

Cite this: *Chem. Commun.*, 2011, **47**, 12176–12178

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## COMMUNICATION

Selective and tuneable recognition of anions using  $C_{3v}$ -symmetrical tripodal urea-amide receptor platforms†Cidalia Maria Gomes dos Santos,<sup>a</sup> Elaine M. Boyle,<sup>a</sup> Stefano De Solis,<sup>ab</sup> Paul E. Kruger<sup>c</sup> and Thorfinnur Gunnlaugsson<sup>\*a</sup>

Received 23rd August 2011, Accepted 29th September 2011

DOI: 10.1039/c1cc15233e

The synthesis and binding investigations of first generation  $C_{3v}$ -symmetrical hydrogen bonding urea-amide based tripodal receptors, **1–6**, with various anions such as acetate, phosphate, sulfate and chloride in DMSO-*d*<sub>6</sub> are presented. Analysis of the <sup>1</sup>H NMR titrations of **1–6** showed on all occasions the selective formation of 1 : 1 stoichiometries.

The design and synthesis of receptors for the selective recognition and sensing of anions, through the use of weak interactions such as hydrogen bonding, is an active area of research within supramolecular chemistry.<sup>1–4</sup> Structures based on urea and thiourea recognition sites are of particular interest due to their strong, and tuneable hydrogen binding abilities,<sup>4–7</sup> and their relatively easy syntheses, which facilitates their use in both simple and complex systems.<sup>8</sup> Incorporation of such moieties into the tripodal molecular platform can give rise to the formation of preorganised structures,<sup>9</sup> which can allow for cooperative hydrogen bonding interactions to take place from several binding sites.<sup>10</sup> Hence, such systems have also been employed for studying transport of anions<sup>11</sup> such as sulfate across lipid bilayers.<sup>12</sup> To date, only a limited number of tripodal anion receptors have been reported in the literature, but these are highly attractive for the formation of anion receptors that possess high coordination requirements such as halides, sulfates and phosphates.<sup>13,14</sup> We have recently demonstrated that simple amido-urea<sup>15</sup> and thiourea<sup>16</sup> receptors can be designed that enable positive cooperative binding of anions. Herein we present the synthesis and anion binding studies of six new tripodal receptors, **1–6**, Fig. 1. Each receptor consists of three urea moieties, connected to a central  $C_{3v}$  symmetrical phenyl platform *via* amide linkage. This central *N*-arylbzamide motif has previously been identified by Lewis *et al.*,<sup>17</sup> as a candidate for developing extended geometries<sup>18</sup> for molecular recognition, but to the best of our knowledge, have not been used

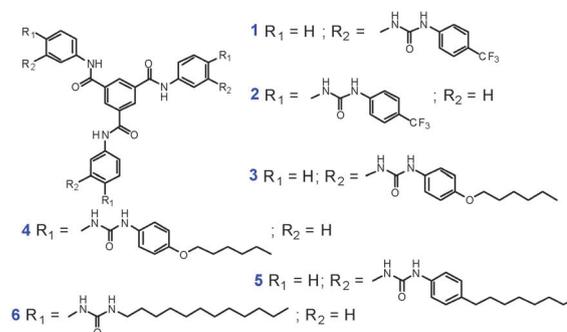


Fig. 1 Structures **1–6** employed in the current study.

as part of an anion receptor platform of the kind presented here. We anticipated that for **1–6**, this central platform would enable cooperative or synergetic binding of anions by all three urea sites. We also foresaw that this binding would affect the chemical shifts of the amide protons in the <sup>1</sup>H NMR due to the conformational changes that these structures would undergo. While **1** and **2** possess electron withdrawing groups, **3–6** all have long alkyl chains which we hoped would facilitate the use of these structures as potential membrane transporters.

The synthesis of receptors **1–6** (see Scheme S1 in ESI†) was achieved in a few steps from 1,3,5-benzenetricarbonyl trichloride. In general, these were first reacted with either *meta* or *para* nitroaniline, followed by reduction to the corresponding amines, using 10% Pd/C and hydrazine monohydrate. The final receptors **1–6** were then formed by suspending these amines into hot CH<sub>3</sub>CN followed by the addition of the desired isocyanates, and heating the resulting mixtures at reflux under an inert atmosphere overnight. This resulted in the formation of precipitates, which were filtered and washed with cold CH<sub>3</sub>CN giving **1–6** in 91%, 85%, 89%, 95%, 91% and 67% yields respectively (see ESI†).

