

The substrate-binding site in Cu nitrite reductase and its similarity to Zn carbonic anhydrase

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The following omissions were inadvertently made in our paper and are corrected below:

Table 1 The explanation of superscript 'b' was omitted. This should have read:

^b Godden *et al.*, *Science* **253**, 438–442 (1991). the Cu-ligand distances are identical for each monomer and are taken from unrefined coordinates of a monomer provided by Dr. E. Adman in November 1991. These distances are the same as given in the Brookhaven Protein Data Bank (INRD). The NiR trimer was generated by crystallographic symmetry. Figures 2 and 3 are also based on these coordinates.

Dr Adman has also recently brought to our attention a preliminary report indicating the structural similarity of AcNiR and AcT2DNiR (Adman, E.T. & Turley, S. (1993) *Acta Crystallogr. A* **49** Suppl p. 75) and that the superposition of Asp 98 and His 255 with copper ligand residues of ascorbate oxidase was published in a preliminary form in reference 35 in our paper. The coordinates of our proposed model of nitrite bound Cu are available on request.

Novel metal-binding proteins by design

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Nature Structural Biology, **2** 368–373 (1995).

The symbols for the Z β 1 variants Z β 1M and Z β 1L in the legends for Figures 3 and 4 were inadvertently switched. The corrected figure legends are printed below:

Fig. 3 Structural changes of the Z β 1 variants in response to metal. *a*, CD spectra of the apo form of Z β 1Z (circles), Z β 1M (squares) and Z β 1L (triangles) acquired at 2 °C. *b*, CD spectra of the proteins at 2 °C in the presence of 2.5 equivalents of CdCl₂: Z β 1A (circles), Z β 1M (squares) and Z β 1L (triangles). Zn(II) and Cd(II) bound forms of the proteins gave similar spectra.

Fig. 4 The effect of metal binding on the stability of the Z β 1 variants. *a*, Thermal denaturation of the apo form of Z β 1A (circles), Z β 1M (squares) and Z β 1L (triangles). Ellipticity at 220 nm is plotted as a function of temperature. The raw ellipticity data is shown, because Z β 1A and Z β 1M are not fully folded in the absence of metal, even at 2 °C. *b*, Thermal denaturation of the Z β 1 variants in the presence of 1.1 molar equivalents of CdCl₂: Z β 1A (circles), Z β 1M (squares) and Z β 1L (triangles). The fraction of unfolded protein is plotted as a function of temperature.

The structure of calyculin reveals a novel homodimeric fold for S100 Ca²⁺-binding proteins

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Nature Structural Biology **2**, 790–796.

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