Copper(II) coordination outside the tandem repeat region of an unstructured domain of chicken prion protein.

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Streszczenie

Combined potentiometric, calorimetric and spectroscopic methods were used to investigate the Cu^{2+} binding ability and coordination behaviour of some peptide fragments related to the neurotoxic region of **ch**icken **Pr**ion **P**rotein. The systems studied were the following protein fragments: $chPrP_{106–114}$, $chPrP_{119–126}$, $chPrP_{108–127}$, $chPrP_{105–127}$ and $chPrP_{105–133}$.The complex formation always starts around pH 4 with the coordination of an imidazole nitrogen, followed by the deprotonation and binding of amide nitrogens from the peptidic backbone. At neutral pH, the $\{N_{im}, 3N^{-}\}$ binding mode is the preferred one. The amide nitrogens participating in the binding to the Cu^{2+} ion derive from residues from the N-terminus side, with the formation of a six-membered chelate ring with the imidazolic side chain. Comparison of thermodynamic data for the two histydyl binding domains (around His-110 and His-124), clearly indicates that the closest to the hexarepeat domain (His-110) has the highest ability to bind Cu^{2+} ions, although both of them have the same coordination mode. Conversely, in the case of the human neurotoxic peptide region, between the two binding sites, located at His-96 and His-111, the farthest from the tandem repeat region is the strongest one. Finally, thermodynamic data show that chicken peptide is a distinctly better ligand for coordination of copper ions with respect to the human fragment.

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