

## Supplementary Material

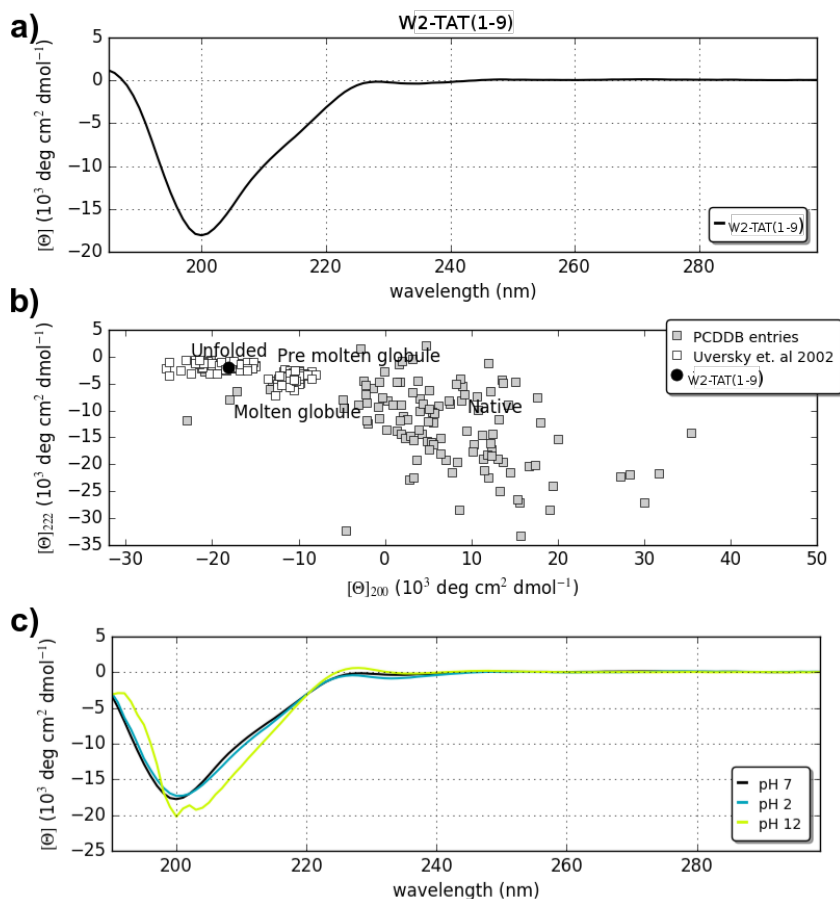
# NMR spectroscopic studies of a TAT-derived model peptide in imidazolium-based ILs: influence on chemical shifts and the *cis/trans* equilibrium state

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**Fig. S 1:** **a)** Far UV-CD spectra of the W2-TAT(1-9) peptide dissolved in water. Circular dichroism (CD) spectra were recorded on a JASCO J-710 CD spectropolarimeter at 303.2 K in a 1 mm quartz cuvette to estimate the secondary structure content. The instrument was calibrated with D-10-camphorsulphonic acid (Sigma Aldrich). The peptide concentration was 157  $\mu\text{M}$  and verified spectrophotometrically at 280 nm with the extinction coefficient calculated using ProtParam (<http://web.expasy.org/protparam/>). Each CD spectrum represents the average of 3 accumulated scans at 20 nm/ min with a 1 nm slit width and a time constant of 2 s for a nominal resolution of 0.7 nm. Data were collected between 185 and 320 nm by taking points every 1 nm. No further zeroing was applied after background subtraction. Data were processed and visualized with CAPITO [1]. **b)** The ‘double wavelength’ plot ( $[\Theta]_{200}$  plotted versus  $[\Theta]_{222}$ ) allows to deduce the folding state of TAT(W2) [2]. **c)** Far UV-CD spectra of the TAT(W2) collected at pH 7 (black), pH 2 (blue) and pH 12 (green). Experimental conditions as described above.

**Table S 1:** The secondary structure elements of W2-TAT(1-9) estimated from CD spectrum. Estimation of structural contents are given in percent.

	helical	$\beta$ -strand	irregular
CAPITO <sup>a</sup>	4–13	18–41	55–69
SELCON3 <sup>b</sup>	10	29	61
CONTIN <sup>b</sup>	8	33	59
CDSSTR <sup>b</sup>	6	33	61
DSSP <i>trans</i> W2-TAT(1-9) <sup>c</sup>	0	33	67
DSSP <i>cis</i> W2-TAT(1-9) <sup>c</sup>	0	55	45

<sup>a</sup> [1]

<sup>b</sup> included in the software CDPro [3]

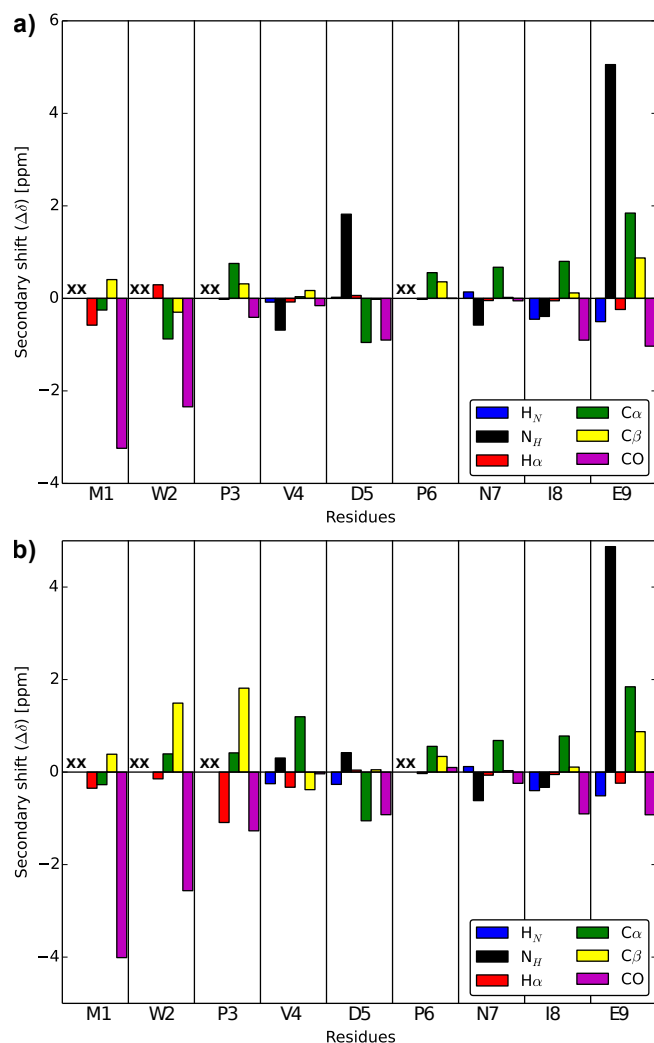
<sup>c</sup> secondary structure determination based on the ROE calculated structures [4]

**Table S 2:**  $^1\text{H}$ ,  $^{13}\text{C}$  and  $^{15}\text{N}$  chemical shift assignments of the *trans* configured W2-TAT(1-9) peptide in aqueous solution (90%  $\text{H}_2\text{O}$ /10%  $\text{D}_2\text{O}$  (v/v), pH 6.5) at 303.2 K