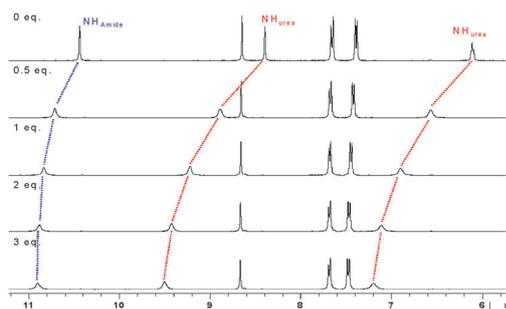
In order to evaluate the binding affinity of **1–6** for various anions, we initially carried out UV-Vis absorption studies using acetate (AcO<sup>−</sup>), sulfate (SO<sub>4</sub><sup>2−</sup>), dihydrogen phosphate (H<sub>2</sub>PO<sub>4</sub><sup>−</sup>) and chloride (Cl<sup>−</sup>), respectively, as their TBA (tetrabutyl ammonium) salt solutions. However, to our surprise, the changes in the absorption spectra were minor, and it was difficult to assess the binding affinity of these receptors for the above anions accurately. Consequently, the anion recognition of **1–6** was instead examined by using <sup>1</sup>H NMR titrations

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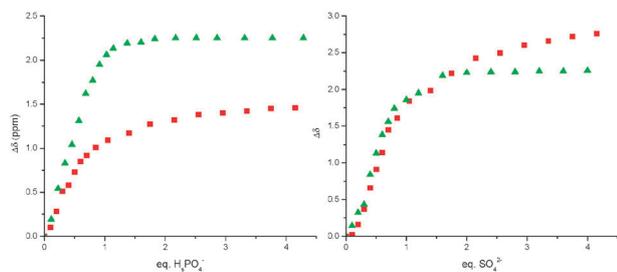
† Electronic supplementary information (ESI) available: Experimental part, detailed photophysical studies. See DOI: 10.1039/c1cc15233e



**Fig. 2** The  $^1\text{H}$  NMR (400 MHz) titration of receptor **6** with  $\text{H}_2\text{PO}_4^-$  (0  $\rightarrow$  3 eq.) in  $\text{DMSO-}d_6$ .

in  $\text{DMSO-}d_6$ , which allowed the changes in the chemical environment of all of the  $N\text{-Hs}$  of **1–6** to be monitored upon anion recognition. An example of such a titration is shown as a stack plot in Fig. 2, for the titration of **6**, where it is clear that the anion binding is in fast exchange on the NMR time scale.<sup>19</sup>

The anion induced changes for the  $N\text{-H}$  resonances of **1–6** were analysed by non-linear regression analysis, and fitted to various host : guest stoichiometries. The changes observed for the urea  $N\text{-H}$  resonances (only one of each shown) of **1** and **2** upon binding of  $\text{H}_2\text{PO}_4^-$  and  $\text{SO}_4^{2-}$  are shown in Fig. 3, expressed as  $\Delta\delta$  vs. anion equivalents. From these changes, it can be clearly seen that both structures bind these anions in a 1 : 1 stoichiometry, where the  $N\text{-H}$  protons are shifted by 1.5–2.5 ppm upon hydrogen binding to the anions. Similar behaviour was observed for  $\text{Cl}^-$  and  $\text{AcO}^-$  for both receptors (see ESI $^\dagger$ ), where the largest changes in the  $^1\text{H}$  NMR were observed upon the addition of one equivalent of these anions. As we had observed in our previous work,<sup>15,16</sup> the amide proton (*meta* to the urea) of **1** also experienced a significant downfield shift upon titration with  $\text{H}_2\text{PO}_4^-$  and  $\text{Cl}^-$ , being shifted by *ca.* 0.6 ppm within the addition of one equivalent of these anions. In contrast, these chemical shifts were less significant upon titration with  $\text{SO}_4^{2-}$  and  $\text{AcO}^-$ , being shifted by *ca.* 0.1 ppm (see ESI $^\dagger$ ). Moreover, for the structural *para* isomer **2**, only  $\text{Cl}^-$  gave rise to such shifts, being *ca.* 0.15 ppm, after the addition of one equivalent. Molecular modeling using MM2 of the binding of **1** and **2** (see Graphical Abstract) to these anions showed the formation of closely associated host–guest complexes, where the amide protons are directed away from the anion-binding side (*i.e.* ‘receptor pocket’). Hence, these shifts are conformationally induced, signifying the binding of the anions to the urea moieties, and are not due to direct binding of the anions to the amides themselves.



