It is known that bone and tendon are piezoelectric, and it is believed that the piezoelectric charges produced under mechanical deformation in these tissues have a potential role in mechanoelectric transduction leading to their growth and remodeling. With high resolution PFM we probe piezoelectric properties in bone and show that single collagen fibrils are responsible for piezoelectric behavior of bone and behave predominantly as shear piezoelectric materials. Furthermore, we show that there is an intrinsic electromechanical heterogeneity in axial direction of individual fibrils that holds even for the collagen fibrils embedded in bone matrix. Such heterogeneity may have implications in regulating the ionic environment in bone responsible for bone remodeling.

3953-Plat
SAXS: Structure Verification of an S-Layer Protein using a Fractal Mean Force Potential
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Using a combination of SAXS and molecular dynamics simulations we get an integrated picture of the structure of S-layer proteins, for which no crystallized structure is currently available. S-layers are the most commonly observed cell surface structure of prokaryotic organisms and they are made up of identical protein subunits. One of the most striking properties of S-layers is that they are able to self-assemble into crystalline lattices in suspension and on various solid substrates. The resulting ordered molecular layer provides a matrix for the binding of various biomolecules and nanoparticles. Due to the complex biochemical properties of these proteins, classical techniques such as NMR or X-ray crystallography have not been able to provide an atomistic structural model for S-layer proteins. Motivated by the results obtained through the use of a fractal concept for the analysis of SAXS data in cluster physics, here we employ such fractal concept for the investigation of the structure of S-layer proteins. We fit the SAXS intensity as a function of the scattering angle using both a fractal form factor and a fractal structure factor. We compute the form factor by a Fourier transform of an average fractal delta function of characteristic units, thereby allowing us to investigate the presence of local, rather than global, electron densities in the structure of S-layer protein monomers. The structure factor is calculated by a Fourier transform of a fractal potential of mean force. Using this fitting function, we calculate the shape of the monomers, which is in good agreement with the shape obtained using molecular dynamics simulations. Our approach reveals itself as a novel means to get a detailed insight into the structure of proteins that adopt a fractal self-assembly and that lack of crystallized structure.

3954-Plat
Is Theory Leading Neutron Diffraction in Macromolecular Solvent Networks?
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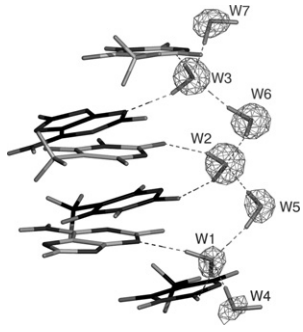
Standard crystallographic practice models electron scattering as a spherically symmetric phenomenon about atoms in the absence of any external effects. We have recently developed a polarizable atomic multipole refinement method for macromolecular crystallography that presents a significant improvement to the resultant information contained in an atomic model. We apply this method to high resolution lysozyme and trypsin data sets and validate its utility for precisely describing biomolecular electron density as indicated by a decrease in 5-6% in the R and Rfree values relative to the deposited values. The resultant models also illustrate the ability of force field electrostatics to orient water networks and catalytically relevant hydrogens that can be used to make predictions regarding active site function and activity. Finally, a DNA model generates the zig-zag spine pattern of hydrogen bonding in the minor groove without manual intervention. Comparison of the solvent networks with macromolecular neutron models suggest the hydrogen bonding patterns and distances generated by our protocol are more consistent with condensed phase measures and more likely to yield energetically favorable hydrogen bonds. The refinement technique proposed should be useful in applications to enzymology, drug design, and protein folding.



3955-Plat
Identification of Functional Surfaces of Proteins from Sequences
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The identification of protein functional surfaces is important for understanding enzyme mechanism, protein function prediction, compound-protein docking, and drug design. As the speed of rapid accumulation of protein sequence information far exceeds that of structures, it is important to construct accurate models of protein functional surfaces and identify key residues on these surfaces. A promising approach is to build comparative models from sequences using known structural templates. We assess how well this approach works by building three-dimensional comparative models of proteins using standard tools and determine how well functional surfaces can be accurately reproduced. We use the pocket algorithm based on alpha shapes computed for the modeled protein structures and characterize potential binding surfaces on these structures. Based on a large scale study, we give general criteria on when such comparative models can give accurate information on functional surfaces. We also provide assessment on the applicability of this approach to the universe of currently known protein sequences. We further point out methods for improved models of protein functional surfaces.

Platform BI: Imaging & Optical Microscopy II

3956-Plat
Self-Organization of the Escherichia Coli Chemotaxis Network Imaged with Super-Resolution Light Microscopy
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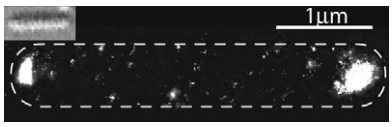
The Escherichia coli chemotaxis network is a model system for signal transduction and processing. Chemotaxis receptors assemble into large clusters containing tens of thousands of proteins which have been observed at cell poles and future division sites. Despite extensive study, it remains unclear how chemotaxis clusters form, what controls cluster size and density, and how the cellular location of clusters is robustly maintained in growing and dividing cells. Here, we use a super-resolution optical technique called photoactivated localization microscopy (PALM) to map the cellular locations of three proteins central to bacterial chemotaxis (the Tar receptor, CheY, and CheW) with a precision of 15 nm. We find that cluster sizes are approximately exponentially distributed, with no characteristic cluster size. One-third of receptors are part of smaller lateral clusters that have not been previously observed. Analysis of the relative cellular locations of 1.1 million individual proteins (from 326 cells) suggests that clusters form via stochastic self-assembly. The super-resolution PALM maps of E. coli receptors support a growing collection of evidence that stochastic self-assembly can create and maintain periodic structures in biological membranes, without direct cytoskeletal involvement or active transport.



3957-Plat
K-Space Image Correlation Spectroscopy of Quantum dot Labeled T Cell Receptors Characterizes their Nanoscale Clustering in Living Cells
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Changes in distribution of membrane receptor organization are used by cells to modulate the dynamic range of their responses to environmental cues. Consequently, it is important to develop experimental methods that can accurately measure receptor transport and aggregation. We used quantum dot (QD) labeling of T cell receptors (TCR) and a recently developed technique, k-space image correlation spectroscopy (kICS) to characterize TCR state as a function of cell differentiation. We developed kICS to measure transport coefficients of fluorescently labeled membrane proteins while taking into account nanoparticle emission blinking. We use kICS to measure T cell receptor (TCR) aggregation in live cells by characterizing quantum dot (QD) blinking and distribution on the cell surface. 2C TCR transgenic cells in culture were observed from the naïve state to 12 days after activation by antigen. Cells were labeled