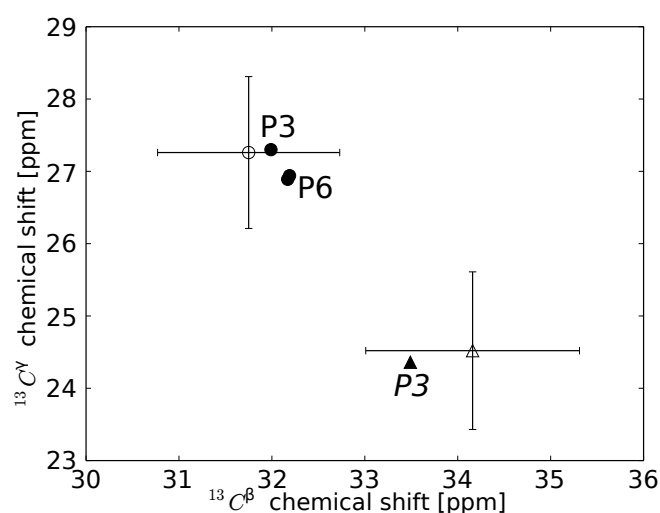
	H	N	$\text{N}^\delta$	$\text{N}^\epsilon$	$\text{H}^\alpha$	$\text{H}^\beta$	$\text{H}^\gamma$	$\text{H}^\delta$	$\text{H}^\epsilon$	$\text{H}^\zeta$	$\text{H}^\eta$	C	$\text{C}^\alpha$	$\text{C}^\beta$	$\text{C}^\gamma$	$\text{C}^\delta$	$\text{C}^\epsilon$	$\text{C}^\zeta$	$\text{C}^\eta$
M1					3.92	2.03,2.03	2.48,2.48		2.02			172.62	55.31	33.18	30.93		16.76		
W2				129.38	5.02	3.15,3.34		7.29	10.13,7.71	7.18,7.51	7.26	174.10	55.14	29.10	111.33	129.47,127.70	120.97,138.89	122.25,114.86	124.83
P3					4.45	2.24,1.89	1.96,1.96	3.78,3.49				176.48	63.31	31.99	27.30	50.86			
V4	8.00	119.83			4.09	2.01	0.92,0.92					175.65	62.05	33.03	20.48,20.48				
D5	8.31	125.63			4.84	2.54,2.79						174.81	52.06	41.54	179.94				
P6					4.41	2.22,1.93	1.95,1.95	3.81,3.81				176.80	63.50	32.19	26.94	50.88			
N7	8.52	118.03	114.08		4.68	2.80,2.75		7.76,6.90				175.08	53.74	38.96	177.29				
I8	7.75	120.40			4.19	1.90	0.90,1.42,1.16	0.86				175.19	61.34	38.97	27.07,17.50	12.98			
E9	7.89	129.76			4.11	1.99,1.88	2.18,2.18					180.92	58.19	31.30	36.67	184.64			

**Table S 3:**  $^1\text{H}$ ,  $^{13}\text{C}$  and  $^{15}\text{N}$  chemical shift assignments of the *cis* configured W2-TAT(1-9) peptide in aqueous solution (90%  $\text{H}_2\text{O}$ /10%  $\text{D}_2\text{O}$  (v/v), pH 6.5) at 303.2 K

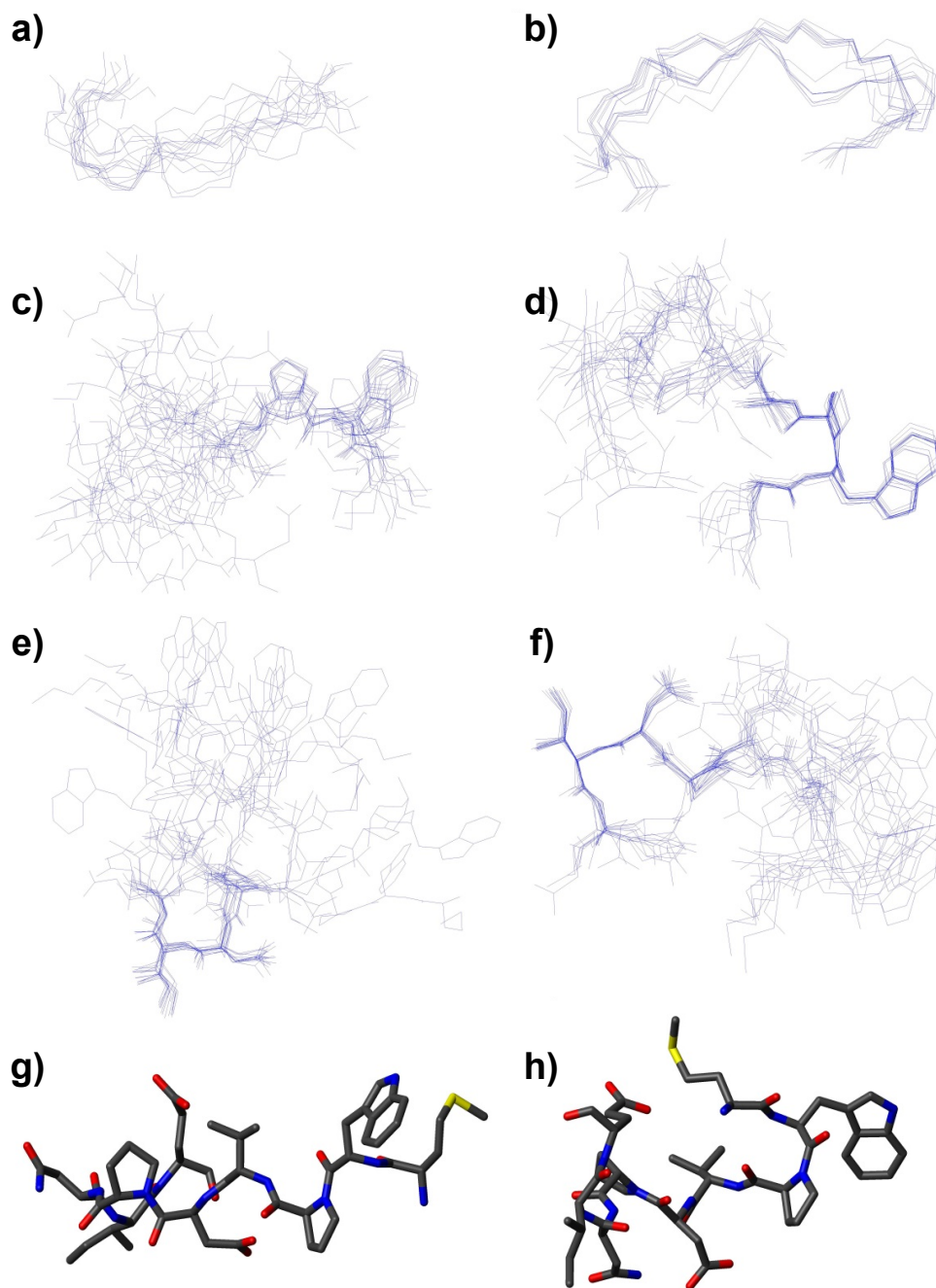
	H	N	$\text{N}^\delta$	$\text{N}^\epsilon$	$\text{H}^\alpha$	$\text{H}^\beta$	$\text{H}^\gamma$	$\text{H}^\delta$	$\text{H}^\epsilon$	$\text{H}^\zeta$	$\text{H}^\eta$	C	$\text{C}^\alpha$	$\text{C}^\beta$	$\text{C}^\gamma$	$\text{C}^\delta$	$\text{C}^\epsilon$	$\text{C}^\zeta$	$\text{C}^\eta$
M1					4.15	2.16,2.16	2.61,2.61		2.15			171.85	55.29	33.16	30.89		16.81		
W2				130.13	4.58	3.29,3.16		7.27	10.21,7.60	7.17,7.52	7.26	173.88	56.41	30.89	110.89	129.41,127.48	120.86,138.97	122.25,114.86	124.81
P3					3.38	1.60,1.07	1.42,1.47	3.21,3.37				175.62	62.97	33.49	24.36	49.99			
V4	7.83	120.82			3.84	1.99	0.89,0.89					175.77	63.21	32.48	21.07,21.07				
D5	8.02	124.23			4.82	2.74,2.47						174.79	51.96	41.61	179.74				
P6					4.40	2.22,1.95	1.93,1.93	3.77,3.77				176.90	63.50	32.17	26.89	50.84			
N7	8.50	117.99	114.03		4.66	2.80,2.74		7.72,6.89				174.89	53.75	38.97	177.38				
I8	7.80	120.46			4.19	1.90	1.16,1.42,0.88	0.85				175.19	61.32	38.96	27.06,17.46	12.98			
E9	7.88	129.58			4.11	2.00,1.87	2.18,2.18					180.90	58.19	31.30	36.67	184.59			



