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## Towards the prediction of global solution state properties for hydrogen bonded, self-associating amphiphiles

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Abstract: Through this extensive structure-property study we show that critical micelle concentration correlates with self-associative hydrogen bond complex formation constant, when combined with outputs from low level, widely accessible, computational models. Herein, we bring together a series of 39 structurally related molecules obtained through stepwise variation of a hydrogen bond donor-acceptor amphiphilic salt. The self-associative and corresponding global properties for this family of compounds have been studied in the gas, solid and solution states. Within the solution state we have shown the type of self-associated structure present to be solvent dependent. In DMSO, this class of compound show a preference for hydrogen bonded dimer formation, however moving into aqueous solutions the same compounds are found to form larger self-associated aggregates. This observation has allowed us the unique opportunity to investigate and begin to predict selfassociation events at both the molecular and extended aggregate level.

#### Introduction

Supramolecular self-assembly relies on the formation of noncovalent bonds. The formation of these bonds, combined with hydrophilic/hydrophobic solvent interactions, stabilise and direct the formation of any resultant aggregate, which in turn will dictate the global solution or solid state properties.<sup>[1]</sup> These noncovalent interactions include, but are not limited to, electrostatics, charge transfer, and hydrogen bond formation.<sup>[2]</sup> Gaining an understanding of the supramolecular interactions involved within the self-assembly process at the molecular level will allow informed construction of monomeric units, which will in turn enable the production of designer supramolecular functional materials, exhibiting global properties of choice. Enabling predictable control of these self-associative interactions at a fundamental level not only influences the fields associated with nanostructure formation,<sup>[3]</sup> specifically two-component selfassociated systems,<sup>[4]</sup> but will also enable a step-change in the fields of supramolecular materials<sup>[5]</sup> and supramolecular organic frameworks (SOFs).<sup>[6]</sup>

Within the extensive area of non-covalent self-associated material design, there is a growing interest in the focused use of intermolecular hydrogen bonds. Specific examples include those

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form Ikkala and co-workers who have used this class of noncovalent complex formation to drive the self-assembly of cobalt nanostructures for capsid production;<sup>[7]</sup> Yagai and co-workers who have used hydrogen bond formation within the construction of novel molecular semi-conductors;<sup>[8]</sup> Steed and co-workers who have shown that hydrogen bonds can act as a substitute for covalent bonds in the production of novel supramolecular gels;<sup>[9]</sup> and Zhou and co-workers who have used hydrogen bonded amphiphile self-association processes to drive the construction of novel drug/gene delivery systems.<sup>[10]</sup>

The use of low molecular weight (< 500), neutral, hydrogen bond donator (HBD) receptors for the selective coordination of anion guest species is well known.<sup>[11]</sup> However, the development of covalently linked, low molecular weight, anionic, HBD systems is not well advanced. One of the few examples, produced by Gale, Sambrook and co-workers, uses this motif to encourage the selective hydrogen bonded coordination of neutral over anionic phosphate centred quest species.<sup>[12]</sup> A separate body of work produced by Faustino and co-workers explores the use of an urea-spacer-anion motif as a novel class of surfactant.[13] During these studies the competitive critical micelle concentration (CMC) values observed for these amphiphiles were attributed to the formation of intermolecular. selfassociative hydrogen bonds. We have since extended this work through the synthesis of a second family of structurally related amphiphile (1-39) based around the general structure shown in Figure 1. Our initial studies have shown that this class of amphiphile to self-associate in DMSO through the formation of intermolecular hydrogen bonds, and that the hydrogen bonding mode can be manipulated in the solution state through the addition of competitive HBD or hydrogen bond accepting (HBA) species.<sup>[14]</sup> We have also shown the potential for this motif to instruct the formation of novel DNA aggregates<sup>[15]</sup> and conducted a solid state study in which we were able to control the self-associative hydrogen bonding mode observed through the alteration of R, X and Z (Figure 1).<sup>[16]</sup> More recently, we have focused on the synthesis and self-associative properties for the series of intrinsically fluorescent amphiphiles 28-31.<sup>[17]</sup> We were able to provide evidence that in DMSO these compounds principally appear to form hydrogen bonded dimers, for which dimerization constants were determined. These hydrogen bonded dimers were also shown to exist in the gas phase (with the exception of 30) and solid state through a combination of high resolution electrospray mass spectrometry and single crystal X-ray diffraction studies. However, in H<sub>2</sub>O/EtOH 5% larger self-associated aggregates > 100 nm in diameter were shown to exist. These structures were studied through a combination of dynamic light scattering (DLS), <sup>1</sup>H NMR, tensiometry (to derive CMC) and directly visualised through microscopy studies. These data showed a correlation between increasing strength of dimerization and a decrease in CMC value, which could be estimated through the use of low level computational modelling techniques, in a comparable but more

accessible format than those predictive studies conducted by Nagarajan and Ruckenstein.<sup>[18]</sup>

Herein, we widen the scope of our preliminary work<sup>[17]</sup> to include 39 structurally related compounds. This study not only verifies and extends our original hypothesis but has enabled us to improve our predictive models and define the associated limitations. These results bring us ever closer towards being able to predict the global and molecular level self-associated properties for this class of amphiphile using low level computational modelling methods. Within this series of 39 compounds, **18** could not be stabilised so has been excluded from this study whereas, **32-39** were synthesised to allow the exploration of ion-pair effects within our systems'.



#### **Results and Discussion**

tetrahexvlammonium.

The self-associative binding modes of **1-31** were first explored within the solid state, through the use of single crystal X-ray diffraction techniques. Crystal structures previously obtained for **8** and **16** show hydrogen bonded self-association through the formation of urea-anion tapes,<sup>[16]</sup> whilst **1**, **4**, **15**, **17**, **28**, **30**, **31** have been shown to dimerize through (thio)urea-anion hydrogen bond formation.<sup>[16-17]</sup> In contrast, a previous structure obtained for **7** showed hydrogen bonded self-association through the formation of urea-urea hydrogen bonded tapes.<sup>[16]</sup> This demonstrates that for this sub-class of anionic-HBD amphiphile,

self-association, and particularly dimerization, through hydrogen bonded (thio)urea-sulfonate complex formation to be the most common self-association mode within the solid state, except when anion pair effects were found to override this motif, causing urea-urea hydrogen bond formation to dominate.

