

Spotlights on Recent JACS Publications

■ A SWEET APPROACH TO ANALYTE DETECTION

Personal glucose meters, or glucometers, are among the limited number of widely used point-of-care devices, offering ease of use, low cost, and reliable quantitative results. For this reason, Chaoyong James Yang and co-workers turn to glucometers to help them develop a new method to detect a wide range of non-glucose analytes in solution (DOI: 10.1021/ja3114714).

The team employs hydrogels cross-linked with aptamers, or DNA strands with specific ligand-binding capabilities. The cross-linking occurs in the presence of glucoamylase—an enzyme that catalyzes the hydrolysis of amylose into glucose—such that the enzyme becomes physically trapped inside the gel. When the aptamer's target ligand is introduced to the hydrogel immersed in an amylose-rich solution, the aptamer–target binding event causes the breakdown of the hydrogel and release of glucoamylase. The free enzyme converts amylose into glucose, which is then rapidly quantified by the portable glucometer.

The team thus combines the convenience and reliability of a simple glucometer with the selective binding capabilities of aptamers. The result is a cost-effective approach to quantifying non-glucose analytes, with the potential to be extended to detect any analyte for which an aptamer exists or can be developed. **Christine Herman, Ph.D.**

■ GOOD VIBRATIONS: HOW BOND VIBRATIONS IN ENZYMES HELP CATALYSIS

Enzymes can speed up reactions as much as 10^{20} -fold, which is an amazing display of efficiency that scientists have strived for decades to understand. Biochemists know that motions of different enzyme parts and various non-covalent interactions are important for creating the proper environment for the reactions on substrates to take place. Now Michael D. Toney and colleagues demonstrate the importance of bond vibrations in enzyme catalysis (DOI: 10.1021/ja3101243).

The investigators study alanine racemase, an enzyme that reversibly catalyzes the interconversion between L- and D-alanine isomers. They compare the activities of the native enzyme with those of a version in which some of the hydrogen atoms are swapped for the heavier isotope deuterium, which has a measurable impact on the rate of the reaction.

From their data, the researchers conclude that vibrational motions on the femto- to picosecond time scale within bonds of the enzyme help it tackle the transition state barrier—an energetic equivalent of an uphill walk. The vibrational motions are critical for generating a high-energy structure between the enzyme and its substrate which effectively reduces the size of the hill and helps to complete the reaction. The work underscores the importance of understanding the molecular fundamentals of enzyme catalysis because these details could be exploited in developing ways to halt enzymes involved in diseases, such as the HIV protease. **Rajendrani Mukhopadhyay, Ph.D.**

■ BIG EFFECTS ON SMALL TIME SCALES

The molecular motions of proteins are inextricably linked to their functions. Sam Hay, Nigel Scrutton, and co-workers offer new insight into this elusive relationship by exploring whether fast protein motions are involved in the transfer of a hydrogen atom in the oxidation of the coenzymes NADH and NADPH (DOI: 10.1021/ja311277k). Though it has been speculated that fast motions—in the range of femto- to picoseconds (one trillionth to one quadrillionth of a second!)—might facilitate certain biological processes, little direct experimental evidence exists to support this hypothesis.

In this work, the researchers study the protein pentaerythritol tetranitrate reductase (PETNR), an enzyme whose H-transfer reaction is characterized by an unusual temperature dependence. The authors use sophisticated structural and kinetic characterization methods to show that this temperature dependence is linked to vibrations in the enzyme, providing compelling experimental evidence of a causal relationship between fast motions and enzyme chemistry.

One use for PETNR has been in the biodegradation of organic pollutants. Understanding the interplay between protein dynamics and function may facilitate more effective industrial use of this enzyme, and offer a means to investigate this relationship in other proteins. **Eva J. Gordon, Ph.D.**

■ DIRECT OBSERVATION OF REACTIONS IN SOLUTION

Hytcherl Ihee, Michael Wulff, and their co-workers show evidence of the direct measurement of iodine atoms reacting in either cyclohexane or carbon tetrachloride solvent, adding to our atomic-level understanding of what occurs when a reaction takes place in solution (DOI: 10.1021/ja312513w).

Solution-based reactions are known to be solvent dependent, with the solvent affecting the pathway and rate of the chemical reaction. The time scale for observing reactive species is very short, and the development of picosecond pump–probe techniques has facilitated these investigations. Pump–probe experiments use one signal to create (or pump) a reactive species— I_2 becomes $2I$ in this case and subsequently reacts to re-form I_2 —while a second pump some picoseconds later probes for signal from the reactive species.

The researchers use time-resolved X-ray liquidography to directly measure the position of iodine atoms with respect to each other as well as the solvent cage enclosing the iodine. The results demonstrate that the newly formed I–I bond distance is larger in cyclohexane, the lighter solvent, while the I–I vibrations relax more quickly in carbon tetrachloride. These measurements give insight into the atomic workings of the solute–solvent relationship. **Polly Berseth, Ph.D.**

Published: March 13, 2013

■ DNA NANO-MORSE CODES AND NANOMATERIAL ASSEMBLY

Capitalizing on the weaker affinity between streptavidin and a biotin derivative called desthiobiotin, Yi Lu and colleagues reveal a secret message that they had encrypted using DNA scaffolds (DOI: 10.1021/ja3122284).

In the burgeoning field of bionanotechnology, DNA is often used as a structural tool. To control placement of DNA scaffolds for applications such as building and customizing metal nanoparticles, carbon nanotubes, and proteins, researchers often take advantage of the strong binding affinity between the protein streptavidin and a water-soluble compound called biotin. However, the biotin–avidin conjugation pair is nearly impossible to separate, which limits its applications when a reversible assembly is required.

To demonstrate their selective and reversible DNA binding process, the researchers encode their message by adding desthiobiotinylated DNA and biotinylated DNA to specific locations on tile scaffolds. When incubated with streptavidin, both anchor pairs grab up the protein, making them indistinguishable to an atomic force microscope (AFM). To decode, a biotin wash selectively competes off the desthiobiotin-bound proteins, while biotin-bound proteins remain attached. The difference in molecular structure becomes visible by AFM, revealing the previously encrypted message. Though the authors used the technique to decode an encrypted message and a letter pattern, the method could be applied to basically every situation where one might reversibly attach any streptavidin-modified nanomaterials to any biotin/desthiobiotin-modified nanostructures. **Jenny Morber, Ph.D.**