#### **Electronic Supplementary Information**

#### for

## Self-Assembly of a Triple-Zwitterion in Polar Solutions: hierarchical Formation of Nanostructures

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### 1. <sup>1</sup>H NMR dilution studies



*Figure S1.* Inversion of the <sup>1</sup>H NMR signal integral by changing binding mode from *intra*- to *inter*molecular with increasing concentration: pyrrole  $NH_{intra}$ : pyrrole  $NH_{inter} \approx 1.2 : 1.9 (1 \text{ mM})$  and 2 : 0.9 (40 mM).



*Figure S2.* <sup>1</sup>H NMR dilution row for triple-zwitterion 1 in a concentrations range from 1 to 40 mM in DMSO- $d_6$  (from bottom to top).

## 2. <sup>1</sup>H DOSY NMR studies

	1 (2 mM)	1 (20 mM)	7 (2 mM)
PULPROG	dstebpgp3s	dstebpgp3s	dstebpgp3s
TD[F2]	64K	64K	64K
TD[F1]	32	32	32
NS	384	128	512
DS	64	64	64
D20	50 ms	50 ms	100 ms
D21	5 ms	5 ms	5 ms
P30	5.4 ms	5.4 ms	5.4 ms
P19	1.1 ms	1.1 ms	1.1 ms
GPZ6	100 %	100 %	100 %
GPZ7	-13.17	-13.17	-13.17
GPZ8	-17.13	-17.13	-17.13

#### *Table S1.* Acquisition parameters for the DOSY experiments

#### *Table S2.* 1 (2 mM, *T* = 303.4 K)

$\delta$ [ppm]	$D \cdot 10^{-11}  [\text{m}^2/\text{s}]$	$\log D$	
14.673	8.905	-10.050	
12.628	9.131	-10.039	
12.371	9.042	-10.044	
11.069	7.150	-10.146	
3.758	7.937	-10.100	
3.326	$8.068 \cdot 10^{-10}$	-9.093	water
2.868	7.643	-10.117	
2.503	$6.196 \cdot 10^{-10}$	-9.208	DMSO
2.188	7.847	-10.105	
2.096	7.725	-10.112	
0.000	$6.029 \cdot 10^{-10}$	-9.220	TMS

*Table S3.* **1** (20 mM, *T* = 303.4 K)

$\delta$ [ppm]	$D \cdot 10^{-11}  [\text{m}^2/\text{s}]$	$\log D$	
14.627	8.688	-10.061	
12.625	6.185	-10.209	
12.383	8.470	-10.072	
11.069	7.150	-10.146	
7.998	6.817	-10.166	
3.760	6.650	-10.177	
3.339	$7.820 \cdot 10^{-10}$	-9.107	water
2.870	6.320	-10.199	
2.504	$6.083 \cdot 10^{-10}$	-9.216	DMSO
2.179	6.050	-10.218	
0.000	5.735 · 10 <sup>-10</sup>	-9.241	TMS

$\delta$ [ppm]	$D \cdot 10^{-11} [\text{m}^2/\text{s}]$	$\log D$	
7.691	1.154	-9.953	
4.246	1.096	-9.960	
3.326	8.417	-9.075	water
3.057	1.098	-9.959	
2.924	1.082	-9.966	
2.505	6.535	-9.185	DMSO
2.432	1.112	-9.954	
2.262	1.089	-9.963	
2.160	1.093	-9.961	
1.469	1.091	-9.962	
1.290	1.105	-9.957	
0.003	6.213	-9.207	TMS

#### *Table S4.* 7 (2 mM, *T* = 303.4 K)

*Table S5.* Mean diffusion coefficients and corresponding hydrodynamic radii

	$\emptyset D [m^2/s]$	$r_H \cdot 10^{-9}  [m]$
1 (2 mM)	8.15 · 10 <sup>-11</sup>	1.37
1 (20 mM)	6.98 · 10 <sup>-11</sup>	1.60
7 (2 mM)	$1.59 \cdot 10^{-10}$	0.70

#### 3. Molecular Modelling



*Figure S3.* Calculated structure of dimeric 1. The *intermolecular* binding motive is shown in green. Both *intramolecular* binding motives are shown in yellow. Non-polar hydrogen atoms are omitted for clarity.



*Figure S4.* End-capped tetramer as repeating element for the self-assembly of 1 (one capped dimer is highlighted in yellow; non-polar hydrogen atoms are omitted for clarity).

*Table S6.* Distances between the central nitrogen atoms of the *tren*-linker (A-A) and the maximum distance of the exterior binding motifs (B-B) as derived from the molecular mechanics calculations [Å].

A-A	B-B
23,5	34,6
22,6	33,5
24,2	33,2
22,1	20,6
19,9	32,4
24,9	29,8

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24.5	20.5
24,5	23,3
20,3	27,1
24,7	26,5
22,3	20,8
24,5	29,7
20,3	27,3
22,5	33,4
23,9	33,9
25	34,6
23,2	30,5
25,4	36,4
23,7	37,2
22,8	30
24,3	35,4
18,2	27,8
24,4	26
22,2	34,8
23,2	32,9
19,1	27,1
23,4	34,4
22	34,4
24,1	22,1
22,3	31,9
20,9	30
21,7	24,3
24,5	33,4
22,7	35,7
20,9	23,9
22,8	32,8
21,1	30,1
19,4	25,5
22,9	21,7
23,5	37,5
23,6	27,8
23,3	33,8
16,5	34,7
21	27,6
24,1	32,7
23,6	36,7
23	24,7
33,4	33,5
17,6	30,3
20.5	28,9
20,3	<i>.</i>
20,5	28,9
20,5 22,6 23,5	28,9 34,9

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22,2	34,6
19,9	30,4
23,3	31,1
23,4	32,8
19,6	28,6
22,8	24,4
23,3	33,2
24,1	31,9
Ø 22,7	Ø 30,6











