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Solvent, Hydration, and Protein - Interactions and Motions

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Proteins exist in a large number of different conformations or conformational substates, described by an energy landscape which depends also on the protein environment. The dynamics in this energy landscape is rich and incompletely explored. Large-scale protein motions, such as the exit of a ligand from the protein interior, follow the dielectric fluctuations in the bulk solvent. The mean-square displacements (msd) from Mössbauer and neutron-scattering experiments probe protein fluctuations on the time scale of the experiment and show that fluctuations in the hydration shell control fast fluctuations in the protein. We call the first type solvent-slaved fluctuations, the second hydration-shell-coupled fluctuations. Solvent-slaved motions are similar to the alpha fluctuations in glasses. Their temperature dependence can be approximated by a Vogel-Tammann-Fulcher relation and they are absent in a solid environment. Hydration-shell-coupled fluctuations are similar to the beta relaxation in glasses. They can be approximated by a Ferry or an Arrhenius relation, are much reduced or absent in dehydrated proteins, and occur in hydrated proteins even if embedded in a solid. They can be responsible for internal processes such as the migration of ligands within myoglobin. The existence of at least two functionally important fluctuations in proteins, one slaved to bulk motions, the other coupled to hydration shell fluctuations, implies that the environment can control protein functions through different interactions. Recent theoretical treatment of the mosaic energy landscapes of liquids applied to protein dynamics sheds light on the solvent-slaved fluctuations. A similar understanding of the hydration-shell-coupled motions is not yet in hand.