

Protein Destabilisation by Ruthenium(II) Tris-Bipyridine Based Protein-Surface Mimetics

Supporting Information

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Section	Page
Additional CD Spectra	2
Additional Proteolysis Data	3

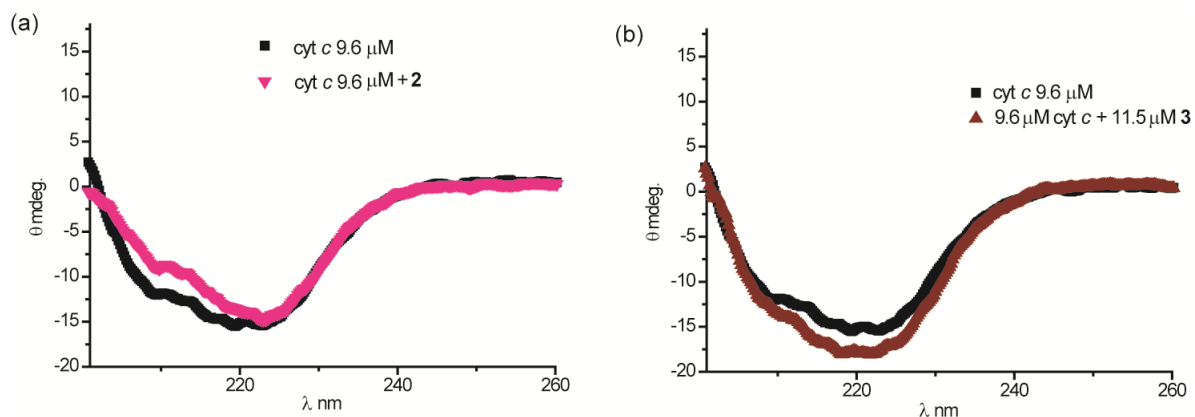


Figure ESI1. Perturbations to secondary structure of cyt *c* in the presence of **2** and **3** (5 mM sodium phosphate, pH 7.4) (a) circular dichroism spectra of cyt *c* (9.6 μM) in the absence and presence of **2** (9.6 μM) at 25°C (b) circular dichroism spectra of cyt *c* (9.6 μM) in the absence and presence of **3** (9.6 μM) at 25°C,

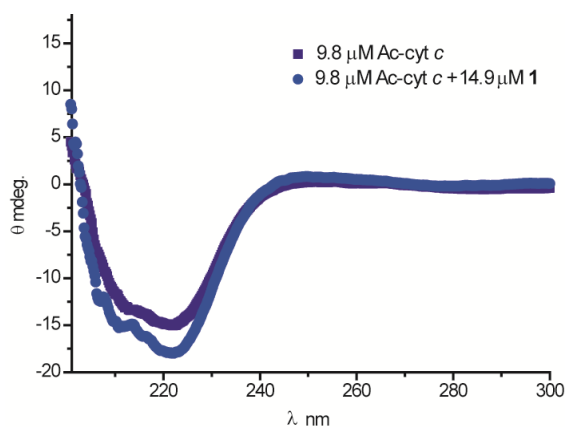


Figure ESI2. Perturbations to secondary structure of different proteins in the presence of **1** (5 mM sodium phosphate, pH 7.4); circular dichroism spectra of Ac-cyt *c* (9.8 μM) in the absence and presence of **1** (14.9 μM) at 25°C)