**Fig. 3** Changes in the chemical shifts ( $\Delta\delta$ ) of one of the urea protons of **1** (■) and **2** (▲) ( $7 \times 10^{-3}$  M) upon titration with  $\text{H}_2\text{PO}_4^-$  (left) and  $\text{SO}_4^{2-}$  (right) in  $\text{DMSO-}d_6$ .

**Table 1** Binding constants determined for **1–6** from NMR titrations in  $\text{DMSO-}d_6$

Receptor	Anion	$\log K_{1:1}$ (N–H urea)
1	$\text{AcO}^-$	$2.81 \pm 0.07$
	$\text{SO}_4^{2-}$	$2.78 \pm 0.05$
	$\text{H}_2\text{PO}_4^-$	<b><math>3.10 \pm 0.10</math></b>
	$\text{Cl}^-$	$2.39 \pm 0.06$
2	$\text{AcO}^-$	$2.79 \pm 0.07$
	$\text{SO}_4^{2-}$	<b><math>3.70 \pm 0.20</math></b>
	$\text{H}_2\text{PO}_4^-$	<b><math>4.20 \pm 0.10</math></b>
	$\text{Cl}^-$	$2.10 \pm 0.07$
3	$\text{AcO}^-$	<b><math>3.70 \pm 0.10</math></b>
	$\text{SO}_4^{2-}$	$2.15 \pm 0.08$
	$\text{H}_2\text{PO}_4^-$	<b><math>3.19 \pm 0.08</math></b>
	$\text{Cl}^-$	— <sup>a</sup>
4	$\text{AcO}^-$	<b><math>3.25 \pm 0.04</math></b>
	$\text{SO}_4^{2-}$	$2.10 \pm 0.10$
	$\text{H}_2\text{PO}_4^-$	<b><math>3.50 \pm 0.10</math></b>
	$\text{Cl}^-$	$2.81 \pm 0.07$
5	$\text{AcO}^-$	<b><math>3.70 \pm 0.10</math></b>
	$\text{SO}_4^{2-}$	$2.06 \pm 0.09$
	$\text{H}_2\text{PO}_4^-$	<b><math>3.20 \pm 0.10</math></b>
	$\text{Cl}^-$	— <sup>a</sup>
6	$\text{AcO}^-$	— <sup>a</sup>
	$\text{SO}_4^{2-}$	— <sup>a</sup>
	$\text{H}_2\text{PO}_4^-$	<b><math>2.84 \pm 0.07</math></b>
	$\text{Cl}^-$	$2.05 \pm 0.04$

<sup>a</sup> Isotherm could not be fitted to a 1 : 1 or 1 : 2 binding model.

From the titration profiles in Fig. 3, it is also clear that the recognition of  $\text{H}_2\text{PO}_4^-$  did not result in any further measurable shifts in the urea N–H resonance after the formation of the 1 : 1 host : guest complex. This 1 : 1 stoichiometry was also confirmed using MALDI-TOF mass spectrometry, (see ESI) for the binding of **2** to  $\text{H}_2\text{PO}_4^-$ , with a  $m/z$  peak observed at 1138.2332, which had an isotopic distribution pattern matching that calculated for  $[\mathbf{2} + \text{H}_2\text{PO}_4]^-$ . The binding affinity of **1** and **2** for the aforementioned anions was further assessed by fitting the changes in the  $N\text{-H}$  resonances of the urea protons using the program WinEq NMR<sup>19</sup> to 1 : 1 and 1 : 2 binding stoichiometries. On all occasions the best fit was obtained using a 1 : 1 stoichiometry and the binding constants obtained from this analysis (expressed as  $\log K_{1:1}$ ) are shown in Table 1, where the binding constants of anions such as  $\text{H}_2\text{PO}_4^-$  which displayed high affinity for these receptors are displayed in bold. Moreover, similar results were obtained for fitting either of the two  $N\text{-H}$  urea protons (see ESI $^\dagger$ ). With the exception of  $\text{Cl}^-$ , **2** gave rise to higher binding affinity for these ions than **1**, which in the case of  $\text{H}_2\text{PO}_4^-$  resulted in a  $\log K_{1:1} = 4.20$  ( $\pm 0.10$ ), for **2**, while an order of magnitude lower binding constant, of  $\log K_{1:1} = 3.10$  ( $\pm 0.10$ ), was observed for **1**. This clearly demonstrates the importance of the substituted pattern of the di-aryl urea part (*e.g.* *meta* vs. *para*) of these receptors and that **1** and **2** have high affinity for tetrahedral anions. For both, the highest affinity was also found to be for  $\text{H}_2\text{PO}_4^-$  of the anions tested. However, the interaction between **2** and  $\text{SO}_4^{2-}$  was also strong with  $\log K_{1:1} = 3.70$  ( $\pm 0.20$ ), again, being a magnitude larger than that seen for **1**.