Novel single crystal X-ray structures acquired for 2, 3, 5, 6, 9, 14, 21, 22 and 23, through the slow evaporation of EtOH : H<sub>2</sub>O solutions, allow us to extend these initial observations. The crystal structures obtained for 2, 3, 6, 21 and 14 (Figure 2) show (thio)urea-sulfonate hydrogen bonded dimer formation. Compound 2 (Figure 2a) also shows evidence of an intramolecular hydrogen-bond between the alkyl N-H and the sulfonate group. This is made possible by the increase in length of the alkyl chain connecting the urea and sulfonate groups from n = 1 to n = 2. Interestingly, the analogous thiourea structure (5, Figure 3a) shows a hydrogen bonded thiourea-sulfonate tape rather than a hydrogen bonded dimer. This difference in hydrogen bonding mode is attributed to either the instability of the dimer due to the formation of intramolecular hydrogen bonds. or crystal packing forces. Further extension of the connective alkyl chain from n = 2 to n = 3 (Figures 2b and 2c) show the intramolecular hydrogen bonding mode to no longer be favourable. The presence of an extra primary amino HBA/HBD group within 14 (Figure 2d) results in a structure which exhibits two different self-associative hydrogen bonding modes, the common urea-sulfonate dimer and a hydrogen bonded aminosulfonate tetramer. The interior angle of dimerization, calculated from the intersecting planes of the two (thio)urea functionalities contained within these dimers illustrated in Figure 2, show these structures to be planar in nature (interior angle of dimerization ≈ 180 °) with the acceptation of 21 (Figure 2e). This dimer exhibits an interior angle of dimerization =  $24.6(2)^{\circ}$  which is comparable to that obtained for the analogous urea  $\boldsymbol{17}^{[16]}$  (interior angle of dimerization =  $19.9(1)^{\circ}$ ).

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Figure 2. Single crystal X-ray structures of: a) 2, illustrating intramolecular and intermolecular dimerization through urea-anion complexation. Interior dimerization angle =  $180.0^{\circ}$ ; b) 3, illustrating dimerization through urea-anion complexation. Interior dimerization angles =  $170.9(5)^{\circ}$  and  $175.7(5)^{\circ}$ ; c) 6, illustrating dimerization through thiourea-anion complexation. Interior dimerization through thiourea-anion complexation. Interior dimerization angle =  $180.0^{\circ}$ ; d) 14, illustrating dimerization through urea-anion complexation angle =  $180.0^{\circ}$ ; e) 21, illustrating dimerization through thiourea-anion complexation. Interior dimerization angle =  $24.6(2)^{\circ}$ . TBA counter cations and solvent molecules have been omitted in all cases for clarity.

As with 5 (Figure 3a), 9 (Figure 3b) also shows selfassociative hydrogen bonded tape formation through (thio)ureasulfonate complexation. In this instance, this binding mode is favoured due to the competitive electrostatic interactions between the anionic sulfonate functionality and the TMA counter cation. Compound 22 (Figure 3c) does not contain an anionic functionality. In this comparative example, the anionic group is instead protected as the tert-butyl ester. This compound exhibits no hydrogen bonded self-association but instead forms a hydrogen bonded complex with a water molecule acting as the principle HBA. Subsequent removal of the tert-butyl ester give rise to the corresponding carboxylate, resulted in the structure shown in Figure 3d. Here the CF<sub>3</sub> group has been converted to a carboxylic acid functionality during the crystallisation process giving rise to 24a. This is a process which occurred over many weeks. As a result of this discovery, solutions containing compounds 23, 24, 26 and 27 were checked for purity before use. The study of this process is ongoing. High resolution mass spectrometry experiments performed with the remaining crystal liquor verified the presence of 24a but did not show the presence of the anion contained in 24. Again, the structure exhibited in Figure 3d shows self-association occurring though the formation of urea-anion complexes however, in this instance tape formation is preferred over dimer formation presumable due to anion geometry. It is hypothesised that the trigonal planar carboxylate moiety favours end-on urea-anion interactions, while the analogous tetrahedral sulfonate group favours dimer formation through the creation of four urea-anion hydrogen bonds, as illustrated in Figure 4.

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Figure 4. A possible effect of anion geometry (a) tetrahedral sulfonate and b) trigonal planar carboxylate) on hydrogen bonding mode.

Moving from the solid into the gas phase, Table 1 shows the occurrence of dimerized (thio)urea species as observed through a series of high resolution -ve electrospray mass spectrometry experiments. Here M, in the case of 22, 23, 25 and 27, represents the conjugate base of the neutral molecule. For all other compounds listed [M]<sup>-</sup> represents the anionic component of the corresponding amphiphilic salt. The mass to charge ratio means that we are unable to distinguish [M]<sup>-</sup> from [M+M]<sup>2-</sup>, however we are able to distinguish the presence of the dimeric [M+M+H]<sup>-</sup> or [M+M+Na]<sup>-</sup> ion from the monomeric species. The presence of self-associated dimers was observed for 1-31 with the exception of 22, 25 and 30. It is hypothesised that the urea-anion hydrogen bonded dimer could not be stabilised for 30 because of the presence of a strong intramolecular hydrogen bond.<sup>[17]</sup> The presence of a dimer is not observed with 22 and 25 due to the lack of an anionic or ionisable carboxylic acid residue within the molecular structure. This means the formation of the respective conjugate base involves deprotonation of the HBD array. As a result the hydrogen bonded dimer cannot be supported.

**Figure 3.** Single crystal X-ray structures of: a) **5**, illustrating polymerisation through thiourea-anion complexation; b) **9**, illustrating polymerisation through urea-anion complexation. Disorder of the CF<sub>3</sub> functionality has been omitted for clarity; c) compound **22**; d) **24a** from a solution of **24**, illustrating self-association through urea-anion complexation. TBA counter cations (where present) have been omitted in all cases for clarity.

15

519.0861

Table 1. High resolution ESI negative mass spectrometry theoretical andexperimentally derived values obtained for $1 - 31$ .						
No.	m/z [M+M+H⁺]⁻		No	m/z [M+M+H <sup>+</sup> ] <sup>-</sup>		
	theoretical	actual	INO.	theoretical	actual	
1	595.0397	595.0408	16 <sup>[a]</sup>	459.0578	459.0649	
2	623.0710	623.0689	17	549.0351	549.0352	
3	651.1023	651.0996	19 <sup>[b]</sup>	573.0224	573.0431	
4	626.9941	626.9940	20 <sup>[b]</sup>	513.0012	512.984	
5	655.0254	655.0236	21 <sup>[b]</sup>	602.9714	602.997	
6	683.0567	683.0529	22	Not observed		
7	595.0397	595.0418	23	523.1058	523.1025	
8	595.0397	595.0410	24 <sup>b</sup>	545.0877	545.1039	
9	595.0397	595.0408	25	Not observed		
10	595.0397	595.0423	26	555.0601	555.0577	
11	595.0397	595.0385	27	555.0601	555.0591	
12	595.0397	595.0377	28 <sup>[a]</sup>	559.0890	558.9373	
13	595.0397	595.0347	<b>29</b> <sup>[a]</sup>	659.1204	659.1210	
14	489.0868	489.0533	30 <sup>[a]</sup>	Not observed		

[a] Previously published results.<sup>[17]</sup> [b] Obtained as the [M+M+Na<sup>+</sup>]<sup>-</sup> ion.