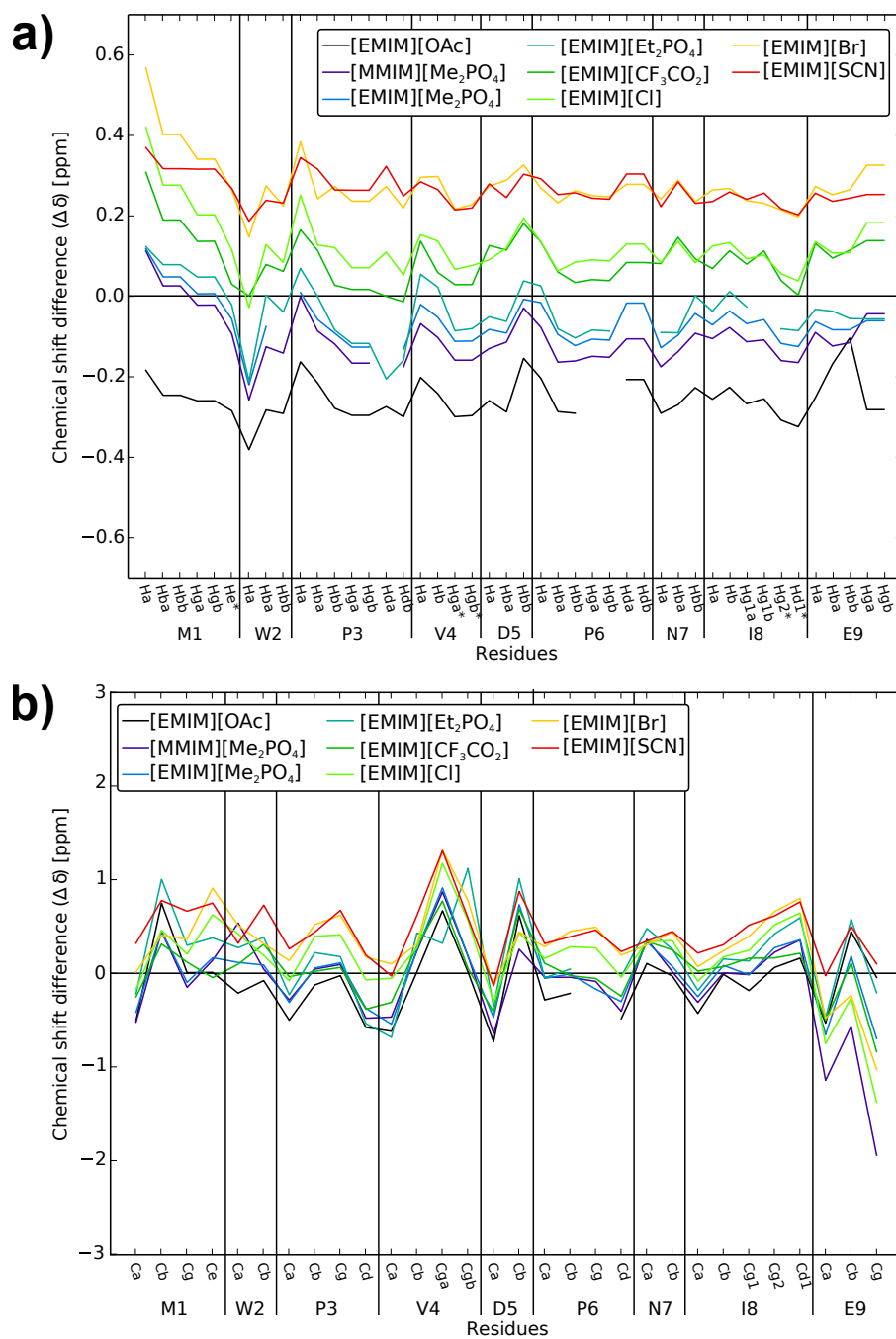
**Fig. S 2:** Secondary chemical shifts of the W2-TAT(1-9) *all-trans* (a) and *cis* (b) isoform. Secondary shifts are defined as the difference between the observed chemical shift and the corresponding random coil value. Random coil chemical shifts of the W2-TAT(1-9) peptide were calculated using the CamCoil webserver [5].



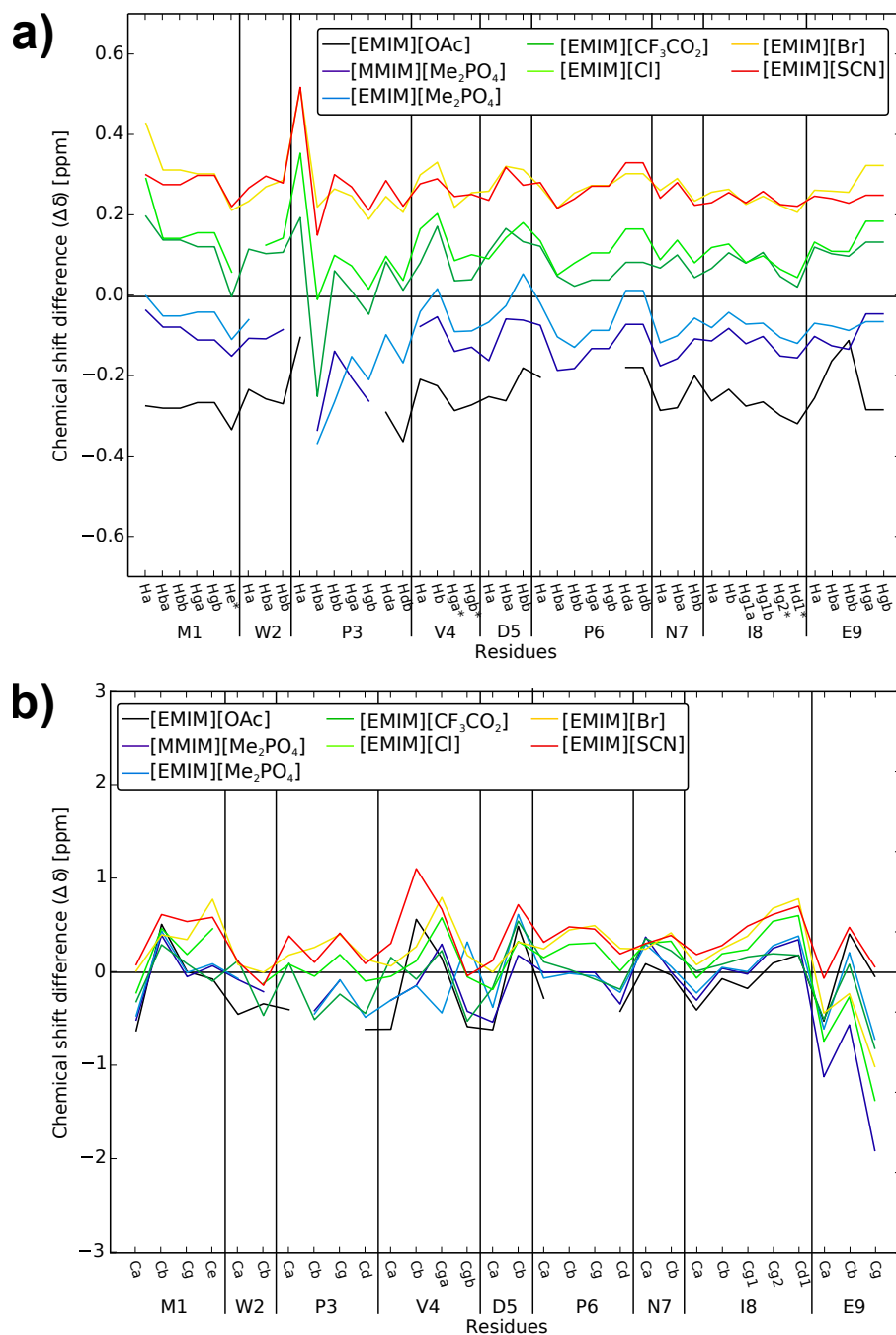
**Fig. S 3:** Proline  $^{13}\text{C}^\beta$  and  $^{13}\text{C}^\gamma$  chemical shift analysis for the *cis*- and *all-trans*-configured W2-TAT(1-9) peptide. Filled circles and filled triangle correspond to the chemical shifts characteristics of the numbered amino acids. The average  $^{13}\text{C}^\beta$  and  $^{13}\text{C}^\gamma$  chemical shifts for *cis* and *trans* proline is given by open triangle and open circle, respectively [6, 7]. Standard deviations are indicated by bars.



