

## Specificity of the Zn<sup>2+</sup>, Cd<sup>2+</sup> and Ni<sup>2+</sup> ion binding sites in the loop domain of the HypA protein.

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The zinc binding loop domain of *Helicobacter pylori*'s HypA protein consists of two CXXC motifs with flanking His residues. These motifs bind metal ions and thus they are crucial for the functioning of the whole protein. The N-terminal site, where His is separated from CXXC by Ser residue is more effective in binding Zn<sup>2+</sup> and Ni<sup>2+</sup> ions than the C-terminal site, in which His is next to CXXC motif. Studies on various modifications of the peptide sequence within the Ac-ELECKDCSHVFKPNALDYGVCCKCHS-NH<sub>2</sub> loop show the role of the residues in the linker between CXXC motifs and the effect of length of the linker on the stability of the complexes it forms with Zn<sup>2+</sup>, Cd<sup>2+</sup> and Ni<sup>2+</sup> ions. The proline residue in the linker between two CXXC binding sites plays a distinct role in the metal ion binding ability of the loop, lowering the efficacy of metal ion coordination. Deletion of the aliphatic residues from the linker between CXXC motifs remarkably improves the binding efficacy of the loop.

### Adres publiczny

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### Strona internetowa wydawcy

<https://www.rsc.org/>

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