PROTEIN SEQUENCE- AND PH-DEPENDENT HYDRATION PROBED BY THZ SPECTROSCOPY.

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Here we use THz spectroscopy to probe directly the effect of site-specific mutations and solvent pH on the hydration shell-protein interaction.

Global perturbations of the protein hydration shell by pH and local perturbation by surface site-specific mutation both produce significant changes in the terahertz absorption spectrum of aqueous protein. The pseudo-wild-type proteins have a much more pronounced effect on long-distance solvation water than mutants replacing a single polar glutamine side chain with aromatic residues. This is true both in the context of enhanced and decreased helix stability. Unfolding the pseudo-wild-type protein at pH 2 likewise reduces the long distance solvation effect.

To complement the experimental data, we studied the approximate dynamics of the protein and explicit solvent water by molecular dynamics (MD) simulation and normal-mode analysis.

In the future the observed changes can be used as sensitive probes of protein-solvent dynamics, opening up the possibility of using THz absorption as a probe for protein folding kinetics and functional dynamics measurements. The development of quantitative models for the THz spectra will make it possible to understand local solvation of proteins at the molecular level.