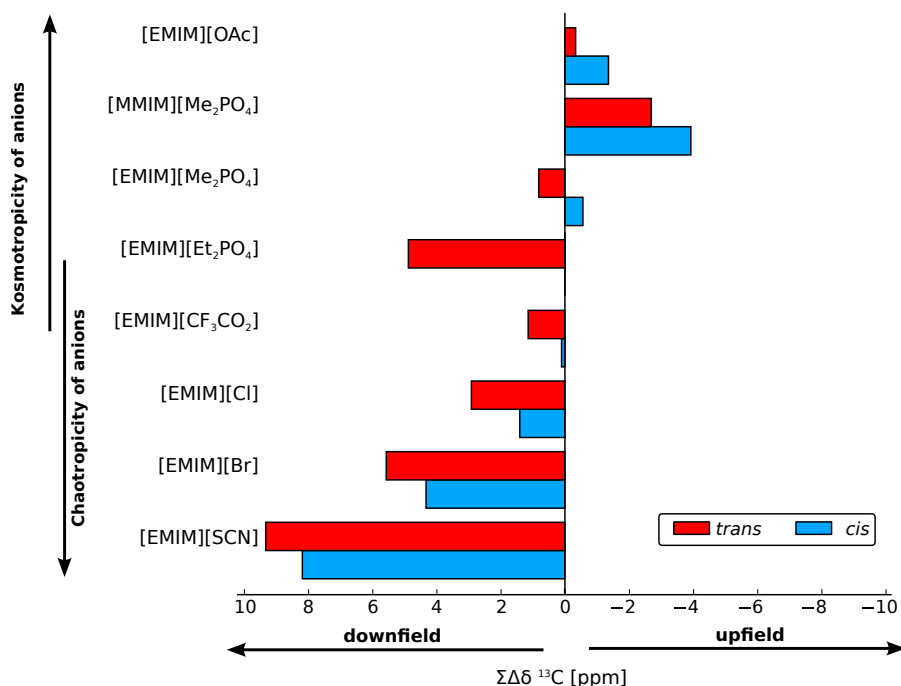
**Fig. S 4:** NMR solution structures of the *all-trans* (a,c,e,g) and *cis* (b,d,f,h) isoform of the W2-TAT(1-9) peptide. (a,b) Superimposed backbone traces for the 15 structures with the lowest energy after OPAL refinement. In the *all-trans* conformer residues 6-9 superimpose with a backbone r.m.s.d. of 0.58 and resemble a turn-like structure (e) whilst the more N-terminal residues are disordered (c). In contrast, in the *cis* conformer the residues M1-V4 (d) and P6-E9 (f) superimpose with r.m.s.d. values of 0.23 and 0.30, respectively, indicating the higher structural definition of the *cis* conformer. Although no standard turn elements could be deduced, in both, the N- and C-terminal stretches these loop elements revert the backbone direction by 180° (*all-trans* (g), *cis* (h)).



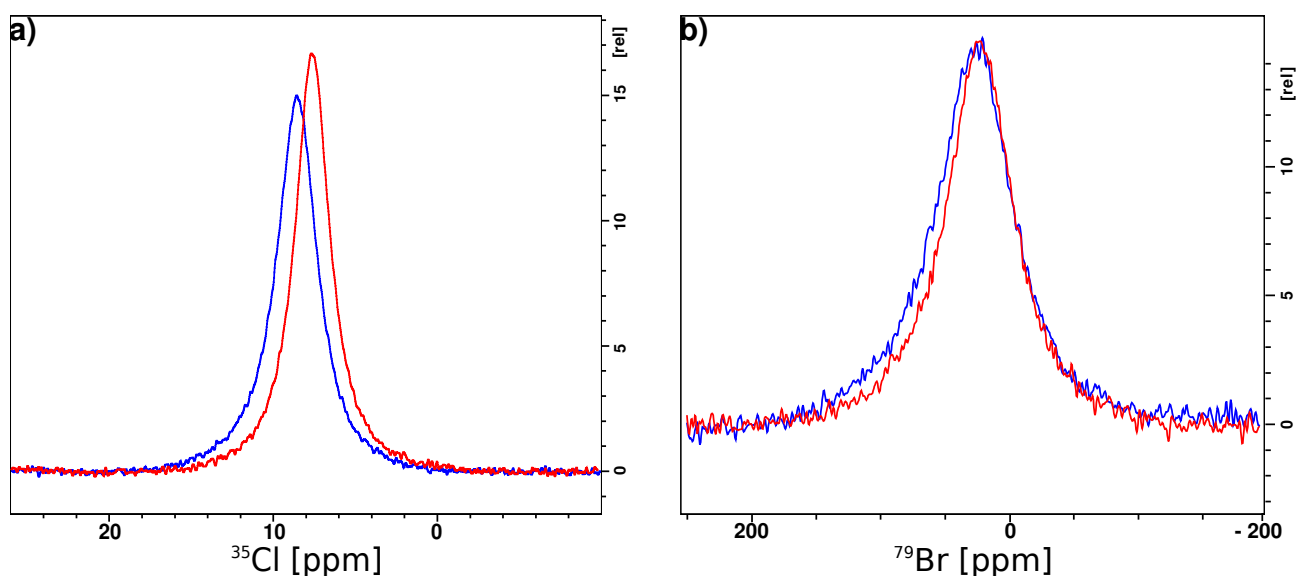
**Fig. S 5:**  $^1\text{H}$  (a) and  $^{13}\text{C}$  (b) NMR chemical shift differences ( $\Delta\delta$ ) of *all-trans*-configured W2-TAT(1-9) in various IL/ solvent systems at 303 K. W2-TAT(1-9) concentration in IL/ solvent systems was 90 mM and 10 mM in the reference water system, respectively. The IL concentration was 3 M (approximately 70% IL/30% D<sub>2</sub>O v/v). In all experiments pH was adjusted to 6.5.



