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Electronic Supplementary Information

Exploring Cyclohexane/Piperazine-urea Motifs for Spherical Halides (X= Cl⁻ / Br⁻) Recognition: Effect on Anion Coordination, Photoluminescence, and Morphological Tunability

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Characterisation of L₁



Figure S1: HRMS spectra of L_1 in 1:1 water-acetonitrile in positive ionization mode.



Figure S2: ¹H NMR spectra of L_1 in DMSO-d₆ at room temperature.



Figure S3: ¹³C NMR of L_1 in DMSO-d₆ at room temperature.



Figure S4: FTIR spectrum of L_1 recorded in KBr pellet at room temperature.

Characterisation of L₂



Figure S5: HRMS spectra of L_2 in 1:1 water-acetonitrile in positive ionization mode.



Figure S6: ¹H NMR spectra of L_2 in DMSO-d₆ at room temperature.



Figure S7: ¹³C NMR of L₂ in DMSO-d₆ at room temperature.



Figure S8: FTIR spectrum of L₂ recorded in KBr pellet at room temperature.

Characterisation of complex 1a



Figure S9: ¹H NMR spectra of chloride complex of $L_1(1a)$ in DMSO-d₆ at room temperature.



Figure S10: FTIR spectrum of chloride complex of $L_1(1a)$ recorded in KBr pellet at room temperature.

Characterisation of complex 1b



Figure S11: ¹H NMR spectra of bromide complex of $L_1(1b)$ in DMSO-d₆ at room temperature.



Figure S12: FTIR spectrum of bromide complex of $L_1(1b)$ recorded in KBr pellet at room temperature.



Figure S13: Comparative PXRD analysis of L_1 varying the chain length of halogen salts (a). in presence of TBACl, TEACl and NH₄Cl. (b) in presence of TBABr, TEABr and NH₄Br.

Characterisation of complex 2a



Figure S14: ¹H NMR spectra of chloride complex of $L_2(2a)$ in DMSO-d₆ at room temperature.



Figure S15: FTIR spectrum of chloride complex of $L_2(2a)$ recorded in KBr pellet at room temperature.

Characterisation of complex 2b



Figure S16: ¹H NMR spectra of bromide complex of $L_2(2b)$ in DMSO-d₆ at room temperature.



Figure S17: FTIR spectrum of bromide complex of $L_2(2b)$ recorded in KBr pellet at room temperature.



Figure S18: Comparative PXRD analysis of L_2 varying the chain length of halogen salts (a). in presence of TBACl, TEACl and NH₄Cl. (b) in presence of TBABr, TEABr and NH₄Br.



Figure S19: X-ray structure analysis of complex **1a** showing coordination environment of anion as well as extra stabilization through C-H_{aliphatic}...O_{urea} interaction with proper bond distances in Angstrom.



Figure S20: X-ray structure analysis of complex **1b** showing coordination environment of anion as well as extra stabilization through two C-H_{aliphatic}...O_{urea} with proper bond distances in Angstrom.



Figure S21: X-ray structure analysis of complex **2a** showing coordination environment of anion as well as extra stabilization through two C-H_{aliphatic}...O_{urea} with proper bond distances in Angstrom.



Figure S22: X-ray structure analysis of complex **2b** showing coordination environment of anion as well as extra stabilization through two C-H_{aliphatic}...O_{urea} with proper bond distances in Angstrom.



Figure S23: Partial ¹H NMR spectra (600 MHz, DMSO-d₆) of L_1 and L_2 and the maximum observable shifts in urea-NH protons upon the addition of excess Cl⁻, Br⁻, I⁻, F⁻ in the form of their TEA/n-TBA salts.

Anion binding analysis by ¹H-NMR titrations

The ¹H NMR titration of L_1 and L_2 was performed in DMSO-d₆ solvent. The stock solutions of the compound (L_1 and L_2 ; 10 mM), tetrabutyl ammonium Chloride (TBACl; 2 M) and tetrabutyl ammonium Bromide (TBABr; 2 M) were prepared in DMSO-d₆. The TBACl and TBABr were used as the source of Cl⁻ and Br⁻ ion. The changes in chemical shift ($\Delta\delta$) value of the N-H protons of the urea-moieties were analysed. Significant extents of chemical shift ($\Delta\delta$) of both N-H protons were observed during titration with chloride solution. All ¹H NMR spectra were stacked through the MestReNova software. Changes in chemical shift against the concentration of Cl⁻ ion were fitted using BindFit v 0.5 program.¹



Figure S24: (a) Expanded partial ¹H NMR spectra of L_1 upon titration with n-TBACl in DMSO-d₆. (b) Showing the raw vs. fitted data (fitted to 1:1 NMR binding data) (top) and the corresponding residual plot (bottom). Binding constant (K) = 4.50 M⁻¹ (Ref. 2).