Next the electron donating receptors *m*- and *p*-urea-phenylalkoxy chain derivatives, **3** and **4**, were investigated. The interaction with  $\text{AcO}^-$  and  $\text{SO}_4^{2-}$  showed very similar results with the urea protons experiencing a large downfield shift of

2.5–3 ppm before reaching a plateau. In contrast, the amide proton of both receptors experienced, however, a significantly smaller shift to that seen for **1** and **2** above. The formation of only the 1:1 species for receptor **4** with  $\text{AcO}^-$  was also evident in the MALDI-TOF mass spectrum (ESI<sup>+</sup>). Similar shifts were seen for  $\text{H}_2\text{PO}_4^-$ . The smallest spectral changes were observed upon titration with  $\text{Cl}^-$ . The results from these NMR titrations were fitted to 1:1 binding, from which  $\log K_{1:1}$  was determined, Table 1. Here, receptor **4** showed a slightly higher affinity for these anions than **3**; albeit the difference in  $\log K_{1:1}$  was to a lesser extent than seen for **1** and **2**. Interestingly, the binding of  $\text{AcO}^-$  was significantly higher for both compared to **1** and **2**. For both, the smallest  $\log K_{1:1}$  was observed for  $\text{SO}_4^{2-}$ .

With the view of further investigating the effect that the various substituents had on the anion affinity of these tripodal systems, the *m*-urea-phenyl-alkyl chain and the *p*-urea-alkyl chain based receptors **5** and **6** were also analysed in an analogous manner. Here, **5**, a slightly modified version of **3**, was determined to have higher affinity for the anions than **6**, which is to be expected, as **6** lacks the second aryl group, which through inductive effects makes the protons in **5** more acidic and hence, better hydrogen bonding donors, Table 1. In fact, comparison of **3** and **5** showed that both display similar affinity for these anions. Analysis of the binding of  $\text{AcO}^-$  and  $\text{SO}_4^{2-}$  to **6** did not result in a full plateau being reached after the addition of excess anions, making accurate determination of  $\log K_{1:1}$  difficult. From the analysis of **5**, slightly higher affinity was seen for  $\text{AcO}^-$ , over  $\text{H}_2\text{PO}_4^-$ ; the latter being of similar magnitude, to that seen for **1** and **3** above. In contrast the binding of  $\text{SO}_4^{2-}$  was significantly weaker for **5** than seen for **1**; but of similar to that seen for **3**. Receptor **6** also showed a significant interaction with  $\text{H}_2\text{PO}_4^-$  and  $\text{Cl}^-$ , but in contrast to that seen for **1–5** it was the lowest in the series.

In summary, we have developed six novel tripodal receptors, **1–6**, possessing highly organised urea binding sites, and determined their binding properties with various anions using <sup>1</sup>H NMR titrations. These showed high binding affinities for  $\text{H}_2\text{PO}_4^-$  and  $\text{AcO}^-$ . Moreover, **2** also showed high affinity for  $\text{SO}_4^{2-}$ . The results clearly show that our simple design principle facilitates the development of novel anion receptors possessing tuneable cooperative binding. We are currently developing this anion binding motives in greater details.

We thank the Science Foundation Ireland for SFI RFP 2008 and 2009 grants, HEA-PRTL Cycle 4 (CSCB), TCD and Ministero per l'Università e la Ricerca Scientifica e Tecnologica (Rome, Italy) for financial support.

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