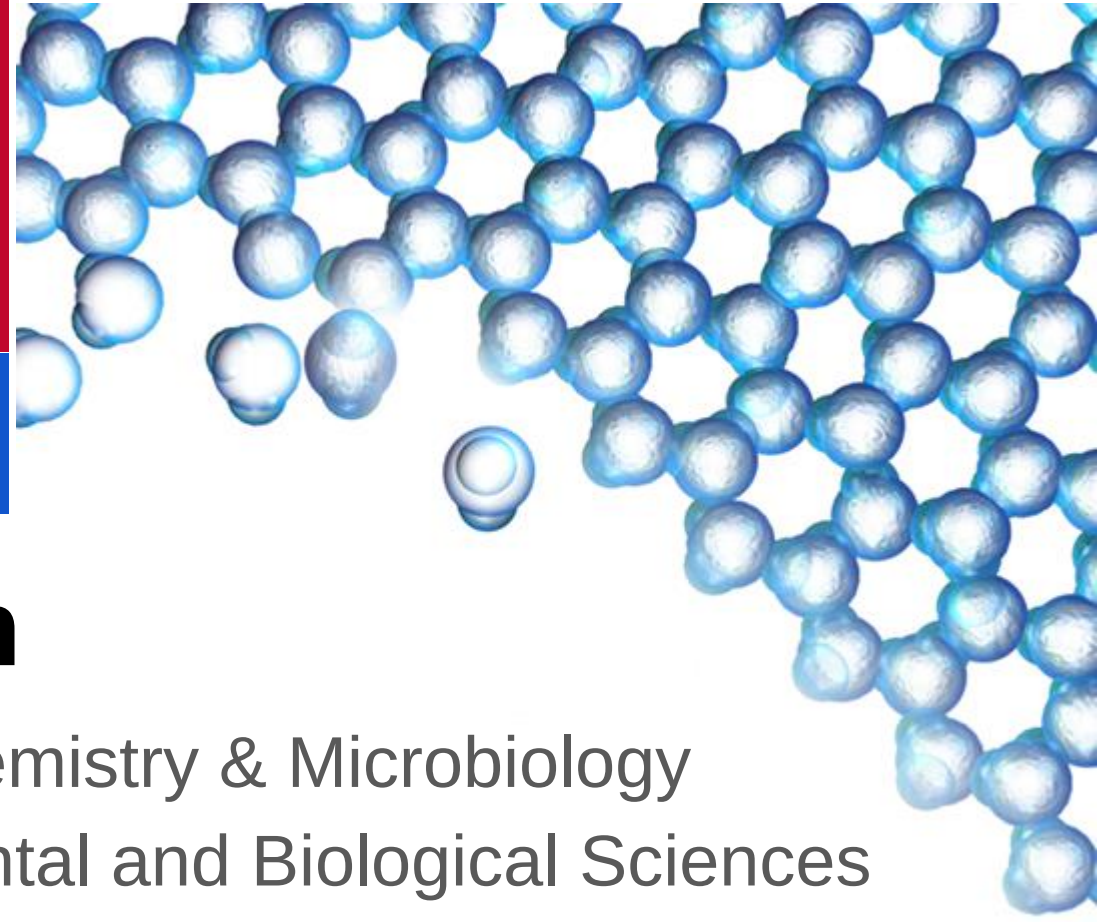
Physical Chemistry Seminar Series

Spring 2017



Peter C. Kahn

Department of Biochemistry & Microbiology
School of Environmental and Biological Sciences
Rutgers University

Friday, May 5 • 12:00 pm
Proteomics, Room 120

How Big is a Water Molecule, and Why Does It Matter? Studies in Protein Hydration

Nearly all processes in cells begin with non-covalent interactions between biomolecules, the exception being those occurring wholly within non-aqueous regions such as membrane interiors. Even when covalent reactions ensue, the initial step in protein folding, ligand binding, association of proteins with nucleic acids, enzyme catalysis, etc., all start with the association of hydrated biomolecular surfaces with one another. Water of hydration is thereby expelled from the surfaces into the bulk solution. That water undergoes profound changes in its thermodynamic properties. Compared to bulk solvent, hydrating water has a lower entropy, a higher heat capacity, a much lower freezing point, and, usually, a greater density. These changes have imposed the constraints within which Nature has evolved the biochemical apparatus.

We use measurements of volume changes as a probe into the nature of hydrating water in association with spectroscopic measurements and, where possible, analyses of solvent exposed surface area changes for proteins of known structure. Data will be presented on the molten globule transitions of cytochrome-c, ligand binding to dehydrogenases, the role of buried charge in protein conformational stability, and other systems if time allows. An aim of the work is to estimate the number of water molecules displaced, as that is the starting point for statistical mechanical understanding.

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