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STRUCTURAL MODEL OF A Ni(II) COMPLEX WITH A 30-AMINOACID PEPTIDE THROUGH AN NMR STUDY

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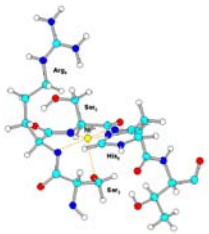
Multidimensional NMR spectroscopy is a useful tool for the calculation of structures or structural models of metal-peptide complexes in solution.[1] We applied bidimensional NMR techniques to study the interactions of Ni(II) ions with a 30-aminoacid peptide, a fragment of the C-terminal tail of Cap 43 protein. This protein is strictly connected to nickel exposure in cells, since it seems to be specifically expressed as a response to the presence of this metal in the cellular medium[2,3] and it is also related to cancer development; an abnormal level of Cap43 protein has been detected in a number of tumour tissues.[2,4] The striking feature of Cap 43 is a three-repeated decapeptide sequence at its C-terminus; each 10-aminoacid fragment (TRSRSHTSEG) bearing a histidinic residue, which has been indicated as an anchoring site for metal binding in numerous cases. We previously reported that each fragment is able to coordinate a Ni(II) ion in a very effective way.[5,6]

Structure calculations for the peptide-metal complex were performed for a single mono-histidinic fragment on the basis of the ROE cross-correlations observed in the 2D ^{1}H-^{1}H ROESY spectra at pH = 10. The metal complex involves an imidazolic nitrogen of histidine residue, three amidic nitrogens of the backbone and an oxygen atom from a deprotonated serine residue which takes part to the formation of a square pyramidal structure.



The structural model calculated (figure below) allowed us a better understanding of the features of nickel coordination with the C-terminal region of Cap43 protein.

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