From α-helix to β-sheet – a reversible metal ion induced peptide secondary structure switch

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Supporting information:

Peptide synthesis and purification: All peptides were synthesized by standard Fmoc chemistry on Fmoc-Leu-OWang resin (0,68/0,71 mmol/g) using a 431 A peptide synthesizer (Applied Biosystems, USA). Purification was carried out by preparative reversed phase high-performance liquid chromatography (HPLC) on a Vydac C4 column. The molecular weight of the products was determined by MALDI-TOF mass spectrometry using a Voyager MALDI-TOF Mass spectrometer (PerSeptive Biosystems) and its purity was determined by analytical HPLC.

CD-spectroscopy: CD measurements of peptides in buffer/TFE were carried out on a J-715 spectrometer equipped with a temperature controller (Jasco inc., Easton, MD) using a quartz cell of 1 mm path length. Spectra were recorded at 25 °C from 190-240 nm at 0.5 to 0.2 nm resolution with a scan rate of 20 nm/min and a sensitivity of 50 to 100 mdeg, respectively. Three respectively six scans were acquired and averaged for each sample. Raw data were manipulated by smoothing and subtraction of buffer spectra. CD values were expressed as the mean residue molar ellipticity. As buffer solution 10 mM Tris-HCl-buffer in water adjusted to pH 7,4 was used. Peptide concentration of peptide stock solution was determined by HPLC with UV detection and Abz calibration.

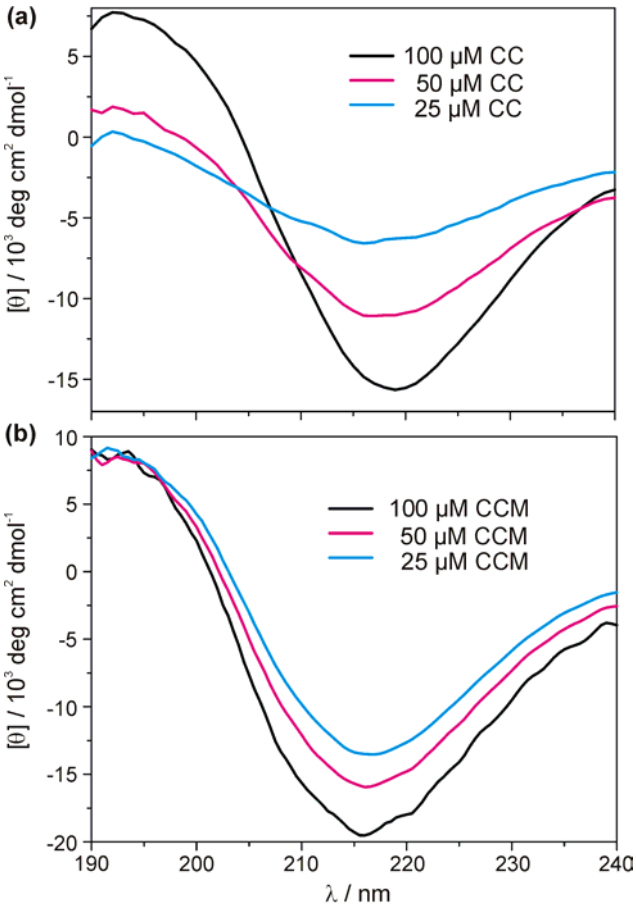

Fig. S1 CD spectra of peptide (a) CC and (b) CCM. All samples were masured in 10 mM Tris-HCl buffer pH 7.4.

CD-spectroscopic investigation of the concentration dependence: To investigate a possible concentrational dependence of the secondary structure of the peptides CC and CCM were measured at different concentrations. Figure S1 show the acquired CD-spectra for peptide CC and CCM respectively.

Influence of TFE on secondary structure: To investigate the influence of TFE on peptide conformation different amounts of TFE were added in order to generate formation of helical peptide folding (see Figure S2).

CD-spectroscopic data for the Cu^{2+} and Zn^{2+} triggered conformational switch: Analogous to peptide CCM Cu^{2+} and Zn^{2+} was added to peptide CC. As shown in Figure S3 the addition to CC does not result in any significant change of its secondary structure. Figure S4 shows the titration of peptide CCM with Cu^{2+}.

Determination of the secondary structure elements content: The calculation of the percentage values for the secondary structure elements α-helix, β-sheet and random coil was carried out with the PEPFIT program.[1] The determined values for the shown CD-spectra are given in Table S1.