**Fig. S 6:**  $^1\text{H}$  (a) and  $^{13}\text{C}$  (b) NMR chemical shift differences ( $\Delta\delta$ ) of *cis*-configured W2-TAT(1-9) in various IL solvent systems at 303 K. W2-TAT(1-9) concentration in IL/ solvent systems was 90 mM and 10 mM in the reference water system, respectively. The IL concentration was 3 M (approximately 70% IL/30% D<sub>2</sub>O v/v). In all experiments pH was adjusted to 6.5. The spectral quality of the 3M [EMIM][Et<sub>2</sub>PO<sub>4</sub>] sample allows only the assignment of a few unambiguous *cis*-configured W2-TAT(1-9) signals.

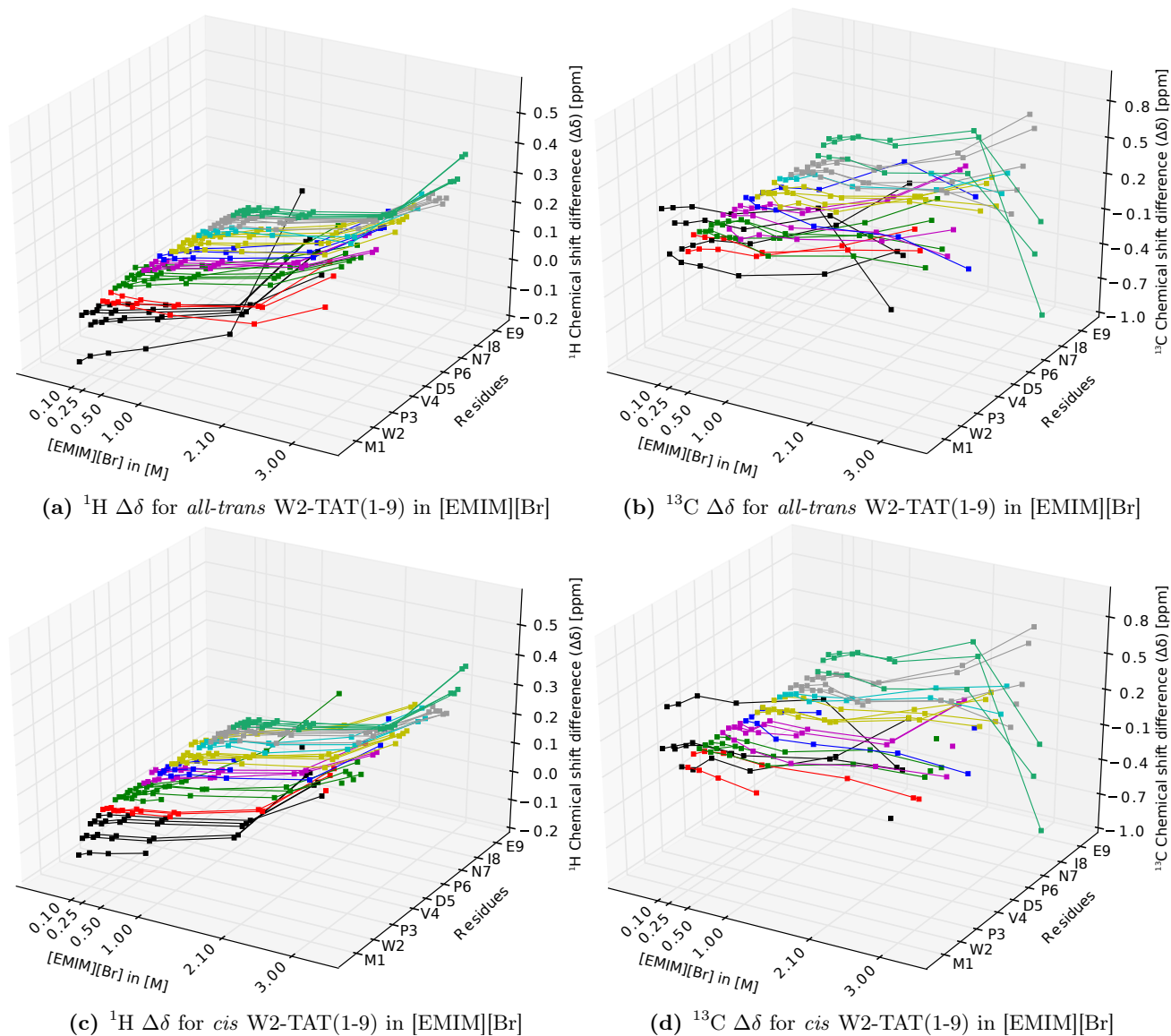


**Fig. S 7:** Summed up  $^{13}\text{C}$  chemical shift differences ( $\sum \Delta\delta$ ) of selected carbons for *cis*-(blue) and *all-trans*-configured (red) W2-TAT(1-9) peptide in different IL solvent systems.

