H), 8.09 (br, 3H), 7.97 (d, J = 1.2 Hz, 6H), 3.42–3.22 (br, 12H), 1.81 (br, 6H), 1.34 Hz (s, 27H); ^{13}C NMR (50 MHz, [D$_6$]DMSO): δ = 166.24 (4°), 151.16 (4°), 134.67 (4°), 126.54 (3°), 123.22 (3°), 36.89 (2°), 34.76 (4°), 31.01 (1°), 29.30 ppm (2°). HRMS (ESI): m/z calcd for $C_{60}H_{80}N_8O_8Na$ $[M+Na]^+$: 1063.5991, found: 1063.6008.

Reaction of 5-*tert*-butylisophthalic acid chloride with 1,4-diaminobutane: A solution of 5-*tert*-butylisophthalic acid chloride (2591 mg, 10.0 mmol) in dry CH_2Cl_2 (20 mL) and a solution of 1,4-diaminobutane (881 mg, 10.0 mmol) in dry CH_2Cl_2 (20 mL) were slowly added by syringe pump over several hours at the same rate to a mixture of triethylamine (2.6 mL) and dry CH_2Cl_2 (250 mL). The next day, the mixture was filtered and the filtrate evaporated. The dry residue was boiled with water (ca. 150 mL) and then left for 24 h at room temperature. The solution was then decanted and the precipitate was again washed with water in a similar manner and dried. The residue was purified by chromatography on 60 g of silica gel using 2–3% CH_3OH in CH_2Cl_2 to yield tetraamide **7**. Further elution with 3% methanol gave a mixture of hexaamide **9** and octaamide **12**. We were unable to separate these two compounds due to their very similar chromatographic properties. Hexaamide **7**: Yield: 412 mg, 15.0%. M.p. >350 °C. ^{1}H NMR (200 MHz, [D$_6$]DMSO): δ = 8.37 (t, J = 5.2 Hz, 4H), 8.03 (br, 2H), 7.90 (d, J = 1.1 Hz, 4H), 3.40–3.25 (br, 8H, overlapping with water), 1.57 (br, 8H), 1.32 ppm (s, 18H); ^{13}C NMR (50 MHz, [D$_6$]DMSO): δ = 166.34 (4°), 151.03 (4°), 134.89 (4°), 126.34 (3°), 123.12 (3°), 38.59 (2°), 34.64 (4°), 30.96 (1°), 26.45 ppm (2°); HRMS (ESI): m/z calcd for $C_{32}H_{44}N_4O_4Na$ $[M+Na]^+$: 571.3255, found: 571.3265.

Reaction of 5-*tert*-butylisophthalic acid chloride with 1,5-diaminopentane: The reaction was carried out by the high-dilution technique as described above. The mixture of products (free from triethylamine hydrochloride) was chromatographically separated. Tetraamide **8**: Yield: 330 mg, 11.4%. M.p. >350 °C. ^{1}H NMR (200 MHz, [D$_6$]DMSO): δ = 8.41 (t, J = 5.2 Hz, 4H), 8.05 (br 2H), 7.89 (d, J = 1.2 Hz, 4H), 3.40–3.25 (br, 8H) 1.55 (br, 8H), 1.42–1.04 (br, 4H), 1.27 ppm (s, 18H); ^{13}C NMR (50 MHz, [D$_6$]DMSO): δ = 166.01 (4°), 150.75 (4°), 134.54 (4°), 126.42 (3°), 123.29 (3°), 39.38 (2°), 34.67 (4°), 30.96 (1°), 29.12 (2°), 24.64 ppm (2°). HRMS (ESI): m/z calcd for $C_{34}H_{48}N_4O_4Na$ $[M+Na]^+$: 599.3568, found: 599.3558. Hexaamide **11**: Yield: 53 mg, 1.8%. M.p. 338–342 °C (with decomp). ^{1}H NMR (200 MHz, [D$_6$]DMSO): δ = 