

Supporting Information

The influence of protein folding on the copper affinities of trafficking and target sites

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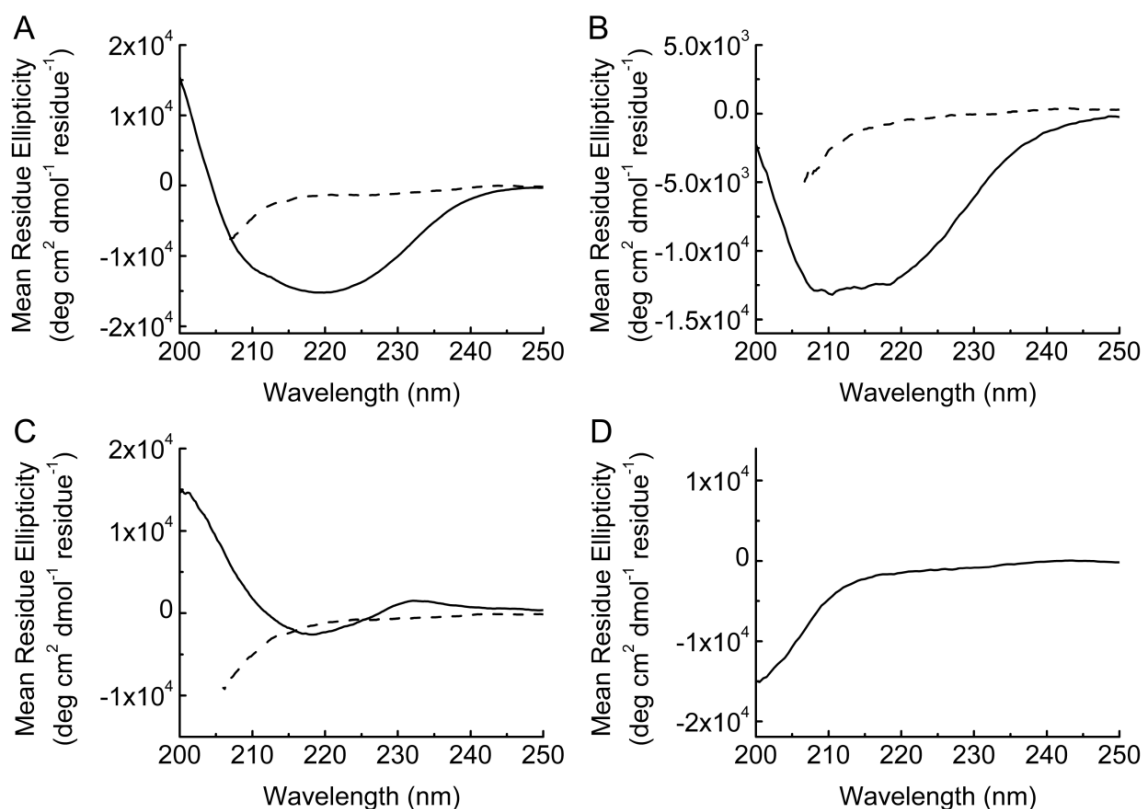


Fig. S1 Far-UV circular dichroism (CD) spectra of apo-HAH1 (A), *S. cerevisiae* apo-Atx1 (B), apo-plastocyanin from *Synechocystis* PCC 6803 (C) and human β -secretase C-terminal domain peptide (BACE1-CTD) (D) in the absence (solid line) and presence (dashed line) of 7 M urea. Protein concentrations were 0.5 mg/ml, except for BACE1-CTD (0.4 mg/ml), and the spectra measured in 20 mM 4-(2-hydroxyethyl)piperazine-1-ethanesulfonic acid (Hepes) containing 200 mM NaCl (200 mM KCl for BACE1-CTD) at pH 7.0.

