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Solvent Viscosity at the Protein Surface SHEILA KHODADADI, MARIAN PALUCH, SEBASTIAN PAWLUS, YOSHIHITO HAYASHI, ALEXEI SOKOLOV, Department of Polymer Science, University of Akron — Biochemical activity of biological macromolecules depends on solvent's viscosity, η, at their surface. The latter might differ from the bulk solvent viscosity due to preferential hydration. In order to estimate η at the protein surface, we studied dielectric relaxation spectra of lysozyme-water-glycerol mixtures. Additional relaxation process that appears in the presence of proteins has been assigned to their rotation. Employing Debye-Stokes-Einstein relationship [$\tau_R = (4\pi \mathrm{R}_R^3 \eta/\mathrm{KT})$],and assuming that hydrodynamics radius of protein, R_R, does not change, we estimated η at the protein surface. Analysis of the obtained results indeed reveals a significant difference between bulk solvent's viscosity and the viscosity experienced by a protein. The water concentration appears to be significantly enhanced at the protein surface, in agreement with earlier thermodynamics study. Using the viscosity data, we estimate solvent composition at the protein surface.We expect that the developed approach will help to unravel the role of the solvent and its viscosity in dynamics, stability and biochemical activity of proteins.

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