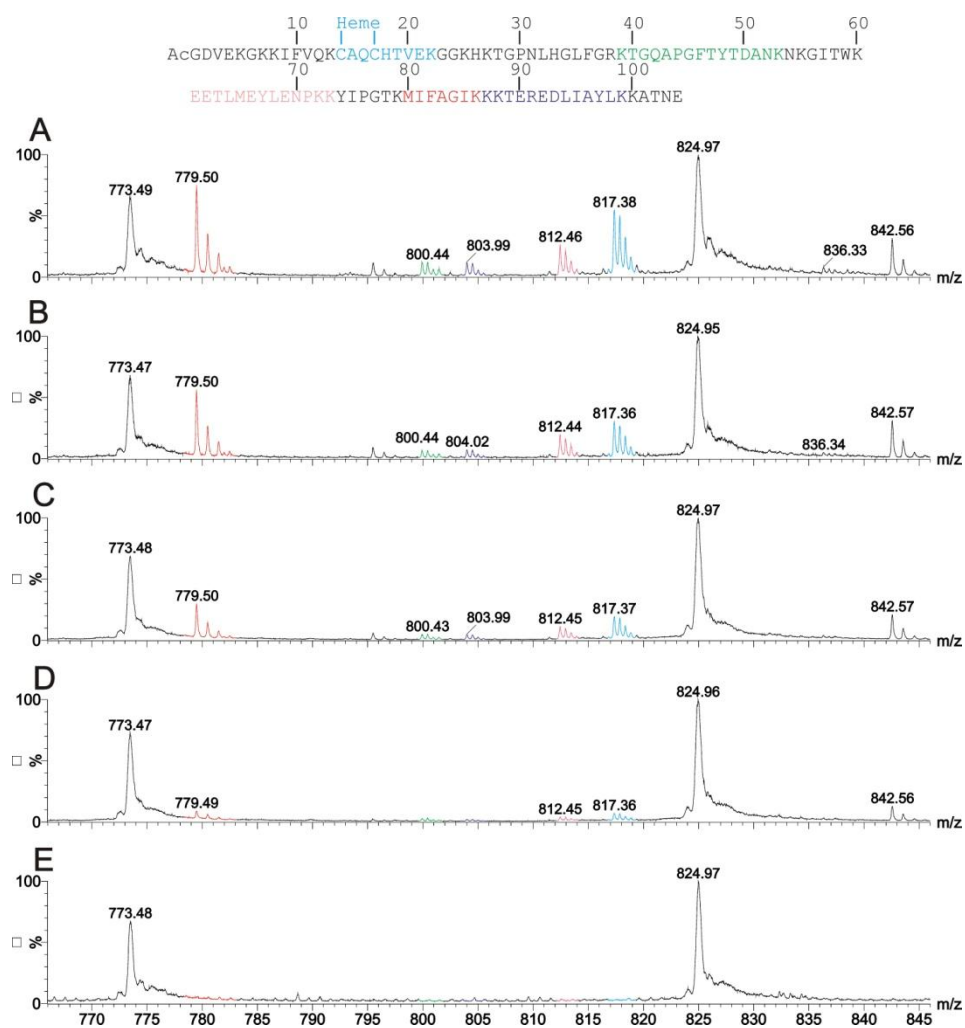


Figure ESI3. Electrospray mass spectra (m/z 765-845) of proteolysis samples after 120 min trypsin digestion showing different rates of proteolysis of cytochrome c in the presence of 2 equivalents of receptor (A), 1 equivalent of receptor (B), 0.2 equivalents of receptor (C) and no receptor (D). A control containing no trypsin and no receptor was also analysed (E). Tryptic peptide signals in the MS are colour coded corresponding to their sequence in the protein (top).

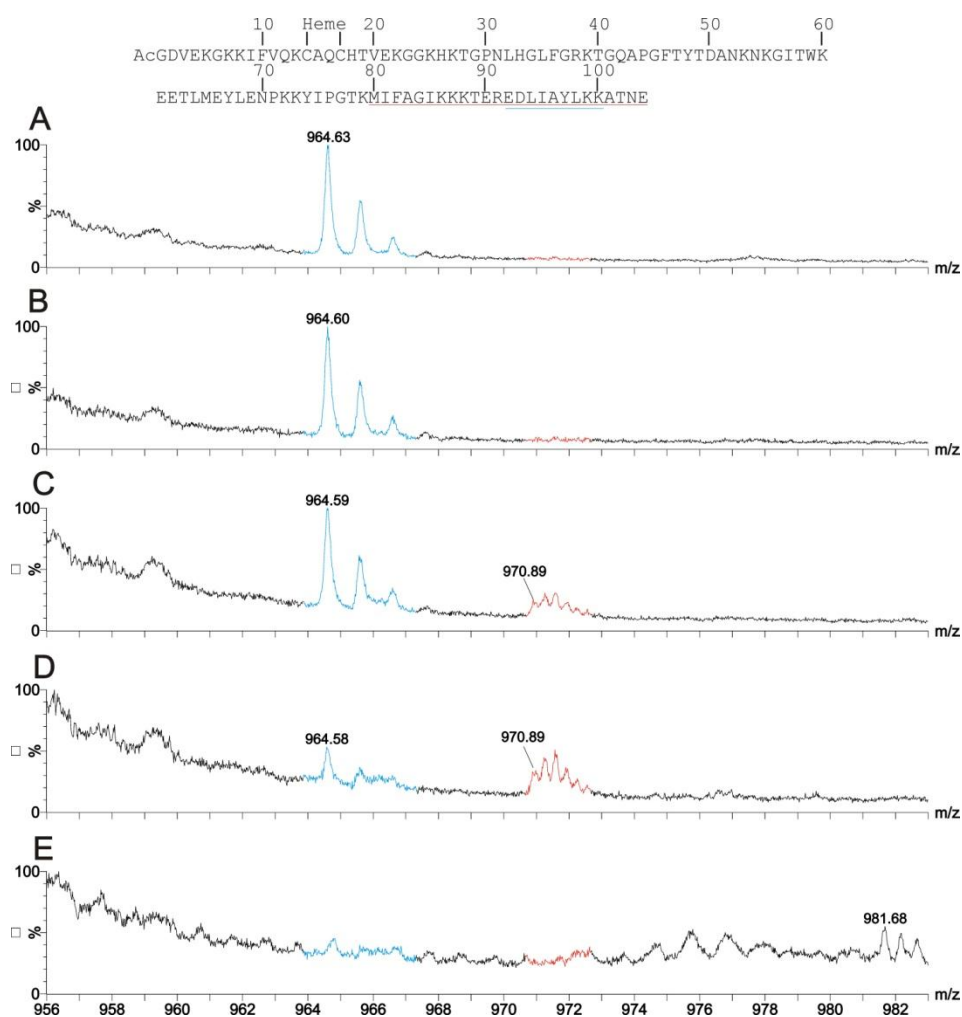


Figure ESI 4. Electrospray mass spectra (m/z 956-983) of proteolysis samples after 120 min trypsin digestion showing different rates of proteolysis of cytochrome c in the presence of 2 equivalents of receptor (A), 1 equivalent of receptor (B), 0.2 equivalents of receptor (C) and no receptor (D). A control containing no trypsin and no receptor was also analysed (E). Tryptic peptide signals in the MS are colour coded corresponding to the sequence underlined in the protein (top).