Two-Metal Ion, Ni(II) and Cu(II), Binding \[\alpha\]-helical Coiled-coil Peptide

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1. Size exclusion chromatography

![Graph a) and b)](image)

Figure S1. A mixture of IZ(5)-2a3aH (20 \(\mu\)M) and CuCl\(_2\) (10 \(\mu\)M) or a mixture of NiCl\(_2\) (10 \(\mu\)M) and CuCl\(_2\) (5 \(\mu\)M) were dissolved in 0.2 ml of 10 mM sodium phosphate buffer at pH 7.0. The samples were applied on Sephadex G-50 (0.6 (i.d.) X 9 cm), and were eluted with the same buffer at pH 7.0. The 90 ml fractions were collected and monitored at a wavelength of 230 nm. As the peptide standards, GCN4-pLI, \(^{1}\) IZ, \(^{2}\) and GCN4-p11 were used for tetramer, trimer, and dimer, respectively. The numbers, 4, 3, and 2, at the top indicate the places where the peptide standards were eluted.

References
2. Sedimentation equilibrium Analysis

Figure S2. Sedimentation equilibrium analysis of the mixture of IZ(5)-2a3adH and Ni(II). It was performed with a Beckman XL-1 Optima Analytical Ultracentrifuge equipped with absorption optics. The total concentrations of the peptide and NiCl₂ were 20 µM and 100 µM, respectively. The sample was centrifuged at 25,000 rpm for 20 hrs at pH 7.0 and 20 °C, and the absorbance was monitored at 280 nm. The oligomerization state was determined by fitting the data to a single species using Origin Sedimentation Equilibrium Single Data Set Analysis (Beckman). The partial specific volume used for the data analysis was 0.756 mL/g for IZ(5)-2a3adH. The data fit to a single ideal species. Apparent molecular mass were 13,122 Da (the calculated molecular mass is 13,279 Da).