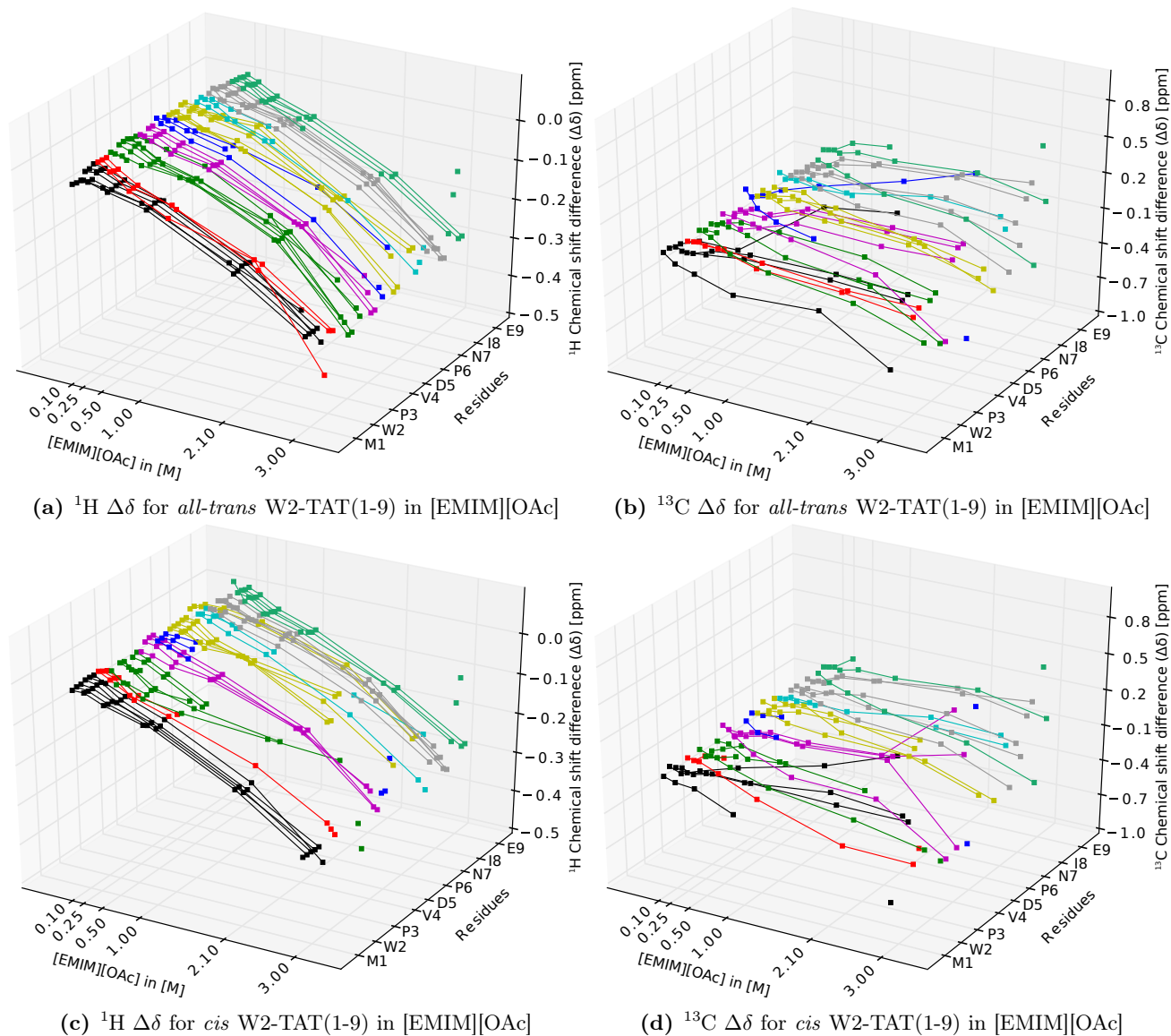


**Fig. S 8:** **a)**  $^{35}\text{Cl}$  chemical shifts of pure [EMIM][Cl] (7.66 ppm, red line) and in the presence of 10 mM W2-TAT(1-9) peptide (8.56 ppm, blue line). **b)**  $^{79}\text{Br}$  chemical shifts of pure [EMIM][Br] (23.6 ppm, red line) and in the presence of 10 mM W2-TAT(1-9) peptide (30.7 ppm, blue line). Spectra were collected at 303 K on a Bruker 400 MHz AvanceIII system equipped with a 5 mm room-temperature double resonance broad band probe and 32 transients. The probe was tuned to the appropriate frequencies. The spectral width for  $^{35}\text{Cl}$  was 2354 Hz with transmitter frequency offset of 0 Hz and acquisition time was 0.217 s with a recycle delay of 1 s. The  $^{35}\text{Cl}$  pulse length was 14  $\mu\text{s}$  at 90 W. The spectral width for  $^{79}\text{Br}$  was 10 kHz with transmitter frequency offset of 1303.23 Hz and acquisition time was 0.00512 s with a recycle delay of 1 s. The  $^{79}\text{Br}$  pulse length was 8  $\mu\text{s}$  at 60 W. The  $^{35}\text{Cl}$  chemical shifts were referenced to 0.1 M NaCl solution in  $\text{D}_2\text{O}$ . The  $^{79}\text{Br}$  chemical shifts were referenced to 0.1 M KBr solution in  $\text{D}_2\text{O}$ .

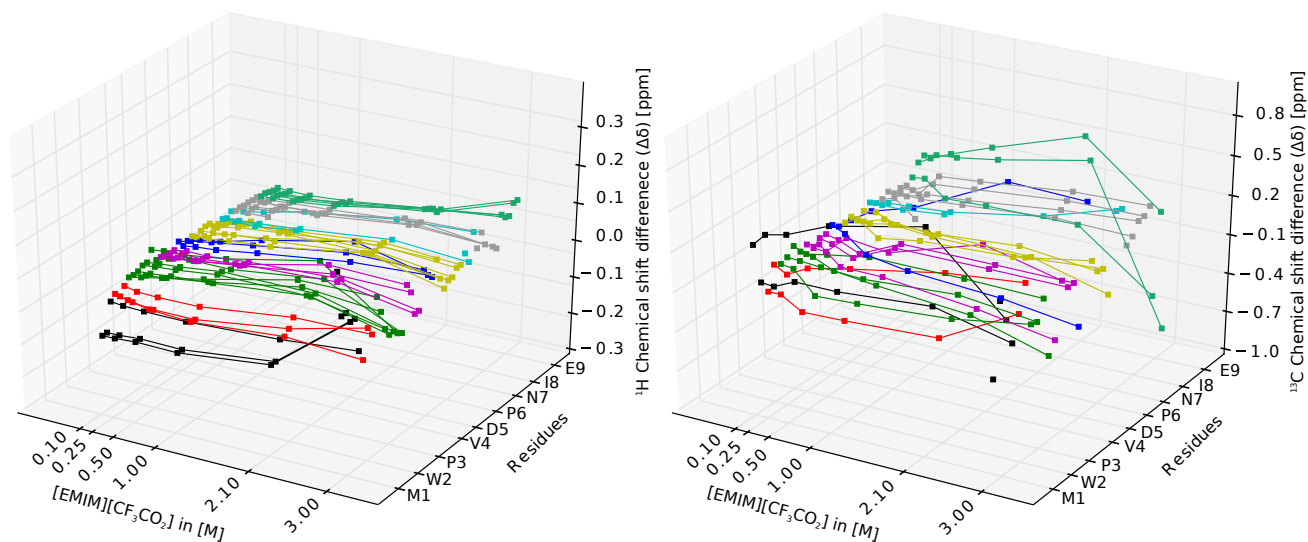




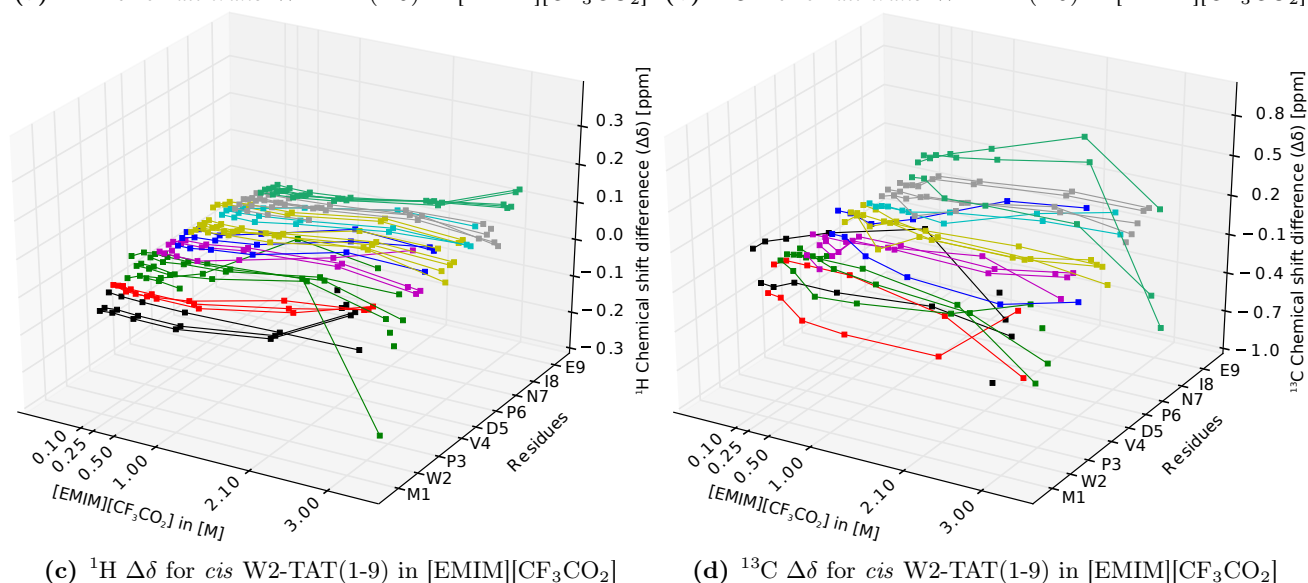
**Fig. S 9:**  $^1\text{H}$  and  $^{13}\text{C}$  chemical shift differences ( $\Delta\delta$ ) of protons and carbons for *all-trans*- (upper panel) and *cis*-configured (lower panel) W2-TAT(1-9) as function of [EMIM][Br] concentration. The reference system was 10 mM W2-TAT(1-9), pH 6.5, in 90/10%  $\text{H}_2\text{O}/\text{D}_2\text{O}$ . The peptide concentration was 10 mM for samples up to 2.1 M [EMIM][Br] and experiments were carried out with a 5 mm room-temperature BBI-probe. Spectra for 3 M [EMIM][Br] were carried out with a 4 mm triple resonance HR-MAS probe at 6 kHz spinning rate and a W2-TAT(1-9) concentration of 90 mM. All NMR experiments were acquired at 303 K and the pH was adjusted to 6.5. Depicted are all  $^1\text{H}$  and  $^{13}\text{C}$   $\Delta\delta$  in sequential order per residue as given in Fig. S5 and S6.