519 0867

31<sup>[a]</sup>

753.0862

753.0864

Within the solid state the molecular interactions observed are influenced by crystal packing forces, whereas these same interactions within the gas phase can be subject to experimental conditions. However, in the solution state, the presence and stability of self-associated structures are influenced by solventsolute interactions. For example, a solvent with HBD or HBA groups will compete with those of a solute, creating solventsolute hydrogen bonded complexes which must be disrupted to enable the formation of hydrogen bonded self-associated complexes. The conformation of the aggregate formed will also be dependent on maximizing hydrophobic or hydrophilic (as appropriate) interactions with the surrounding environment.

The presence of extended (> 50 nm) self-associated aggregates formed by 1-31 in a H<sub>2</sub>O/EtOH 5% mixture were verified through DLS studies. The addition of the EtOH was required to aid compound solubility. Table 2 gives an overview of the results obtained for average size intensity studies at 5.56 mM. Before these studies were conducted, the samples underwent an annealing process to obtain aggregates that had achieved a thermodynamic minimum. Compound solubility issues prevent inclusion of 12, 13, 22 and 25 within these studies. For the purposes of these discussions, the aggregate sizes observed by DLS have been grouped into three different classes. The first are those with a hydrodynamic diameter  $(d_{H})$ between 100-550 nm. This size of structure was observed for every compound studied at 5.56 mM except for 17 (91 nm). The existence of this size of self-associated structure, reported by these DLS studies, have already been confirmed through a combination of complimentary fluorescence and transmission microscopy studies, utilising the intrinsic fluorescent properties of 30 and 31. These previously published results obtained with these representative systems confirm the presence and type of aggregate structure present within these comparable systems.[17] The second class of aggregates exhibit  $d_{\rm H}$  between 10-100 nm and were only observed with solutions containing 2, 17 and 31.

For **2** and **31**, results indicate two distinct aggregate size distributions coexisting within the solution. The third class of aggregate exhibit  $d_{\rm H}$  from 1-10 nm and were only observed with **1** and **21**, giving evidence for the presence of low order aggregates, containing few monomeric units.

To elucidate the stability of the self-associated aggregates observed at 5.56 mM, zeta potential measurements were obtained. Reproducible measurements could not be produced for solutions containing 17, 21 or 23, which suggests aggregate instability in these cases. The measurements obtained with solutions containing 8, 9, 10, 16, 26, and 27 also showed evidence of unstable aggregate formation (zeta potential  $< \pm 30$ mV). In general, these observations suggest that the presence of a strongly coordinating, less hydrophobic or HBD counter cation such as pyridinium (PyrH<sup>+</sup>), TMA or TEA, and the replacement of the sulfonate anion with the neutral carboxylic acid functionality destabilise the resultant aggregate formed. These are both structural alterations that will weaken any selfassociative hydrogen bond formation process. The presence of a nitro group (17 and 21) was also found to destabilise aggregate formation, as was the exchange of the sulfonate anion of 4 (-92 mV) for the carboxylate group in 27 (-4 mV). This change in anion geometry and basicity may also affect the hydrogen bonding mode and therefore overall aggregate stability, as illustrated in Figure 4, supported by the information shown in Figure 3d. Here we see both end on and side on carboxylateurea self-associative hydrogen bonding modes, which are dissimilar to those observed for the sulfonate analogue 4<sup>[16]</sup>.

**Table 2.** Peak maxima obtained from an average intensity particle size distribution of **1** - **31** and corresponding zeta potential measurements obtained at 5.56 mM in a H<sub>2</sub>O/EtOH 5 % system by DLS. Hydrodynamic aggregate diameter is given in nm. An annealing process was applied in which the samples were heated to approximately 40 °C before being allowed to cool to a measurement temperature of 25 °C.

Annual Contraction					
No.	Size (nm)	Zeta potential (mV)	No.	Size (nm)	Zeta potential (mV)
1	160, 4	-76	16 <sup>[a]</sup>	220	-19
2	460, 59	-78	17	91	[c]
3	120	-94	19	220	-30
4	340, 300	-92	20	190	-66
5	140	-34	21	110, 1	[c]
6	120	-38	22	[b]	[b]
7	530	-55	23	400	[c]
8	220	-28	24	220	-37
9	160	-24	25	[b]	[b]
10	190	-26	26	460	-23
11	190	-48	27	160	-4
12	[b]	[b]	28 <sup>[a]</sup>	160	-96
13	[b]	[b]	<b>29</b> <sup>[a]</sup>	220	-82
14	340	-30	30 <sup>[a]</sup>	300	-79
15	190	-98	31 <sup>[a]</sup>	300, 59	-101

[a] Previously published results.<sup>[17]</sup> [b] Not calculated due to sample insolubility. [c] Could not be accurately determined due lack of reproducibility.

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The CMC and corresponding surfactant properties for solutions of **1-11**, **15-17**, **19**, **20**, **24** and **28-31** in H<sub>2</sub>O/EtOH 5% were observed using the pendant drop method. The CMC value was determined as the point at which the surface tension was no longer found to decrease with increasing concentrations of compound,<sup>[19]</sup> as illustrated in Figure 5. A full overview of these results is given in Table 3. With the exception of 6, 29 and 31, the CMC value derived for these systems was found to be higher than the concentrations at which the DLS and associated zeta potential measurements were performed, however this does not mean that stable aggregates do not exist in solution.<sup>[20]</sup>



Figure 5. Calculation of CMC for 11 in a  $H_2O$ /EtOH 5% mixture using surface tension measurements. Red = linear relationship between Log(Conc.) and surface tension. Green = surface of droplet saturated, minimum surface tension reached.

Table 3. CMC and surface tension (obtained at CMC) measurements for 1 -	_
<b>31</b> (except for <b>18</b> ) at 25 °C. CMC = mM. Surface tension = mN m <sup>-1</sup> .	

No.	СМС	Surface tension	No.	CMC	Surface tension
1	10.39	37.45	16 <sup>[a]</sup>	40.89	47.90
2	10.70	38.49	17	30.29	44.94
3	8.85	36.78	19	65.83	45.05
4	24.14	34.35	20	74.59	42.85
5	6.12	42.24	21	[b]	[b]
6	5.61	33.59	22	[b]	[b]
7	96.35	36.65	23	[b]	[b]
8	198.42	36.16	24	11.21	39.33
9	209.98	41.78	25	[b]	[b]
10	103.13	33.75	26	[b]	[b]
11	34.57	36.09	27	[b]	[b]
12	b	b	28 <sup>[a]</sup>	10.67	46.67
13	b	b	<b>29</b> <sup>[a]</sup>	2.52	43.15
14	b	b	30 <sup>[a]</sup>	9.54	48.71
15	92.67	46.14	31 <sup>[a]</sup>	0.50	46.50

[a] Previously published results.  $^{[17]}$  [b] Not calculated due to sample insolubility.