8.56 (brt, 6H), 8.10 (s, 3H), 7.93 (s, 6H), 3.28 (m, 12H, partially overlapping with water signal), 1.58 (m, 12H), 1.46–1.20 (brm, 6H, overlapping with singlet at 1.31), 1.31 ppm (s, 27H); ^{13}C NMR (50 MHz, [D$_6$]DMSO): δ = 166.11 (4°), 150.94 (4°), 134.67 (4°), 126.39 (3°), 123.53 (3°), 39.16 (2°), 34.70 (4°), 30.99 (1°), 28.87 (2°), 23.89 ppm (2°). HRMS (ESI): m/z calcd for $C_{51}H_{72}N_6O_6Na$ $[M+Na]^+$: 887.5406, found: 887.5437. Octaamide **14**: Yield: 80 mg, 2.8%. ^{1}H NMR (200 MHz, [D$_6$]DMSO): δ = 8.55 (t, J = 5.4 Hz, 8H), 8.09 (br, 4H), 7.92 (d, J = 1.0 Hz, 8H), 3.27 (br, 16H), 1.57 (br, 8H), 1.29 ppm (s, 36H); ^{13}C NMR (50 MHz, [D$_6$]DMSO): δ = 166.04 (4°), 150.89 (4°), 134.61 (4°), 126.38 (3°), 123.49 (3°), 39.24 (2°), 34.72

(4°), 31.01 (1°), 28.95 (2°), 24.09 ppm (2°); MS (ESI): *m/z*: 1175 $[M+Na]^+$.

Acyclic tetraamide 15: A solution of 1,3-diaminopropane (5 mmol) and triethylamine (10 mmol) in dry CH_2Cl_2 was slowly added by syringe pump over 2 h to a stirred solution of 5-*tert*-butylisophthalic acid chloride (5183 mg, 20 mmol) in dry CH_2Cl_2 (150 mL). After stirring for about 1 h, the reaction mixture was quenched with methylamine (3 mL, 66 mmol, cooled to about −70 °C). After an additional 1 h of mixing, the precipitate of methylamine hydrochloride was filtered off, and the filtrate evaporated to dryness. The dry residue was boiled with water (ca. 150 mL) and then left for 24 h at room temperature. The water solution was then decanted and the precipitate dissolved in CH_2Cl_2/CH_3OH (1:1), evaporated and again washed with water in a similar manner as above. The mixture of products, free from triethylamine hydrochloride, was purified by chromatography on 200 g of silica gel using 1% CH_3OH in CH_2Cl_2 until the diamide was completely eluted. Then the desired tetraamide was washed with 3% CH_3OH in CH_2Cl_2. Dimethylamide of 5-*tert*-butylisophthalic acid: Yield: 2057 mg, 41.4%. M.p. 126–127 °C. ^{1}H NMR (200 MHz, $CDCl_3$): $\delta = 7.87$ (br, 3H), 6.69 (br, 2H), 2.99 (d, $J = 3.8$ Hz, 6H), 1.31 (s, 9H); HRMS (ESI): *m/z* calcd for $C_{14}H_{20}N_2O_2Na$ $[M+Na]^+$: 271.1417, observed 271.1426. Tetraamide **15**: Yield: 271 mg, 5.3%. ^{1}H NMR (200 MHz, $[D_6]$DMSO): $\delta = 8.67$ (t, $J = 5.5$ Hz, 2H), 8.54 (q, $J = 4.6$ Hz, 2H), 8.13 (br, 2H), 7.97 (br, 2H), 3.28–3.45 (m, 4H), 2.79 (d, $J = 4.4$ Hz, 6H), 1.81 (br m, 2H), 1.33 ppm (s, 18H); ^{13}C NMR (50 MHz, $[D_6]$DMSO): $\delta = 166.50$, 166.12, 151.02, 134.54, 154.51, 126.36, 123.55, 37.21, 34.75, 31.00, 29.33, 26.26 ppm; HRMS (ESI): *m/z* calcd for $C_{29}H_{40}N_4O_4Na$ $[M+Na]^+$: 531.2942, observed 531.2968.

