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Protein folding, stability, and solvation structure in osmolyte solutions hydrophobicity

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The hydrophobic effect between solutes in aqueous solutions plays a central role in our understanding of recognition and folding of proteins and self assembly of lipids. Hydrophobicity induces nonideal solution behavior which plays a role in many aspects of biophysics. Work on the use of small biochemical compounds to crowd protein solutions indicates that a quantitative description of their non-ideal behavior is possible and straightforward. Here, we will show what the structural origin of this non-ideal solution behavior is from expression derived from a semi grand ensemble approach. We discuss the consequences of these findings regarding protein folding stability and solvation in crowded solutions through a structural analysis of the m-value or the change in free energy difference of a macromolecule in solution with respect to the concentration of a third component. This effect has recently been restudied and new mechanisms proposed for its origins in terms of transfer free energies and hydrophobicity.