A comparative decrease in surface tension recorded at CMC for 1-11, 15-17, 19, 20, 24 and 28-31 in general correlates with the presence of a CF<sub>3</sub> substituted aromatic ring system within the molecular structure. Spartan '16 was used to perform simple computational modelling of these systems to enable the derivation of theoretical LogP (Figure 6) and polarizability values.<sup>[21]</sup> These values were calculated for optimised geometries of the aromatic ring substituents and counter cations contained within the molecular structures of 1-31 at the semi-empirical PM6 level. These calculations show trifluoromethyl benzene to have the highest LogP value which is used as a comparative measure of compound hydrophobicity for this study, and we suggest this to be a major contributing factor to explain our previously stated general observation.

We have provided preliminary evidence to support the hypothesis that increasing strength of hydrogen bonded, selfassociative complex formation correlates to a decrease in CMC.<sup>[17]</sup> The expansion of this original study has allowed us to extend these structure-property relationships. With the exception of 2, which has been observed to form a intramolecular hydrogen bond (Figure 2a), an increase in (thio)urea-anion connective alkyl chain length results in a decrease in CMC for 1-6. and the substitution of the more acidic thiourea for the urea HBD group also results in a decrease in CMC. An increase in HBD acidity with simple (thio)urea receptors is known to result in stronger hydrogen bonded receptor:anion complex,<sup>[22]</sup> а supporting our original hypothesis. However, this argument does not hold when comparing the CMC values obtained with 1 (10.39 mM) and 24 (11.21 mM). Carboxylate anions have been shown to from stronger hydrogen bonded complexes with urea functionalities than the hydrogen sulfate ion.<sup>[23]</sup> This is expected to result in 24 exhibiting a lower CMC than 1 but the reverse is observed. In this case, these data may be explained by comparing the differences in potential hydrogen bonding mode shown in Figure 4, and it is possible that the molecular geometry adopted by 24 results in an increased CMC.



**Figure 6.** Calculated values of LogP using Spartan'16 and optimised geometries at the semi-empirical PM6 level. Values for Na<sup>+</sup> were inaccessible by these computational methods.

A correlation is also observed between CMC and compound counter cation (1, 8-11). Here, theoretical values of

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relative polarizability for those counter cations contained within the structures of 1, 8-11 were calculated. The calculated polarizability acts as a measure of potential anion-cation coordination/strength of ion pair effects, within the system. The higher the polarization value, the more diffuse the cationic charge and therefore the weaker any potential ion pair interactions. The weaker the ion pair interactions, the more available the anion is to form self-associative hydrogen bonds. Figure 7 shows the correlation between calculated polarizability and CMC, which again supports the hypothesis that strengthening self-associative hydrogen bonded complex lowers CMC. This may also explain the low CMC calculated for 7 (96.35 mM). In an aqueous solution, the sodium ion exists as the hydrated complex [Na(H<sub>2</sub>O)<sub>6</sub>]<sup>+</sup>. This hydration process decreases the cations relative availably towards the formation of an ion-ion complex and therefore promotes urea-anion hydrogen bond formation in comparison to PyrH<sup>+</sup> (8 198.42 mM), TMA (9 209.98 mM) and TEA (10 103.13 mM). These CMC values obtained for the sub series of compounds may also be influenced by the hydrophobicity of the counter cation. Evidence for this can also be seen in Figure 7, which shows a correlation between increasing calculated counter cation LogP and decreasing CMC.



Figure 7. Comparison of CMC and calculated cation polarizability (black) and LogP (red) values obtained for 1, 8 - 11, using Spartan'16 and optimised geometries at the semi-empirical PM6 level.

To gain some understanding of hydrogen bond mediated, self-association events at the molecular level, a series of <sup>1</sup>H NMR studies were performed with **1-17**, and **19-31** in a DMSO*d*<sub>6</sub>/H<sub>2</sub>O 0.5% solution, which allows the direct observation of the HBD N-H resonances in a competitive solvent environment. A full series of DLS studies conducted with **1-31** in DMSO at both 5.56 mM and 0.56 mM show evidence of aggregates > 100 nm in diameter (see ESI). However, the hydrodynamic diameter (*d*<sub>H</sub>) of the (thio)urea-anion species obtained *via* the Stokes-Einstein equation<sup>[24]</sup> from representative <sup>1</sup>H NMR DOSY studies, with **1** (*d*<sub>H</sub> = 1.15 nm), **4** (1.11 ≤ *d*<sub>H</sub> ≥ 1.12 nm), **24** (1.26 ≤ *d*<sub>H</sub> ≥ 1.29 nm), **27** (1.42 ≤ *d*<sub>H</sub> ≥ 1.43 nm) and **31** (1.61 ≤ *d*<sub>H</sub> ≥ 1.66 nm)<sup>[17]</sup> at 55.56 mM did not show any evidence of these large aggregates. The size of aggregate obtained from both <sup>1</sup>H NMR DOSY and DLS should be treated as an estimate, as these methods assume that the aggregate structures are spherical, large in comparison to the coordinated solvent sphere, <sup>[25]</sup> and in the case of <sup>1</sup>H NMR DOSY experiments maybe further complicated through the presence of fast exchange processes.<sup>[26]</sup> However, given the discrepancy in size (> 100 nm) of the structures observed by these two complimentary methods, it is hypothesised that either the larger species observed by DLS exist in concentrations that are too low to be observed by standard solution state <sup>1</sup>H NMR techniques or, alternatively, the size and consequent slow tumbling of these large aggregates results in signals too broad to be resolved by <sup>1</sup>H NMR.

A series of T<sub>1</sub> <sup>1</sup>H NMR studies conducted in DMSO-*d*<sub>6</sub>, with 1, 4, 24, 27 and 31 at 111.12 mM (with the exception 24 which, for solubility reasons, was performed at 55.56 mM) and spiked with DCM (5 µL) as an internal standard, showed no discernible 'loss' of compound from solution through comparative integration. This suggests that the large species observed by DLS exist in concentrations that are too low to be detected by <sup>1</sup>H NMR methods. An analogous series of <sup>1</sup>H NMR studies performed in D<sub>2</sub>O/EtOH 5% with 1, 4, 24, 27 and 31 at ca. 6 mM to replicate those conditions within the DLS experiments, did show the apparent 'loss' of compound from the NMR sample through comparative integration with the EtOH signals. This apparent compound 'loss' can be attributed to the formation of large structures in solution that are then invisible to the NMR and estimated to be 52%, 50%, 68%, 59% and 10% of the total concentration of 1, 4, 24, 27 and 31 respectively. These results indicate that the larger structures observed by the DLS studies under similar aqueous experimental conditions are significant in number. Therefore, we conclude that a DMSO-d<sub>6</sub>/H<sub>2</sub>O 0.5% solution is not sufficiently hydrophilic to extensively stabilise the larger, self-associated aggregates observed in H<sub>2</sub>O/EtOH 5% solution. Instead the size of the structures identified by <sup>1</sup>H NMR DOSY experiment suggests the formation of low order species, such as urea-anion dimers. The occurrence of these structures are also supported by the results of extensive solid state single crystal X-ray diffraction studies and gas phase mass spectrometry results.