Amidoester 16: The hydrochloride salt of β-alanine methyl ester (2792 mg, 20.0 mmol) was suspended in dry CH_2Cl_2 (200 mL) and cooled to about −55 °C. To this mixture, triethylamine (5.6 mL) was added dropwise to liberate the ester from its salt. Immediately after the addition was finished, a solution of 5-*tert*-butyl-isophthalic acid chloride (2591 mg, 10.0 mmol) in dry CH_2Cl_2 (10 mL) was slowly added. The mixture was left in a cooling bath and allowed to reach slowly room temperature. Then it was washed twice with 10% $NaHSO_4$ (2 × 50 mL) and once with water and dried over $MgSO_4$. The solvent was removed and the residue was purified by chromatography on 150 g of silica gel using 3% CH_3OH in CH_2Cl_2 as an eluent. Yield: 2925 mg, 74.5%. M.p. 88–89 °C. ^{1}H NMR (200 MHz, $CDCl_3$, TMS): $\delta = 7.94$ (d, $J = 1.6$ Hz, 2H), 7.89 (s, $J = 1.5$ Hz, 1H), 7.03 (t, $J = 5.8$ Hz, 2H), 3.80–3.64 (m + s, 10H), 2.67 (t, $J = 6.0$ Hz, 4H), 1.34 ppm (s, 9H); ^{13}C NMR (50 MHz, $CDCl_3$, TMS): $\delta = 173.02$ (4°), 167.07 (4°), 152.42 (4°), 134.47 (4°), 127.28 (3°), 122.14 (3°), 51.84 (1°), 35.51 (2°), 35.01 (4°), 33.68 (2°), 31.13 ppm (1°); elemental analysis calcd (%) for $C_{20}H_{28}N_2O_6$ (392.45): C 61.21, H 7.19, N 7.14; found: C 61.19, H 7.12, N 7.08; HRMS (ESI): *m/z* calcd for $C_{20}H_{28}N_2O_6Na$ $[M+Na]^+$: 415.1840, found: 415.1852.

Tetraamide 18: Sodium (0.25 g) was dissolved in anhydrous methanol (100 mL), and amido ester **16** (1962 mg, 5.00 mmol) and diamine **17** (962 mg, 5.00 mmol) were dissolved in this solution of sodium methanolate. The reaction flask was tightly sealed and left at room temperature for about one month. After this time, the solvent was evaporated and the desired product was isolated by column chromatography on silica gel using 3% CH_3OH in CH_2Cl_2 as eluent. Yield 205 mg, 7.9%. M.p. > 350 °C. ^{1}H NMR (200 MHz, $[D_6]$DMSO): $\delta = 8.32$–8.18 (m, 4H), 7.93 (m, 3H), 7.14 (d, $J = 1.2$ Hz, 2H), 7.08 (bs, 1H), 4.23 (d, $J = 5.0$ Hz, 4H), 3.55 (br m, 4H), 2.48–2.35 (br m, 4H), 1.30 (s, 9H), 1.16 ppm (s, 9H); ^{13}C NMR (50 MHz, $[D_6]$DMSO): $\delta = 170.45$, 166.14, 151.00, 150.64, 138.64, 134.17, 126.96, 125.12, 123.83, 122.13, 43.06, 35.86, 35.40, 34.60, 34.20, 31.08, 30.96 ppm; elemental analysis (%) calcd for $C_{30}H_{40}N_4O_4$: C 69.20, H 7.74, N 10.76; found: C 69.10, H 7.81, N 10.88; HRMS (ESI): *m/z* calcd for $C_{30}H_{40}N_4O_4Na$ $[M+Na]^+$: 543.2942, found: 543.2945.

