Metal ion substitution in prokaryotic zinc finger Ros87

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Zinc ion binding is a principal event in the achievement of the correct fold in eukaryotic classical zinc finger domains since the motif is largely unfolded in the absence of metal. The formation of a small hydrophobic core further helps to stabilize the final structure. In the case of a prokaryotic zinc finger, the larger ββββαα domain contributes to the folding mechanism with a larger hydrophobic core [1]. Thus, following the great attention devoted to unveiling the effect of xenobiotic metal ion replacement in in zinc-containing proteins, the prokaryotic zinc finger domain appears to be an interesting model for studying metal ion interaction with zinc fingers and with metallo-proteins in general [2]. Here, we explore the binding of Co (II), Ni(II), Hg(II), Pb(II) and Cd(II) to Ros87 [3,4]. We measured Ros87-metal ion dissociation constants and monitored the effects of the metal ion replacement on the protein structure. The data reported show how, although all the metals examined bind Ros87 with binding constants lower in terms of magnitude with respect to that for the native zinc ion, this zinc binding domain is capable to adapt its structure in presence of metal ions with different ionic radii. Indeed, Ros87 fold with a small ion like nickel and with a larger metal ion like cadmium. Interestingly the Cd(II) appears to be the highest limit in terms of tolerated dimensions to obtain a structured protein.

References

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