A series of <sup>1</sup>H NMR dilution studies conducted in DMSOd<sub>6</sub>/H<sub>2</sub>O 0.5% solutions with 1-31 were performed to enable the observation and charicterisation of hydrogen bonded selfassociative complexation events, through monitoring the downfield change in chemical shift of those signals corresponding to the HBD N-H resonances with increasing compound concentration. This fast exchange process is indicative of a single self-associative hydrogen bond polymerization process as expected (Figure 8a). However, the introduction of the more acidic HBD thiourea functionality to the methyl linked sulfonate amphiphiles (4, 19-21) resulted in the identification of a second slow exchange process, Figure 8b. This proposed hydrogen bond mediated, reversible slow exchange process was verified through VT NMR (see ESI). Analogous <sup>1</sup>H NMR DOSY NMR experiments involving 4 demonstrated that both the fast and slow exchange thioureasulfonate species were almost identical in size. This, combined

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with the observation that the hydrogen bond donating groups must be comparatively more acidic to allow this process to occur, supports the hypothesis that the slow exchange process represents the formation of an intramolecular hydrogen bonded or tautomeric species. The comparative downfield chemical shift for those resonances corresponding to the HBD groups of this second slow exchange species indicated that these groups are comparatively acidic in nature, while the absence of a change in chemical shift for the N-H resonances upon solution dilution, suggest that this species is not involved in an associative process but exists as an independent species. The study and characterization of this slow exchange process is ongoing.



**Figure 8.** <sup>1</sup>H NMR stack plot of a) **1** the urea, and b) **4** the analogous thiourea in DMSO-*d*<sub>6</sub>/H<sub>2</sub>O 0.5% illustrating the change in chemical shift for those signals corresponding to the N-H residues of A/A<sub>1</sub> and B/B<sub>1</sub> or intramolecular hydrogen bonded/tautomeric species A<sub>2</sub> and B<sub>2</sub> with changing compound concentration.

Within this series of compounds (1-31), we have also included variations in counter cation (7-13). The presence of competitive ion-ion pair effects is well known to be problematic when observing hydrogen bond complexation events. For this reason, within the field of anion coordination chemistry, the 'noncoordinative' TBA counter cation is a popular choice when attempting to establish HBD receptor:anion complexation strength. To establish the extent to which ion pair effects would affect our systems, a second set of <sup>1</sup>H NMR dilution studies were performed using 32-39. Whilst these salts do not contain a HBD (thio)urea group, monitoring the change in chemical shift of the ethyl CH<sub>2</sub> resonance gives a reliable indication for the presence of ion-ion interactions (Figure 9). There is clear evidence of ion pair effects with both Na<sup>+</sup> and PyrH<sup>+</sup> counter cations. There is also arguable evidence of ion-pair effects for the TMA cation, however the TEA, TPA, TBA, TPeA and THA show little evidence of sulfonate-cation coordination. In order to gain an estimation for the strength of ionic interactions between the Na<sup>+</sup>, PyrH<sup>+</sup> or TMA cation and the sulfonate functionality, a series of <sup>1</sup>H NMR titration studies were performed with **37** acting as the 'host' and the PyrH<sup>+</sup> or TMA hexafluorophosphate salt supplied as the 'guest' species. Unfortunately the sodium hexafluorophosphate salt was shown to be insoluble in a DMSO $d_{\rm e}/H_2O$  0.5% solution. Association constants of  $\approx$  10 M<sup>-1</sup> were obtained for both the formation of the pyridinium ethane sulfonate and TMA ethane sulfonate salts, when fitting these data to a 1:1 binding isotherm.



**Figure 9.** Change in chemical shift observed for those <sup>1</sup>H NMR signals corresponding to the ethyl sulfonate CH<sub>2</sub> of compounds **32-39** in a DMSO- $d_e/H_2O$  0.5% mixture at concentrations of 55.56 mM and 0.56 mM.

These data from the <sup>1</sup>H NMR dilution studies, performed with **1-31** were fitted to both the cooperative equal K (CoEK) and dimerization/equal K (EK)<sup>[27]</sup> models to elucidate the corresponding self-association constants. The CoEK model assumes the first association event differs from all subsequent identical association events whereas, the EK or dimerization model assumes all association events to be equal.<sup>[28]</sup> However, these models are limited to one component, one dimensional homogenous aggregation.<sup>[29]</sup> This means that data collected

showing evidence of more than one species, or more than a single type of aggregation event cannot be fitted to these models. This includes 4 and 19-21, which exhibit additional slow exchange processes and 7-8, which exhibit significant competitive ion pair effects. Compound 22 was also excluded as the overall change in chemical shift was too small to be classed as significant when considering the resolution limitations of the NMR spectrometer. Data from the remaining dilution studies were successfully fitted to both the EK and CoEK models to derive the associated association constants (Table 4). However, the values obtained for 9, where there is some suspected sulfonate-TMA coordination and 14, which contains a primary amino group that is free to act as both a HBD or HBA should be treated with caution as the aggregation events may not be homogenous. The associated errors obtained when fitting these data to both the CoEK and EK models suggest that these systems best fit the EK model.

With the exception of 24 and 27, the association constants calculated are all relatively small ( $K_e < 15 \text{ M}^{-1}$ ). These low association constants indicate the formation of lower order complexes, such as dimers. This hypothesis is also supported by the <sup>1</sup>H NMR DOSY, mass spectrometry and single crystal Xray diffraction studies. The association constants derived for carboxylate containing 24 ( $K_{dim} = 41 \text{ M}^{-1}$ ) and 27 ( $K_{dim} = 105 \text{ M}^{-1}$ ) are over an order of magnitude greater than the value obtained for the comparative sulfonate containing 1 ( $K_{dim} = 3 M^{-1}$ ). The anion dependent increase in dimerization constant is thought to be due to the basicity of the anionic species itself and the geometry of self-associated hydrogen bonded complex, Figure 4. Comparatively low dimerization constants (< 0.5 M<sup>-1</sup>) were calculated for 2 and 5. This observation can be explained through consideration of the potential intramolecular hydrogen bonding mode identified within the single crystal X-ray structure of 2 (Figure 2a). The formation of this intramolecular hydrogen bond would prevent self-association of the anionic monomer. However, further increasing the length of this HBD-HBA connective alkyl chain from a methyl (1  $K_{dim} = 5.3 \text{ M}^{-1}$ ) to propyl  $(3 \text{ K}_{dim} = 6.6 \text{ M}^{-1})$  results in an increase in dimerization constant.