CCDC-246610 (**6**·CH_3OH), CCDC-246611 (**6**·Ph_4Cl), CCDC-283441 (**6**·0.5 H_2O), CCDC-283442 (**6**·$TBAPF_6$·TBAF·$C_2H_4Cl_2$·1.8 H_2O), CCDC-283443 (**7**), CCDC-283444 (**8**·TBA^+Cl^-), CCDC-283445 (**8**·TBA^+Cl^-·2 H_2O) and CCDC-283446 (**8**·$(C_2H_5)_2O$) contain the supplementary crystallographic data for this paper. These data can be obtained free of charge from the Cambridge Crystallographic Data Centre via www.ccdc.cam.ac.uk/data_request/cif.

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[1] A. Bianchi, K. Bowman-James, E. Garcia-España, *Supramolecular Chemistry of Anions*, Wiley-VCH, Weinheim, **1997**.
[2] A. Bianchi, K. Bowman-James, E. Garcia-España, *Supramolecular Chemistry of Anions*, Wiley-VCH, Weinheim, **1997,** Chap. 3.
[3] J. D. Watson, J. Milner-White, *J. Mol. Biol.* **2002**, *315*, 171–182.
[4] C. R. Bondy, S. J. Loeb, *Coord. Chem. Rev.* **2003**, *240*, 77–99.
[5] P. A. Gale, *Chem. Commun.* **2005**, 3761–3772.
[6] K. Bowman-James, *Acc. Chem. Res.* **2005**, *38*, 671–678.
[7] For a review on macrocyclic anion receptors based on hydrogen-bonding interactions, see: K. Choi, A. D. Hamilton, *Coord. Chem. Rev.* **2003**, *240*, 101–110.
[8] M. J. Chmielewski, A. Szumna, J. Jurczak, *Tetahedron Lett.* **2004**, *45*, 8699–8703.
[9] M. J. Chmielewski, J. Jurczak, *Chem. Eur. J.* **2005**, *11*, 6080–6094.
[10] M. J. Chmielewski, J. Jurczak, *Tetahedron Lett.* **2005**, *46*, 3085–3088.
[11] K. Kavallieratos, C. M. Bertao, R. H. Crabtree, *J. Org. Chem.* **1999**, *64*, 1675–1683.
[12] Similar behaviour of bis-amide receptors was observed earlier by Hamilton et al. with respect to uncharged hydrogen-bond acceptors: S.-K. Chang, D. Van Engen, E. Fan, A. D. Hamilton, *J. Am. Chem. Soc.* **1991**, *113*, 7640–7645.
[13] V. S. Bryantsev, B. P. Hay, *J. Am. Chem. Soc.* **2005**, *127*, 8282–8283.
[14] A 20-membered macrocyclic tetraamide devoid of *tert*-butyl groups was already synthesized from isophtahlic acid chloride and 1,3-diaminopropane; however, its anion-binding properties were not studied. L. Wambach, F. Voegtle, *Tetrahedron Lett.* **1985**, *26*, 1483–1486.
[15] From isophthalic acid chloride and 1,4-diaminobutane: H. Stetter, L. Marx-Moll, H. Rutzen, *Chem. Ber.* **1958**, 1775–1780.
[16] From 2,6-pyridinedicarboxylic acid chloride and 1,4-diaminobutane: K. Krakowiak, *Pol. J. Chem.* **1988**, *62*, 231–233.
[17] From 2,6-pyridinedicarboxylic acid chloride and 1,5-diaminopentane: K. Krakowiak, *Pol. J. Chem.* **1986**, *60*, 277–281.
[18] From 1,2-diaminobenzene and both isophthalic acid chloride and 2,6-pyridinedicarboxylic acid chloride: Z. Mo, W. Yang, J. Gao, H. Chen, J. Kang, *Synth. Commun.* **1999**, *12*, 2147–2153.