**Fig. S 10:**  $^1\text{H}$  and  $^{13}\text{C}$  chemical shift differences ( $\Delta\delta$ ) of protons and carbons for *all-trans*- (upper panel) and *cis*-configured (lower panel) W2-TAT(1-9) as function of [EMIM][OAc] concentration. The reference system was 10 mM W2-TAT(1-9), pH 6.5, in 90/10%  $\text{H}_2\text{O}/\text{D}_2\text{O}$ . The peptide concentration was 10 mM for samples up to 2.1 M [EMIM][OAc] and experiments were carried out with a 5 mm room-temperature BBI-probe. Spectra for 3 M [EMIM][OAc] were carried out with a 4 mm triple resonance HR-MAS probe at 6 kHz spinning rate and a W2-TAT(1-9) concentration of 90 mM. All NMR experiments were acquired at 303 K and the pH was adjusted to 6.5. Depicted are all  $^1\text{H}$  and  $^{13}\text{C}$   $\Delta\delta$  in sequential order per residue as given in Fig. S5 and S6.

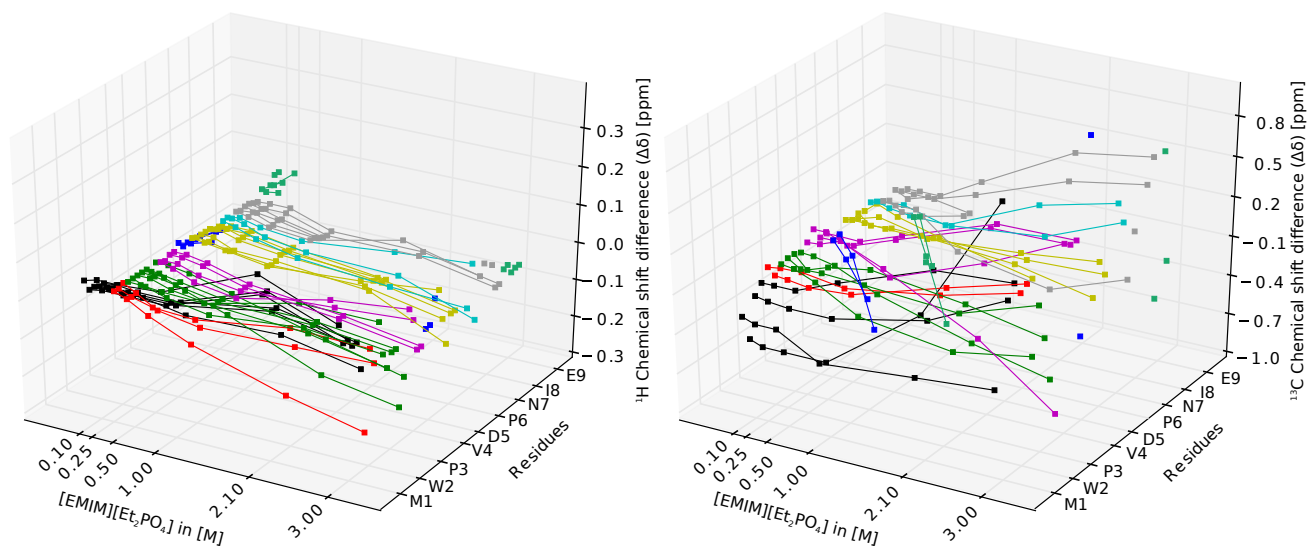


(a)  $^1\text{H}$   $\Delta\delta$  for *all-trans* W2-TAT(1-9) in [EMIM][CF<sub>3</sub>CO<sub>2</sub>] (b)  $^{13}\text{C}$   $\Delta\delta$  for *all-trans* W2-TAT(1-9) in [EMIM][CF<sub>3</sub>CO<sub>2</sub>]

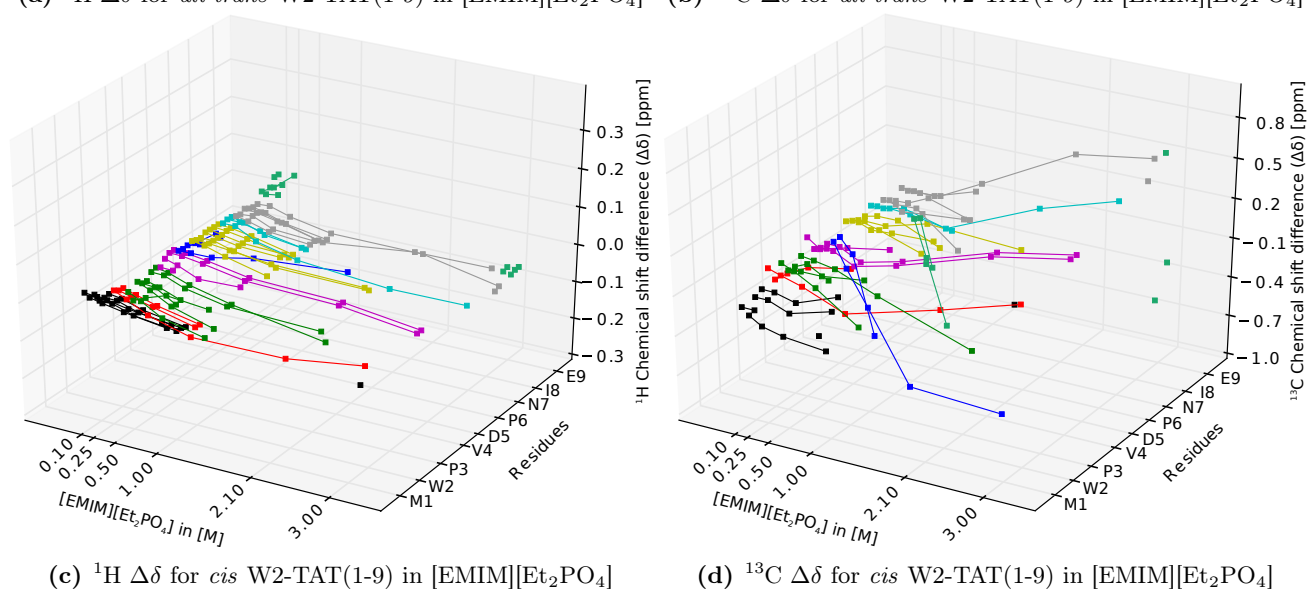


(c)  $^1\text{H}$   $\Delta\delta$  for *cis* W2-TAT(1-9) in [EMIM][CF<sub>3</sub>CO<sub>2</sub>] (d)  $^{13}\text{C}$   $\Delta\delta$  for *cis* W2-TAT(1-9) in [EMIM][CF<sub>3</sub>CO<sub>2</sub>]