**Table 4.** Self-association constants (M<sup>-1</sup>) calculated for **1-3**, **5**, **6**, **9-17** and **22-31** in a DMSO- $d_6/H_2O$  0.5% solution at 298 K. These constants were obtained from the fitting of <sup>1</sup>H NMR dilution data and refined to EK and CoEK models using Bindfit v0.5<sup>[30]</sup>.

-					
No.	EK moo	lel (M <sup>-</sup> ')	Co	EK model (M	')
	Ke 5.2	r <sub>dim</sub>	12.0	K <sub>dim</sub>	ρ
1	5.5 + 0.6 %	+03%	+07%	+04%	10.5 +21%
	± 0.0 %	± 0.3 %	<u>±0.7 %</u>	20	<u> </u>
2	+ 2 0 %	+10%	4.0	2.0	0.4 ± 20.3 %
	<u>12.0</u> %	3.3	20.0	10.0 %	0.3
3	+20%	+ 1.0 %	+27%	+ 1 4 %	+ 11.6 %
	0.3	0.2	19	0.9	0.5
5	+ 4 2 %	+2.1 %	+ 51 0 %	+ 25.5 %	+ 66.3 %
	51	26	14.1	7 1	0.4
6	+2.1%	+ 1.4 %	+ 4.4 %	± 2.2 %	± 14.0 %
	13.5	6.7	18.2	9.1	0.8
<b>9</b> <sup>[a]</sup>	± 0.7 %	± 0.3 %	± 1.0 %	± 0.5 %	± 3.4 %
	6.3	3.2	12.0	6.0	0.6
10	± 0.9 %	± 0.4 %	± 2.0 %	± 1.0 %	± 5.5 %
	6.6	3.3	14.9	7.5	0.5
11	± 1.2 %	± 0.6 %	± 2.1 %	± 1.1 %	± 6.7 %
	4 1	21	88	4 4	0.6
12	± 0.5 %	± 0.3 %	± 1.3 %	± 0.7 %	± 3.0 %
	5.0	2.5	9.6	4.8	0.9
13	± 0.9 %	± 0.5 %	± 2.7 %	± 1.3 %	± 6.3 %
	3.6	1.8	4.6	2.3	0.9
14 <sup>[a]</sup>	± 1.5 %	± 0.7 %	± 8.3 %	± 4.1 %	± 13.4 %
15	1.2	0.6	18.0	9.0	0.1
	± 3.0 %	± 1.5 %	± 4.1 %	± 2.1 %	±21.5 %
16 <sup>[b]</sup>	0.6	0.3	13.0	6.5	0.2
	± 3.0 %	± 1.5 %	± 5.7 %	± 2.9 %	± 23.8 %
[6]	8.9	4.5	32.2	16.1	0.2
17 <sup>[a]</sup>	± 5.1 %	±2.6 %	± 5.1 %	±2.6 %	± 37.5 %
22	[d]	[d]	[d]	[d]	[d]
7			7.1	3.6	0.1
23	<0.1	<0.1	± 18.3 %	± 9.2 %	± 58.4 %
	82.78	41.4	101.8	5.9	2.6
24	± 2.5 %	± 1.3 %	±2.6 %	± 1.3 %	± 11.6 %
	11.9	6.0	23.8	11.9	0.5
25	± 1.5 %	± 0.8 %	± 1.7 %	± 0.9 %	± 7.5 %
	10.8	5.4	4.6	2.3	1.9
26	± 3.5 %	± 1.8 %	± 20.8 %	± 10.4 %	± 31.1 %
	209.3	104.7	226.1	113.0	1.2
21	± 1.3 %	± 0.7 %	± 1.4 %	± 0.7 %	± 3.3 %
<b>28</b> [b,c]	-0.1	-0.1	0.5	0.3	0.0
28 <sup>10,0]</sup>	<0.1	<0.1	± 43.1 %	±21.5 %	± 47.0 %
<b>20</b> [b]	2.9	1.5	8.6	4.3	0.5
29	± 0.5 %	± 0.2 %	± 1.1 %	± 0.5 %	±2.5 %
<b>30[</b> p]	1.2	0.6	6.2	3.1	0.4
30.7	± 2.1 %	± 1.1 %	± 8.8 %	± 4.4 %	± 17.8 %
34[b]	5.3	2.7	13.0	6.5	0.5
21	+06%	+02%	+07%	+02%	+20%

[a] Possibility of more complex binding events than are being modelled. [b] Previously published results.<sup>[17]</sup> [c] Data fitted using L-BFGS-B (quasi-Newtown) rather than Nelder-Mead (Simplex) methods. [d] Could not be fitted.

In order to gain further insight into the molecular behavior of 1-31 in a DMSO solution a series of theoretical studies have also been undertaken. The semi-empirical PM6-D3H4X method using an implicit COSMO solvent model was used to determine the lowest energy stable conformations for a representative group of compounds (1-4, 15-17 and 24) following preliminary searches using MM2 and/or MMFF94. The resulting minimum energy conformers for the compounds are illustrated in Figure 10. In all cases where the urea and sulfate functions were separated by one CH<sub>2</sub> unit (1, 4, 15-17 and 24) the minimum energy structure found was a trans-cis (thio)urea arrangement (relative to the phenyl ring) with an intramolecular hydrogen bond between the N-H proton adjacent to the phenyl ring, and the sulfate anionic group. Stabilisation of the trans-cis conformation over the more common trans-trans conformation for ureas by intramolecular hydrogen bonding has been welldocumented.<sup>[31]</sup> Curiously for these molecules the trans-trans conformers were not stable (via frequency analysis). Where the urea and sulfate were separated by two CH<sub>2</sub> units (2) an intramolecular hydrogen bond between the N-H proton adjacent to the phenyl ring and the sulfate anionic group existed alongside a higher energy trans-trans conformation. When the linker between urea and sulfate was three CH<sub>2</sub> units (3) the alltrans conformation was preferred with the anion able to hydrogen bond to both N-H protons.



Figure 10. (a) Minimum energy conformations found for compounds 1 to 4, 15 to 17 and 24 from PM6-D3H4X in DMSO. (b) Schematic illustrating hydrogen bond motifs observed.

The self-associated complexes of **1-4** and **24** were also modelled using PM6-D3H4X. The initial dimers were set up with aromatic rings close to one another and the urea and anion functions close to each other, head-to-head/tail-to tail (H-H/T-T) and also with the only urea and anion groups close to one another with the aromatic groups separated, tail-to-tail (T-T). Initial geometry optimisation was performed using the MM2 force field followed by optimisation with PM6-D3H4X. As with the monomeric forms considerable manual input was required to optimise structures through manipulation of the dihedral angles.

