How the α-hydroxymethylserine residue stabilizes oligopeptide complexes with nickel(II) and copper(II) ions.

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Streszczenie

Potentiometric, spectroscopic and theoretical studies have shown that the a-hydroxymethylserine (HmS) residue is a very specific amino acid residue when inserted into a peptide sequence. The theoretical calculations as well as evaluated deprotonation microconstants indicated that in the HmS-HmS-His tripeptide the N-terminal ammonium group is more acidic than the imidazole nitrogen. The hydrogen bond formation between the N-terminal amino group and imidazole nitrogen stabilizes the cyclic conformation of the metal-free peptide. The unusual gain in the 4N complex stability in the copper(II) and nickel(II) complexes with HmS-HmS-His ligands seems to derive from the enhancement of the π-electron contribution to the metal-amide nitrogen bond.

Adres publiczny

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