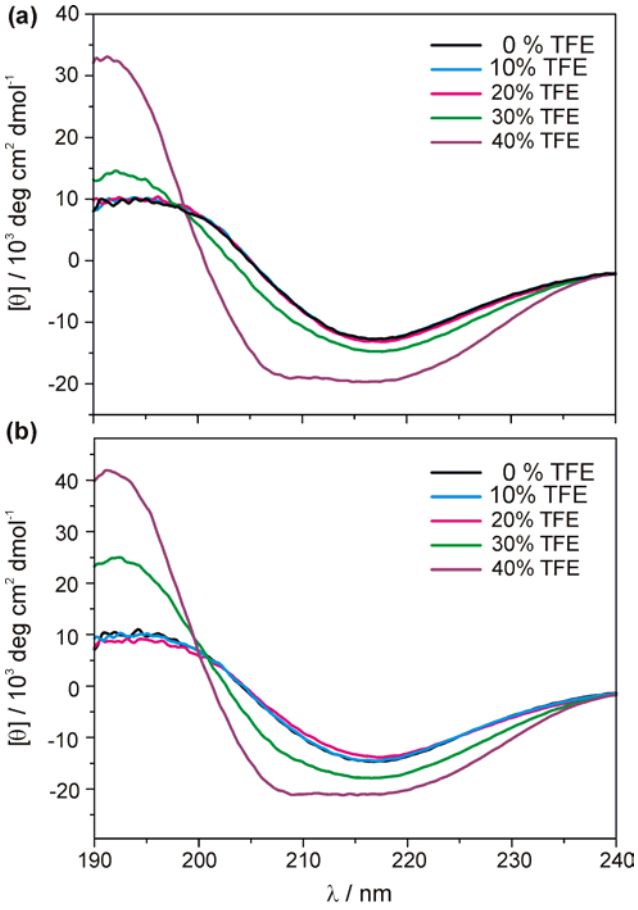

Fig. S2 CD spectra of peptide (a) CC and (b) CCM at different TFE concentrations.

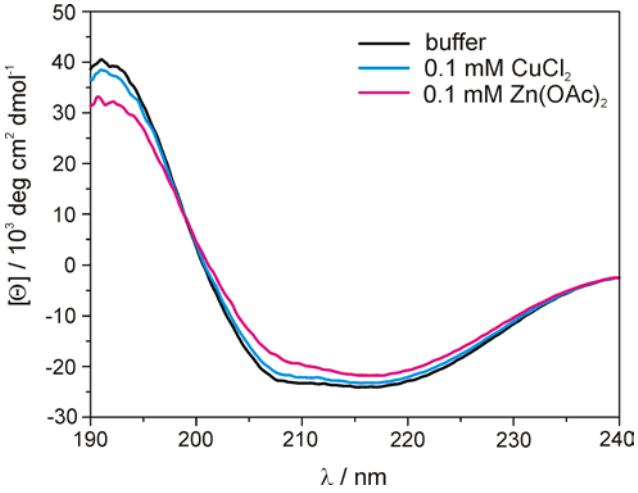

Fig. S3 CD spectra of peptide CC in 40% TFE, in 40% TFE with 0.1 mM $CuCl_2$ and in 40% TFE with 0.1 mM $Zn(OAc)_2$.

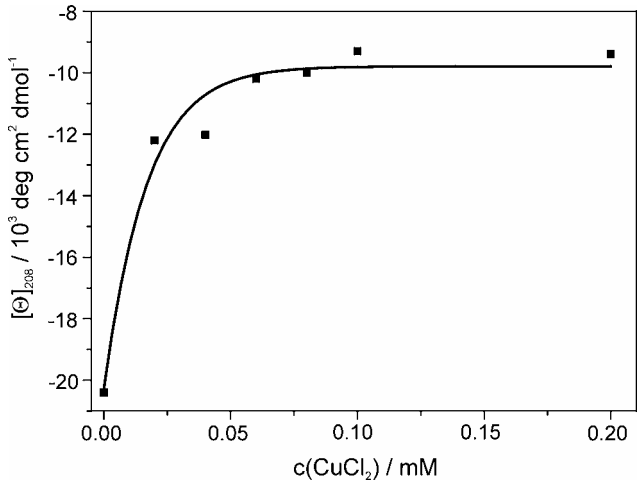

Fig. S4 Cu^{2+} titration profile of 0.1 mM peptide CC (40% TFE, pH 7.4) followed by CD spectroscopy at λ = 208 nm.

Table S1: Content of secondary structure elements determined with PEPFIT.[1]

Figure	Peptide/ Conditions	% α-helix	% β-sheet	% random
2	CC	0	75	25
2	CCM	0	67	33
2	CC 40% TFE	90	10	0
2	CCM 40% TFE	85	15	0
3a	CCM	85	15	0
3a	CCM + Cu^{2+}	10	70	20
3a	CCM + Cu^{2+} + EDTA	90	10	0
3b	CCM	85	15	0
3b	CCM + Zn^{2+}	0	65	35
3b	CCM + Zn^{2+} + EDTA	75	25	0

Notes and references

1 J. Reed, T.A. Reed, *Anal. Biochem.*, 1997, **254**, 36-40.