For 1-4 H-H-/T-T arrangements with trans-trans (thio)urea arrangement were consistently the lowest energy conformation. In all cases the two molecules in a dimer were held together by hydrogen bonding between N-H protons and the oxygens on the sulfate of the other molecule giving a C2 symmetrical arrangement. No stable low energy T-T dimers were found. Side and top views of the dimers of 1-4 are shown in Figure 11 with a schematic of the hydrogen bonding motif. In contrast to 1-4, compound 24 formed a T-T dimer with Ci symmetry. The aromatic rings did not overlap and the hydrogen bonds between one O of a carboxylate group and the N-H furthest from the phenyl ring in the partner molecule (Figure 12). These computational studies focus on the self-associative properties of the hydrogen bond donating anionic component and therefore do not consider the influence of the counter cation and any inherent water within the sample. For these reason the computational results may differ from solution state findings.







Figure 12. Minimum energy conformations found for dimeric complexes formed by 24 in DMSO from PM6-D3H4X. The inset shows a schematic illustrating the hydrogen bonding motif.

It has long been accepted by the supramolecular community that, broadly speaking and where no other factors apply the more acidic the HBD groups the stronger the resultant hydrogen

bonded complex. It is also accepted, with the same caveat, that the greater the comparative basicity of the associated guest species, the stronger the resultant hydrogen bonded complex. In 2004, Hunter showed that electrostatic surface potential maps derived from low level computational modelling using geometry optimised, semi-empirical AM1 structures would produce electrostatic potential surface maxima ( $E_{max}$ ) and minima ( $E_{min}$ ) values which correlate well with those elucidated from experimental data.<sup>[32]</sup> For the purpose of this work, AM1 modelling methods were substituted for PM6 methods in line with work conducted by Stewart.<sup>[33]</sup> Using this method, the E<sub>max</sub> and  $E_{\min}$  values were calculated for linear versions of the (thio)urea containing monomeric units of 1-31 to increase the accuracy of values obtained for the primary HBD and HBA groups. The  $E_{max}$  and  $E_{min}$  values were found to correlate with the principle HBD and HBA functionalities within the molecular structure, Figure 13. These optimised linear geometries also identify the presence of an intramolecular hydrogen bond for 2 and 5. which contain an ethyl linker, in comparison with those linear structures obtained for 1, 3, 4 and 6, which contain either methyl or propyl linkers.

Within the scope of our preliminary studies we were able to show a correlation between these computationally derived  $E_{max}$  and  $E_{min}$  values and corresponding dimerization constant.<sup>[17]</sup> This is not surprising since the comparative acidity and basicity of the principle HBD and HBA groups respectively are a major contributing factor to the strength of the self-associative hydrogen bonded complex formed, where the hydrogen bonding mode is identical. For example, in the formation of hydrogen bonded dimers using a (thio)urea HBD group and a tetrahedral HBA anionic functionality, the comparative acidity and basicity of these groups should control the hydrogen bonded selfassociation process.



**Figure 13.** Electrostatic potential maps calculated for linear: a = 1; b = 2; c = 3 using semi-empirical PM6 modelling methods.  $E_{max}$  and  $E_{min}$  values depicted in the Figure legend are given in KJ/mol..

For 1-3, 5, 6, 9-17 and 28-31, Figure 14a shows the relationship between  $E_{max}$  or  $E_{min}$  and dimerization constant. This comparison shows some correlation between calculated values for  $E_{max}$  and dimerization constant, however there is no discernible correlation observed between those values obtained for  $E_{min}$  and experimentally derived dimerization values. This observation indicates that increasing  $E_{max}$  (HBD acidity) correlates with an increase in dimerization constant. However, this is perhaps unsurprising as we cannot include those data from **22-27** that were discounted due to differentiation in potential binding mode, and therefore we only include the sulfonate derivatives within this comparative study.

There is no denying that, in theory, both the HBD and HBA functionalities contribute to the dimerization process, although the effects of  $E_{min}$  are unclear in Figure 14a. It is hypothesised that this may be due to those monomeric intramolecular hydrogen bond formation events indicated by computational modelling studies (Figure 11).

Figure 14b shows the correlation between the sum of  $E_{max}$ and  $E_{min}$  ( $E_{max} + E_{min}$ ) and dimerization constant. The use of these values allows both the comparative effects of both HBD acidity and HBA basicity to be included. These data show a linear correlation with the exclusion of five outliers corresponding to 2, 5, 6, 9 and 14. For 2 and 5 there is evidence that the

anionic monomers exist in solution in an intramolecular hydrogen bonded form, which all but eliminates intermolecular self-association events. This justifies their exclusion. Compound 9 is believed to experience competitive ion pair effects and was excluded on that basis. The data for 6 were also excluded from the fitting process due to the probable adoption of a slightly twisted geometry due to the thiourea in comparison to the planar urea functionalities (cf. 3). This led us to question the extent to which the self-associative hydrogen bonding mode is comparable which causes the thiourea to violate the fitting criteria. Finally, those data from 14 were also excluded because of the additional primary amine, which can act as an additional HBD or HBA group. The results of these comparative studies shown in Figure 14b led us to conclude that where hydrogen bonded mode, and competitive effects on a hydrogen bonded, self-associative system are the same, simple low level computational modelling methods maybe of use in predicting the strength of the associated complex formed when considering an equal K model.



Figure 14. a) Comparison of  $E_{max}$  and  $E_{min}$  values obtained for the (thio)urea containing components of 1 - 31 with dimerization constant; b)  $E_{max} + E_{min}$  vs. dimerization constant. The data points used in the determination of these correlations are circles in red. Those data points excluded from this fitting process are shown in black only. The green boxes are used to highlight those results which contain different counter cations but the same anionic substituent.

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We previously hypothesised that the comparative increase in strength of the hydrogen bonded dimer formed in DMSO- $d_6/H_2O$  0.5% correlated with a decrease in CMC value obtained in H<sub>2</sub>O/EtOH 5%. Through extension to our preliminary studies, we are now able to propose evidence of linear correlations between dimerization constant (which can be estimated using low level computational modelling) obtained in DMSO- $d_6/H_2O$  0.5% and CMC value obtained in H<sub>2</sub>O/EtOH 5%. We are also able to propose the potential limitations to these modelling methods.

