Abstract

In this work, the influence of three sodium salts on the structure of three proline-based peptide models in aqueous solution was examined by a combination of NMR spectroscopy and molecular dynamics simulations. The sodium salts cover a wide range of the Hofmeister series of ions, and the choice of the peptide models represents a systematic permutation of the residues at N and C termini of proline.

It was shown that the *cis*/*trans* conformational equilibrium, which takes place by rotation around the proline amide bond, can be influenced by the addition of salts, always leading to a higher population of the *cis* conformer. The impact depends on both the identity of the anion and the local chemical structure of the peptide model. Furthermore, it was shown that, in some cases, the conformational equilibria are almost insensitive to temperature changes, implying that the salts are able to fix conformations even within wide temperature ranges up to 80 °C. Corresponding thermodynamic data, ΔG, ΔH and ΔS, were determined for each case.

In order to rationalize these findings, preferred ion binding sites of the peptide models were detected. The results show that the *cis* conformers are able to provide an additional binding site that is determined by both adjacent carbonyl groups, and that is not existing in the *trans* conformers. This situation was partially explained by electrostatic surface potentials of the peptide models, which are different for each conformer.

The information is complemented by the determination of timescales for local ion exchanges.