(http://app.supramolecular.org/bindfit/view/4fc6d6b1-2de2-43c5-af72-bbd18e997501)



Figure S25: (a) Expanded partial ¹H NMR spectra of L_1 upon titration with n-TBABr in DMSO-d₆.



ppm 9.8 9.7 9.6 9.5 9.4 9.3 9.2 9.1 9.0 8.9 8.8 8.7 8.6 8.5 8.4 8.3 8.2 8.1 8.0 7.9 7.8 7.7 7.6 7.5 7.4 7.3 7.2 7.1 7.0 6.9 6.8 6.7 6.6 6.5 6.4

(b)



Figure S26: (a) Expanded partial ¹H NMR spectra of L_2 upon titration with n-TBACl in DMSO-d₆. (b) Showing the raw vs. fitted data (fitted to 1:1 NMR binding data) (top) and the corresponding residual plot (bottom). Binding constant (K) = 12.96 M⁻¹ (Ref. 2).

(http://app.supramolecular.org/bindfit/view/df8b0a98-517a-4b88-88d5-cd99e39c582d)



Figure S27: (a) Expanded partial ¹H NMR spectra of L_2 upon titration with n-TBABr in DMSO-d₆.



Figure S28: (a) UV-Vis changes of L_1 (2 μ M) (b) L_2 (2 μ M) in several solvents at room temperature.



Figure S29: The scatter plot of N-H···A angle vs. H···A distance of the hydrogen bonds in the complexes (1a, 1b, 2a, 2b).



Figure S30: ORTEP diagram of 1a.



Figure S31: ORTEP diagram of 1b.



Figure S32: ORTEP diagram of L₂.



Figure S33: ORTEP diagram of 2a.



Figure S34: ORTEP diagram of 2b.



Figure S35: Solid state fluorescence spectra of L_1 and L_2 .

References:

1. D. Brynn Hibbert and P. Thordarson, Chem Commun, 2016, 52, 12792-12805.

2. http://supramolecular.org

Complex	D-H…A	d(D…H)/Å	d(H…A)/Å	d(D…A)/Å	<d-h····a th="" °<=""><th>Symmetry codes</th></d-h····a>	Symmetry codes
1a	N1-H1N…C11	0.86	2.58	3.367(4)	153	x,1/2-y,1/2+z
	N2-H2N…C11	0.86	2.35	3.192(4)	167	x,1/2-y,1/2+z
	С6-Н6…О1	0.93	2.36	2.930(5)	119	x, y, z
	C11-H11A … Cl1	0.97	2.81	3.763(5)	169	x, y, z
	C23-H23A… O1	0.97	2.56	3.426(5)	148	x, y, z
1b	N1-H1···Br01	0.86	2.65	3.459(3)	157	x,1/2-y,-1/2+z
	N2-H2A…Br01	0.86	2.46	3.309(2)	169	x,1/2-y,-1/2+z
	С4-Н4…О3	0.93	2.36	2.935(4)	120	x,y,z
	C14-H14B…Br01	0.97	2.87	3.816(3)	167	x,y,z
	C26-H26A…O3	0.97	2.54	3.412(4)	150	x,y,z
2a	N1-H1N…C11	0.86	2.32	3.136(6)	160	x,y,z
	N2-H 2N…Cl1	0.86	2.56	3.315(6)	147	x,y,z
	С5-Н5…О1	0.93	2.31	2.865(8)	118	x,y,z
	C14-H 14A… Cl1	0.97	2.81	3.745(8)	163	x,1/2-y,-1/2+z
	C17-H17B…O1	0.97	2.45	3.388(7)	162	x,1/2-y,1/2+z
	C28-H28B… O1	0.97	2.58	3.286(8)	130	x,1/2-y,1/2+z
	С30-Н 30А… С11	0.97	2.73	3.637(6)	157	x,y,z
2b	N1-H1…Br1	0.86	2.47	3.292(6)	161	x,y,z
	N2-H2···Br1	0.86	2.66	3.439(8)	152	x,y,z

Table S1: Hydrogen bonding distances (Å) and Bond angles (°) in the neutral anion-receptor complexes:

	C7-H7…O1	0.93	2.29	2.850(11)	118	x,y,z
	C13-H13B… Br1	0.97	2.90	3.863(10)	174	x,1/2-y,-1/2+z
	C22-H22A… Br1	0.97	2.92	3.850(10)	161	x,1+y,z
	C27-H27A… Br1	0.97	2.85	3.755(8)	156	x,y,z
	C30-H30B…O1	0.97	2.47	3.399(10)	160	x,1/2-y,1/2+z
2	N1-H1N… O1	0.86	2.06	2.893(5)	162	x,1/2-y,1/2+z
	N2-H2N… O1	0.86	2.26	3.035(6)	149	x,1/2-y,1/2+z
	N3-H3N…N2	0.98	2.57	3.205(6)	123	x,y,z
	С6-Н6…О1	0.93	2.47	2.933(6)	111	x,y,z

Table S2: Contact contributions from the d_{norm} surface areas of dipodal segments in free receptors and in anion complexes.

Bond	1a	1b	2a	2b	L ₂
C…H/H…C	3.3/2.4	3.4/2.5	3.0/2.8	4.4/3.0	2.5/2.0
O…H/ H…O	7.0/6.1	7.2/6.3	0.2/0.2	0.2/0.2	3.7/3.3
F…H	0	0	9.4	9.5	15.6
N…H	1.1	1.1	1.0	0.9	1.0
H…H	65.4	63.4	55.3	53.6	31.0
Cl…H	5.0	0	3.5	0	0
BrH	0	5.1	0	4.0	0