[19] Y. H. Kim, J. Calabrese, C. McEwen, *J. Am. Chem. Soc.* **1996**, *118*, 1545–1546.
[20] A. Szumna, J. Jurczak, *Helv. Chim. Acta* **2001**, *84*, 3760–3765.
[21] F. J. Carver, C. A. Hunter, R. J. Shannon, *Chem. Commun.* **1994**, 1277–1280.
[22] A. G. Johnston, D. A. Leigh, L. Nezhat, J. P. Smart, M. D. Deegan, *Angew. Chem.* **1995**, *107*, 1327–1331; *Angew. Chem. Int. Ed. Engl.* **1995**, *34*, 1212–1216.
[23] L. Fielding, *Tetrahedron* **2000**, *56*, 6151–6170.
[24] M. A. Hossain, S. U. Kang, D. Powell, K. Bowman-James, *Inorg. Chem.* **2003**, *42*, 1397–1399.
[25] M. J. Chmielewski, Ł. Dobrzycki, J. Jurczak, K. Woźniak, *Cryst. Growth Des.* **2005**, *5*, 1339–1341.
[26] G. W. Gokel, D. M. Goli, C. Minganti, L. Echegoyen, *J. Am. Chem. Soc.* **1983**, *105*, 6786–6788.
[27] See reference [9] and references therein.
[28] C. A. Hunter, D. H. Purvis, *Angew. Chem.* **1992**, *104*, 779–782; *Angew. Chem. Int. Ed. Engl.* **1992**, *31*, 792–795.
[29] J. F. Malone, C. M. Murray, G. M. Dolan, R. Docherty, A. J. Lavery, *Chem. Mater.* **1997**, *9*, 2983–2989.
[30] For recent example, see: T. Velasco, G. Lecollinet, T. Ryan, A. P. Davis, *Org. Biomol. Chem.* **2004**, *2*, 645–647.
[31] A similar twist of the amide group was calculated earlier for benzamides: M. Čajan, I. Stibor, J. Koča, *J. Phys. Chem. A* **1999**, *103*, 3778–3782.

[32] S. J. Coles, J. G. Frey, P. A. Gale, M. B. Hursthouse, M. E. Light, K. Navakhun, G. L. Thomas, *Chem. Commun.* **2003**, 568–569.
[33] C. A. Schalley, W. Reckien, S. Peyerimhoff, B. Baytekin, F. Vögtle, *Chem. Eur. J.* **2004**, *10*, 4777–4789.
[34] D. A. Leigh, A. Venturini, A. J. Wilson, J. K. Y. Wong, F. Zerbetto, *Chem. Eur. J.* **2004**, *10*, 4960–4969.
[35] The AM1 method has been recently successfully applied to much larger systems containing isophthalamide units.[33]
[36] The only exceptions are found in the largest macrocycle **8**, for example, SS(+,−)SS(+,−) conformations nos. 526 and 647, see Supporting Information.
[37] A. Szumna, D. T. Gryko, J. Jurczak, *Heterocycles* **2002**, *56*, 361–368.
[38] For another example of a PF_6^- complex grown in the presence of an excess of tetrabutylammonium fluoride, see reference [32].
[39] X-ray structure of the receptor **19**–sulfate complex: M. A. Hossain, J. M. Llinares, D. Powell, K. Bowman-James, *Inorg. Chem.* **2001**, *40*, 2936–2937.
[40] Sterically mismatching cation complexes of crown ethers: J. W. Steed, P. C. Junk, *J. Chem. Soc. Dalton Trans.* **1999**, 2141–2146.
[41] M. A. Hossain, J. M. Linares, S. Mason, P. Morehouse, D. Powell, K. Bowman-James, *Angew. Chem.* **2002**, *114*, 2441–2444; *Angew. Chem. Int. Ed.* **2002**, *41*, 2335–2338.
[42] J. L. Sessler, D. An, W.-S. Cho, V. Lynch, D.-W Yoon, S.-J. Hong, C.-H. Lee, *J. Org. Chem.* **2005**, *70*, 1511–1517.