In order to qualify for this comparative analysis step, compounds must have both experimentally derived dimerization constant and CMC value. The compounds must also exhibit the same binding modes, and these binding modes must not be influenced by counter cation effects or intramolecular hydrogen bonded complex formation. The compounds must also share the same counter cation, as the competitive hydrophobicity of a cation will have substantial effects in an aqueous system. Eight of our 31 original compounds were found to meet these criteria. 1, 15-17, and 28-31. Altering solvent systems has enabled us to observe the molecular association events (DMSO-d<sub>6</sub>/H<sub>2</sub>O 0.5%) and the formation of extended aggregates (H<sub>2</sub>O/EtOH 5%) independently of one another. However, the movements of these molecules from a DMSO to aqueous system, and the change in self-associated structure from dimer to extended aggregate will also be driven by the hydrophobic nature of the self-associated, hydrogen bonded complex. To gain an estimate for these effects, we have calculated theoretical LogP values for the parent compounds aromatic substituents (Figure 6). These values have been used as CMC weighting values within the correlation study shown in Figure 15. These eight qualifying amphiphiles were split into two sub groups: those which contain a single aromatic ring; and those which contain > 1 aromatic ring, as again these amphiphile sub-groups have slightly different factors affecting the self-associative bonding mode due to the extension of the aromatic ring systems. The dimerization value obtained in a DMSO-d<sub>6</sub>/H<sub>2</sub>O 0.5% system was then plotted against the LogP-weighted CMC obtained in H<sub>2</sub>O/EtOH 5%. This produced two linear correlations, indicating that hydrogen bonded dimerization strength and the hydrophobicity of the anionic component of this sub-class of compound, which meet the previously stated criteria, are the major contributing factors towards CMC. This set of linear correlations indicates that the higher the dimerization constant and LogP of the aromatic substituent of the anion component of the amphiphilic salt, the lower the CMC. As we have previously discussed, the dimerization constant for these eight compounds may be estimated using computationally derived  $E_{max}$  and  $E_{min}$  values and the LogP value used in Figure 6 may also be derived using the same methods. Therefore, we hypothesise that, for hydrogen bonded systems, it may be possible to predict CMC values using low level, easily accessible computational modelling methods.



Figure 15. Comparison of dimerization values obtained for compounds 28-31 (red) and compounds 1, 15-17 (black). LogP weighted CMC = CMC (mM) x LogP of the aromatic R group (Figure 6).

#### Conclusions

We have expanded our preliminary results, focusing on understanding and predicting the self-associative properties of amphiphilic (thio)urea-anion monomers from five to 39 structurally related compounds. This has allowed the elucidation of structure-property relationships governing the self-associative properties for this class of compound. The extension of previous single crystal X-ray diffraction studies have confirmed that, in the solid state, this class of compounds containing covalently linked HBD-anionic functionalities and a weakly coordinating counter cation show a preference towards the formation of HBD:anion complexes. In the gas phase, all compounds meeting the same criteria were found to form dimeric species except for 30, in which this is prevented due to the formation of a strong intramolecular hydrogen bond. Moving into the solution state, a combination of <sup>1</sup>H NMR dilution, DOSY and T<sub>1</sub> studies showed a tendency for these compounds to form dimeric species in a 0.5% solution although, DMSO-d<sub>6</sub>/H<sub>2</sub>O instances of intramolecular hydrogen bond formation/ tautomerism prevented the elucidation of association constants for those compounds containing the most acidic hydrogen bond donating groups. Ionpair effects were also shown to prevent the determination of some association constants (7-8). Simple, low level computational modelling was used to produce electrostatic surface potential maps. The  $E_{max}$  and  $E_{min}$  values derived from these maps were used in the identification of the principle HBD and HBA sites respectively. The sum of  $E_{max}$  and  $E_{min}$  was found to correlate well with the experimentally derived dimerization constants, where the same hydrogen bonding mode was adopted and ion pair effects were shown to be minimal. In a H<sub>2</sub>O/EtOH 5% solution, the urea containing compounds (where solubility allowed) were shown to form extended self-associated aggregates, in most cases > 100 nm at 5.56 mM. The CMC values calculated for these systems showed correlations with the calculated cation polarizability and LogP; the higher either of these calculated values, the lower the CMC.

For those amphiphiles with the same counter cation and identical binding mode, both dimerization constants and CMC values maybe compared. Two linear correlations were identified, linking dimerization and LogP weighted CMC values. The first linear correlation is composed of compounds where the number of aromatic rings contained in the molecules = 1, and the second where the number of aromatic rings >1. These linear correlations show the potential for the use of simple, readily accessible, low level computational modelling methods for the prediction of hydrogen bond influenced, highly complex, solution state, self-associated systems. The accuracy of these prediction methods will be evaluated experimentally as a part of our ongoing studies, which expand and further investigate this family of self-associating amphiphiles.

#### **Experimental Section**

The synthesis of 1,<sup>[14]</sup> 4, 7 - 8, 15 - 17<sup>[16]</sup> and 28 - 31<sup>[17]</sup> have previously been reported. Compounds 2 - 3, 5 - 6, 19 - 21 were synthesised through the reaction of TBA aminomethane, aminoethane or aminopropane sulfonate with the appropriate isocyanate or isothiocyanate, with yields between 50% - 76%. Compounds 9 - 13 were synthesised through the addition of the appropriate hydroxide salt to compound 8, with yields between 97% - 99%. Compound 14 was obtained in a yield of 96% through the reduction of compound 17 with hydrazine hydrate and 10% palladium on carbon. Compounds 22 and 25 were synthesised through the reaction of tert-butyl 2-aminoacetate with the appropriate isocyanate or isothiocyanate, with yields of 45% and 77% respectively. Compounds 23 and 26 were obtained by the addition of trifluoracetic acid to a solution of 22 or 25 as appropriate, resulting in yields of 65% and 83% respectively. The addition of the TBA hydroxide to a solution of 23 or 26 resulted synthesis of 24 and 27 in yields of 83% and 62% respectively. Compounds 32 - 39 were synthesised through the addition of ethane sulfonic acid to a solution of either the hydroxide salt or pyridine as appropriate resulting in yields of 100 %. Although compound 18 was obtained, it was found to be unstable in the anionic form so could not be investigated further.

For single crystal X-ray diffraction studies a suitable crystal of each amphiphile was selected and mounted on a Rigaku Oxford Diffraction Supernova diffractometer. Data were collected using Cu Ka radiation at 100 K, 270 K or 343 K as necessary due to crystal instability at lower temperatures. Structures were solved with the ShelXT<sup>[34]</sup> or ShelXS structure solution programs via Direct Methods and refined with ShelXL<sup>[35]</sup> on Least Squares minimisation. Olex2<sup>[36]</sup> was used as an interface to all ShelX programs (CCDC 1589879-1589888).

#### **Conflict of interest**

The authors declare no conflict of interest.

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FULL PAPER

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## FULL PAPER

**FULL PAPER** 

A readily accessible step-change towards predicting the global effects of hydrogen bonded self-assembly. Here we experimentally validate the first steps towards predicting the role of hydrogen bonding in extended aggregate formation with the use of simple, low level computational modelling methods.



Lisa J. White, Stilyana N. Tyuleva, Ben Wilson, Helena J. Shepherd, Kendrick K. L. Ng, Simon J. Holder, Ewan R. Clark and Jennifer R. Hiscock\*

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Towards the prediction of global solution state properties for hydrogen bonded, self-associating amphiphiles