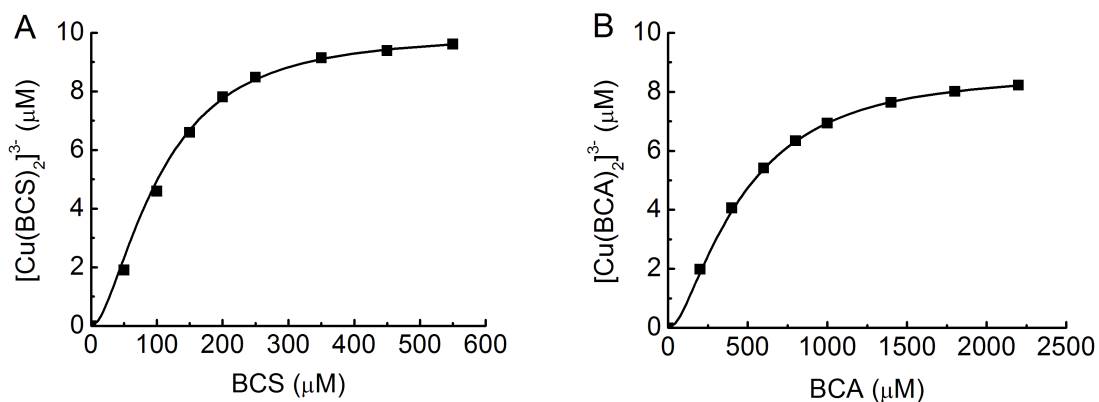


Fig. S2 Titrations of (A) bathocuproine disulfonate (BCS) into Cu(I)-BACE1-CTD (10 μM) plus an excess of apo-peptide (10 μM apo-BACE1-CTD) in 20 mM Hepes containing 200 mM KCl at pH 7.0, and of (B) bicinchoninic acid (BCA) into Cu(I)-thioredoxin (9 μM) plus an excess of apo-protein (5 μM) in 20 mM Hepes containing 200 mM NaCl at pH 7.0. The lines show fits of the data to equation S1 giving K_b values of $(3.1 \pm 0.2) \times 10^{16}$ (A) and $(3.1 \pm 0.1) \times 10^{15} \text{M}^{-1}$ (B).

Table S1 Matrix assisted laser desorption ionization time-of-flight (MALDI-TOF) and Fourier transform ion cyclotron resonance (FT-ICR) mass spectrometry (MS) results for *Synechocystis* His61Lys Atx1 and *S. cerevisiae* Atx1

Protein	MS Analysis	Experimental mass (Da)	Theoretical mass (Da)
<i>Synechocystis</i> His61Lys Atx1	FT-ICR	6542	6545 (-Met)
<i>S. cerevisiae</i> Atx1	MALDI-TOF	8089	8091 (-Met)

Table S2 Elution volumes and corresponding calculated apparent molecular weights for wild type (WT) *Synechocystis* apo-Atx1, His61Lys *Synechocystis* apo- and Cu(I)-Atx1 and *S. cerevisiae* apo-Atx1 determined from analytical gel filtration chromatography

Protein	Elution Volume (ml)	Apparent Mass (kDa)
<i>Synechocystis</i> WT apo-Atx1 ^a	13.90	13.2
<i>Synechocystis</i> His61Lys apo-Atx1	12.86	21.2
<i>Synechocystis</i> His61Lys Cu(I)-Atx1	13.92	13.8
<i>S. cerevisiae</i> apo-Atx1	14.55	10.6

^a Data from reference 1.

Table S3 Comparison of secondary structure content compositions determined from available structures using STRIDE^a with those calculated from far-UV CD spectra of mainly apo-proteins using Dichroweb^b

Protein ^c	Data	Secondary structure element (%)			
		α -helix	β -sheet	Turn	Random
<i>Synechocystis</i> WT Atx1 ^d	Crystal structure	40	21	21	19
	Far-UV CD ^e	48	11	17	25
<i>Synechocystis</i> His61Lys apo-Atx1	Far-UV CD	21	24	19	36
<i>Synechocystis</i> His61Lys Cu(I)-Atx1	Far-UV CD	42	6	30	22
<i>S. cerevisiae</i> Atx1	Crystal structure	32	36	11	21
	Far-UV CD ^e	21	33	22	24
HAH1	Crystal structure	36	36	6	22
	Far-UV CD ^e	42	15	17	26
<i>Synechocystis</i> plastocyanin	Crystal structure	7	53	17	23
	Far-UV CD ^e	7	44	19	30

^aReference 2. ^bReference 3. ^cThe following PDB files were used for the determination of protein secondary structure compositions using STRIDE: 2XMT (WT *Synechocystis* Atx1), 1FEE (HAH1), 1CC8 (*S. cerevisiae* Atx1) and 1PCS (*Synechocystis* plastocyanin). ^dData from reference 1. ^e For reduced apo-proteins.

Determination of Cu(I) affinities

Cu(I) affinities (K_b values) were obtained by fitting data from titrations of BCS or BCA into a mixture of Cu(I)-protein and excess apo-protein to equation S1, where [L], [P] and [Cu] represent the total concentrations of BCS or BCA, protein and Cu(I) respectively, and β is the overall association constant of $[\text{Cu}(\text{BCS})_2]^{3-}$ or $[\text{Cu}(\text{BCA})_2]^{3-}$.^{4,5}

$$[\text{L}] = 2[\text{CuL}_2] + \sqrt{\frac{K_b([\text{P}] - [\text{Cu}] + [\text{CuL}_2])[\text{CuL}_2]}{([\text{Cu}] - [\text{CuL}_2])\beta}} \quad (\text{S1})$$

Supporting References

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