[43] O. Beckstein, K. Tai, M. S. P. Sansom, *J. Am. Chem. Soc.* **2004**, *126*, 14694–14695.
[44] D. H. Burns, K. Calderon-Kawasaki, S. Kularatne, *J. Org. Chem.* **2005**, *70*, 2803–2807.
[45] V. Balzani, A. Credi, J. F. Stoddart, *Angew. Chem.* **2000**, *112*, 3484–3530; *Angew. Chem. Int. Ed.* **2000**, *39*, 3348–3391.
[46] J. F. Stoddart, *Acc. Chem. Res.* **2001**, *34*, 409–522.
[47] A. Petitjean, R. G. Khoury, N. Kyritsakas, J.-M. Lehn, *J. Am. Chem. Soc.* **2004**, *126*, 6637–6647.
[48] M. Barboiu, G. Vaughan, N. Kyritsakas, J.-M. Lehn, *Chem. Eur. J.* **2003**, *9*, 763–769.
[49] M. Büschel, M. Helldobler, J. Daub, *Chem. Commun.* **2003**, 1338–1339.
[50] H. Huang, L. Mu, J. He, J.-P. Cheng, *Tetrahedron Lett.* **2002**, *43*, 2255–2258.
[51] S. B. Suh, C. Cui, H. S. Son, J. S. U, Y. Won, K. S. Kim, *J. Phys. Chem. B* **2002**, *106*, 2061–2064.
[52] J. L. J. Blanco, J. M. Benito, C. O. Mellet, J. M. G. Fernandez, *Org. Lett.* **1999**, *1*, 1217–1220.
[53] R. Martínez-Máñez, F. Sancenón, *Chem. Rev.* **2003**, *103*, 4419–4476.
[54] F.-Y. Wu, Z. Li, Z.-C. Wen, N. Zhou, Y.-F. Zhao, Y.-B. Jiang, *Org. Lett.* **2002**, *4*, 3203–3205.
[55] C. Demuth, O. Zerbe, D. Rognan, R. Söll, A. Beck-Sickinger, G. Folkers, U. E. Spichinger, *Biosens. Bioelectron.* **2001**, *16*, 783–789.
[56] C. M. Keaveney, D. A. Leigh, *Angew. Chem.* **2004**, *116*, 1242–1244; *Angew. Chem. Int. Ed.* **2004**, *43*, 1222–1224.
[57] D. T. Gryko, A. Pecak, W. Koźmiński, P. Piatek, J. Jurczak, *Supramol. Chem.* **2000**, *12*, 229–235.
[58] A. Szumna, D. T. Gryko, J. Jurczak, *J. Chem. Soc. Perkin Trans. 2* **2000**, 1553–1558.
[59] E. Kolomiets, V. Berl, I. Odriozola, A.-M. Stadler, N. Kyritsakas, J.-M. Lehn, *Chem. Commun.* **2003**, 2868–2869.
[60] C. Dolain, V. Maurizot, I. Huc, *Angew. Chem.* **2003**, *115*, 2844–2846; *Angew. Chem. Int. Ed.* **2003**, *42*, 2738–3740.
[61] K. Navakhun, P. A. Gale, S. Camiolo, M. E. Light, M. B. Hursthouse, *Chem. Commun.* **2002**, 2084–2085.
[62] M. D. Covart, I. Sucholeiki, R. R. Bukownik, C. S. Wilcox, *J. Am. Chem. Soc.* **1988**, *110*, 6204–6210.
[63] I. Stibor, D. S. M. Hafeed, P. Lhoták, J. Hodačová, J. Koča, M. Čajan, *Gazz. Chim. Ital.* **1997**, *127*, 673–685.
[64] C. Heim, A. Affeld, M. Nieger, F. Vögtle, *Helv. Chim. Acta* **1999**, *82*, 746–768.

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