



Thermodynamic contributions of peptide backbone unit from water to biocompatible ionic liquids at $T = 298.15$ K

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ABSTRACT

To quantify the biomolecular interactions of protein functional groups with biocompatible ionic liquids (ILs), transfer free energies (ΔG_{tr}^0) of model compounds from water to aqueous ILs solutions have been determined from the solubility measurements, as a function of ILs concentration at $T = 298.15$ K under atmospheric pressure. The aqueous systems investigated contain amino acids of zwitterionic glycine peptides: glycine (Gly), diglycine (Gly₂), and cyclic glycylglycine (c(GG)) with ILs of diethylammonium acetate ([Et₂NH][CH₃COO], DEAA), triethylammonium acetate ([Et₃NH][CH₃COO], TEAA), and trimethylammonium acetate ([Me₃NH][CH₃COO], TMAA). It was found that the solubility of model compounds in aqueous IL solutions decreases with increasing IL concentration (salting-out effect). We observed positive values of ΔG_{tr}^0 for Gly, Gly₂, and c(GG) from water to ILs, indicating that the interactions between ILs and protein surface are unfavourable, which leads to stabilization of the native structure of amino acids. Moreover, our experimental data is used to determine transfer free energies (ΔG_{tr}^0) of the peptide backbone unit ($-\text{CH}_2\text{C}(\text{NH})-$) from water to IL solutions. These results explicitly elucidate that all alkyl ammonium ILs acted as stabilizers for tested model compounds through the exclusion of ILs from surface of model compounds and also reflect the effect of alkyl chain on the stability of protein model compounds. To obtain the mechanism events of the ILs role in enhancing the stability of the model compounds structure, we further studied the UV–vis spectrum analysis.

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1. Introduction

Proteins are polymers made up of specific sequences of model compounds linked together by covalent peptide bonds. The nature and the arrangement of the amino acid side chain along the protein backbone are responsible for the individual characteristics of the biomolecules, and it has been recognised that all of the information pertaining to the proteins is implicit in the amino acid sequence. In a protein, the peptide bond is very stable and has unusual conformational properties [1]. Basically, these bonds are influenced by the aqueous solutions therefore, it is very much important to have a clear idea on the solubility, stability, and thermodynamic properties of these molecules in aqueous solution. It has long been known that dramatic changes in the physical and functional properties of proteins are due to the addition of co-solvents. Their structural and chemical properties have been extensively investigated by both theoretical and experimental techniques thereby providing valuable insights into the chemistry of peptides [1–3]. Understanding

of the protein–solvent interactions is of considerable importance in the development of biotechnologies and industrial processes.

The effects of co-solvents on the solubility and conformational stability of proteins have been of intense interest for decades. Obviously, the stability of biomolecules under co-solvent conditions is dependent on the nature of the co-solvent; which can alter a protein's properties and structural effects through biomolecular interactions between its functional groups and the co-solvent particles [4–7]. During the past decade, ionic liquids (ILs), a class of environmental friendly solvents, has been used for a wide range of industrial and pharmaceutical applications [8–13]. Ionic liquids represent a rather diverse class of co-solvents that are combinations of different ions, which are liquids at or close to room temperature [9,14–16]. The ILs are a relatively new class of compounds, they appear to be replacements for volatile organic compounds (VOCs). Due to the ionic nature of the materials, ILs have essentially negligible vapour pressure and so can be envisioned as being useful in a variety of applications [5,7]. The ILs pose a new option for an excellent co-solvent, not only for preserving proteins stability [17–21] but also as a refolding additive for the biomolecules from a quenched thermal unfolded structure [21,22].

Virtually, there are rapid physiological stresses inside the biomolecules, therefore the biomolecule needs to maintain its

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