

## The specificity of interaction of Zn<sup>2+</sup>, Ni<sup>2+</sup> and Cu<sup>2+</sup> ions with the histidine-rich domain of the TjZNT1 ZIP family transporter.

### Autorzy

Sławomir Potocki

Daniela Valensin

Henryk Kozłowski

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### Streszczenie

The Zrt/Irt-like protein (ZIP) family contributes to the metal homeostasis by regulating the transport of divalent metal cations such as Fe<sup>2+</sup>, Zn<sup>2+</sup>, Mn<sup>2+</sup>, Cd<sup>2+</sup> and sometimes even Cu<sup>2+</sup>. Most ZIP members have a long variable loop between transmembrane domains (TMDs) III and IV; this region is predicted to be located in the cytoplasm and is postulated to be the metal ion binding site. In this study, we looked at the thermodynamic behavior and coordination chemistry of Zn<sup>2+</sup>, Ni<sup>2+</sup> and Cu<sup>2+</sup> complexes with the histidine-rich domain, Ac-(185)RAHAAHHRHSH(195)-NH<sub>2</sub> (HRD), from the yeast TjZNT1 protein, located between TMDs III and IV. The sequence is conserved also in higher species like *Thlaspi japonicum*. The stability of complexes increases in the series Ni<sup>2+</sup> < Zn<sup>2+</sup> ≪ Cu<sup>2+</sup>. The geometry of complexes is very different for each metal and in the case of Zn<sup>2+</sup> complexes, high specificity in binding is observed. Moreover, the stability of HRD–Cu<sup>2+</sup> complexes was compared with the five His residues containing peptide from Hpn protein (*Helicobacter pylori*). The results suggest a high ability of HRD in the binding of all three studied metals.

### Adres publiczny

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### Strona internetowa wydawcy

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