

Supporting Information

The role of the Cys-X-X-X-Cys motif on the kinetics of cupric ion loading to the *Streptomyces lividans* Sco protein

Katie L.I.M. Blundell¹, Michael T. Wilson¹, Erik Vijgenboom² and Jonathan A.R. Worrall¹

¹School of Biological Sciences, University of Essex, Wivenhoe Park, Colchester, CO4 3SQ, UK. ²Molecular Biotechnology, Institute of Biology Leiden, Sylvius Laboratory, Leiden University, PO Box 9505, 2300RA Leiden, The Netherlands.

Correspondence addressed to: Jonathan Worrall, Tel: +44 1206 872095; email: jworrall@essex.ac.uk

Table S1: Output from Dichroweb of average secondary structure content for apo-Sco^{SL} and the two Cys mutants. The data for apo-Sco^{SL} was taken from¹.

Protein	% α -helix ^a	% β -sheet ^a	% Turn ^a	% Unordered ^a
Apo-Sco ^{SL}	35.0	18.7	16.2	30.0
Apo-C86A	30.2	15.7	20.2	34.0
Apo-C90A	38.0	13.5	17.6	31.1
Secondary structure content determined from X-ray structures				
Protein	% α -helix	% β -sheet	% Other	PDB
<i>Bacillus Subtilis</i> Sco	26	22	52	1XZ0
<i>Bacillus anthracis</i> Sco	31	17	52	4HDE

^aAll analysis carried out on far-UV CD spectra recorded at 20 °C and pH 7.0.

References

1. K. L. I. M. Blundell, M. T. Wilson, D. A. Svistunenko, E. Vijgenboom and J. A. R. Worrall, *Open biology*, 2013, **3**, 120163.