**Fig. S 11:**  $^1\text{H}$  and  $^{13}\text{C}$  chemical shift differences ( $\Delta\delta$ ) of protons and carbons for *all-trans*- (upper panel) and *cis*-configured (lower panel) W2-TAT(1-9) as function of [EMIM][CF<sub>3</sub>CO<sub>2</sub>] concentration. The reference system was 10 mM W2-TAT(1-9), pH 6.5, in 90/10% H<sub>2</sub>O/D<sub>2</sub>O. The peptide concentration was 10 mM for samples up to 2.1 M [EMIM][CF<sub>3</sub>CO<sub>2</sub>] and experiments were carried out with a 5 mm room-temperature BBI-probe. Spectra for 3 M [EMIM][CF<sub>3</sub>CO<sub>2</sub>] were carried out with a 4 mm triple resonance HR-MAS probe at 6 kHz spinning rate and a W2-TAT(1-9) concentration of 90 mM. All NMR experiments were acquired at 303 K and the pH was adjusted to 6.5. Depicted are all  $^1\text{H}$  and  $^{13}\text{C}$   $\Delta\delta$  in sequential order per residue as given in Fig. S5 and S6.



(a)  $^1\text{H}$   $\Delta\delta$  for *all-trans* W2-TAT(1-9) in [EMIM][Et<sub>2</sub>PO<sub>4</sub>] (b)  $^{13}\text{C}$   $\Delta\delta$  for *all-trans* W2-TAT(1-9) in [EMIM][Et<sub>2</sub>PO<sub>4</sub>]



(c)  $^1\text{H}$   $\Delta\delta$  for *cis* W2-TAT(1-9) in [EMIM][Et<sub>2</sub>PO<sub>4</sub>]

(d)  $^{13}\text{C}$   $\Delta\delta$  for *cis* W2-TAT(1-9) in [EMIM][Et<sub>2</sub>PO<sub>4</sub>]

**Fig. S 12:**  $^1\text{H}$  and  $^{13}\text{C}$  chemical shift differences ( $\Delta\delta$ ) of protons and carbons for *all-trans*- (upper panel) and *cis*-configured (lower panel) W2-TAT(1-9) as function of [EMIM][Et<sub>2</sub>PO<sub>4</sub>] concentration. The reference system was 10 mM W2-TAT(1-9), pH 6.5, in 90/10% H<sub>2</sub>O/D<sub>2</sub>O. The peptide concentration was 10 mM for samples up to 2.1 M [EMIM][Et<sub>2</sub>PO<sub>4</sub>] and experiments were carried out with a 5 mm room-temperature BBI-probe. Spectra for 3 M [EMIM][Et<sub>2</sub>PO<sub>4</sub>] were carried out with a 4 mm triple resonance HR-MAS probe at 6 kHz spinning rate and a W2-TAT(1-9) concentration of 90 mM. All NMR experiments were acquired at 303 K and the pH was adjusted to 6.5. Depicted are all  $^1\text{H}$  and  $^{13}\text{C}$   $\Delta\delta$  in sequential order per residue as given in Fig. S5 and S6.

**Table S 4:** Linear regression analysis of W2-TAT(1-9)  $^1\text{H}$  and  $^{13}\text{C}$  chemical shifts in different ILs as shown in Figure S9-12. The slope is given in  $\Delta\delta/\text{M}$  [ppm/M] IL.

	<i>trans</i>		<i>cis</i>	
	$^1\text{H}$	$^{13}\text{C}$	$^1\text{H}$	$^{13}\text{C}$
[EMIM][Br]	0.083±0.019	0.119±0.074	0.092±0.029	0.071±0.046
[EMIM][Et <sub>2</sub> PO <sub>4</sub> ]	-0.024±0.034	-0.059±0.153	-0.047±0.037	-0.123±0.252
[EMIM][CF <sub>3</sub> CO <sub>2</sub> ]	0.013±0.021	-0.001±0.083	0.010±0.041	-0.035±0.117
[EMIM][OAc]	-0.096±0.019	-0.108±0.069	-0.067±0.035	-0.101±0.123

**Table S 5:** Effect of ILs and 0.5 M LiCl in TFE on the W2-TAT(1-9) *all-trans/cis* equilibrium state obtained by  $^1\text{H}$  NMR spectroscopy. Presented are the *cis*-population contents. Conditions: 10 mM W2-TAT(1-9), pH adjusted to 6.5, were dissolved in the respective IL. The reference system was 10 mM W2-TAT(1-9), pH 6.5, in 90/10% H<sub>2</sub>O/D<sub>2</sub>O.

Solvent system	IL concentration						
	0 M	0.1 M	0.25 M	0.5 M	1 M	2.1 M	3 M
H <sub>2</sub> O/D <sub>2</sub> O	0.46						
TFE-d <sub>3</sub> / 0.5M LiCl	0.64						
[EMIM][OAc]	0.47	0.48	0.46	0.42	0.38	0.32	0.27
[MMIM][Me <sub>2</sub> PO <sub>4</sub> ]	0.49	0.42	0.39	0.36	0.32	0.30	0.29
[EMIM][Me <sub>2</sub> PO <sub>4</sub> ]	0.47	0.40	0.36	0.33	0.29	0.28	0.29
[EMIM][Et <sub>2</sub> PO <sub>4</sub> ]	0.48	0.48	0.47	0.44	0.43	0.37	0.33
[EMIM][CF <sub>3</sub> CO <sub>2</sub> ]	0.45	0.38	0.34	0.29	0.26	0.27	0.29
[EMIM][Cl]	0.47	0.45	0.42	0.39	0.37	0.35	0.31
[EMIM][Br]	0.47	0.39	0.36	0.35	0.31	0.35	0.30
[EMIM][SCN]	0.46	0.40	0.38	0.35	0.35	0.25	0.29

## References Supplementary Data

- [1] Christoph Wiedemann, Peter Bellstedt, and Matthias Görlach. Capito—a web server-based analysis and plotting tool for circular dichroism data. *Bioinformatics*, 29(14):1750–1757, Jul 2013.
- [2] Vladimir N. Uversky. Natively unfolded proteins: a point where biology waits for physics. *Protein Sci*, 11(4):739–756, Apr 2002.
- [3] N. Sreerama and R. W. Woody. Estimation of protein secondary structure from circular dichroism spectra: comparison of CONTIN, SELCON, and CDSSTR methods with an expanded reference set. *Anal Biochem*, 287(2):252–260, Dec 2000.
- [4] W. Kabsch and C. Sander. Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features. *Biopolymers*, 22(12):2577–2637, Dec 1983.
- [5] Alfonso De Simone, Andrea Cavalli, Shang-Te Danny Hsu, Wim Vranken, and Michele Vendruscolo. Accurate random coil chemical shifts from an analysis of loop regions in native states of proteins. *J Am Chem Soc*, 131(45):16332–16333, Nov 2009.
- [6] Mario Schubert, Dirk Labudde, Hartmut Oschkinat, and Peter Schmieder. A software tool for the prediction of Xaa-Pro peptide bond conformations in proteins based on  $^{13}\text{C}$  chemical shift statistics. *J Biomol NMR*, 24(2):149–154, Oct 2002.
- [7] Yang Shen and Ad Bax. Prediction of Xaa-Pro peptide bond conformation from sequence and chemical shifts. *J Biomol NMR*, 46(3):199–204, Mar 2010.