it was allowed to move freely within the arrays in a supported lipid bilayer. T-cells were plated on arrays comprising individual TCR binding sites, small clusters and extended hexagonal close packed arrays, with spacings ranging from 40 nm and below to 1 μm. TCR signaling strength was monitored by measuring phosphorylated tyrosine (pY) intensity. T-cell adhesion was assessed by the number of cells bound to the arrays, as well as by the area of spread cells.

Systematic variation of the spacing and cluster size of TCR binding sites in the arrays enabled determination of the minimum conditions that support T-cell signaling and the formation of the IS. TCR signaling increased with decreasing spacing below a threshold spacing ~ 60 nm. For clusters with these spacings the formation of the stereotypical “bullseye” geometry that characterizes the immune synapse became evident, with ICAM-1 excluded to the periphery. In terms of stoichiometry, at least 4 TCR-binding sites (within ~ 60 nm) were required for T-cell adhesion and spreading. Further, in the absence of ICAM-1 (or at low concentrations), a threshold density of agonist sites was found above which the TCR apparently plays a dual role of immune activity and adhesion.

3185-Pos Board B615 Voltage Gating in Nanopores Containing Anthraquinone Mimics Biological Membrane Proteins Matthew Pevarnik, Weihin Cui, Luke Theogarajan, Electrical & Computer Engineering, University of California, Santa Barbara, Santa Barbara, CA, USA.

Ion channels formed by membrane bound proteins play a key role in the proper functioning of the human body. These membrane proteins are able to regulate the transport of water, ions, and larger molecules through small openings in the protein under a transmembrane potential. Much study has gone into illuminating how these membrane proteins sense voltage. Some mechanisms include charged residues in proteins that can reorient in an electric field or side chains that have an intrinsic dipole moment. Here we report the first synthetic nanopore to mimic and explore these possible mechanisms. We chemically attached a 9, 10 Anthraquinone (AQ) to the interior of an Alumina nanopore. In the presence of an applied voltage we found the AQ responds in a manner similar to biological pores exhibiting voltage gating. The conductivity versus voltage of the AQ modified nanopore followed a classic sigmoidal gating curve, identical to biological membrane proteins. Through this plot, it is possible determine the exact mechanism of the gating effect. In our system, we determined that the AQ was gaining one electron when the applied voltage reached a certain level. At this voltage level the AQ was reduced to form a radical semiquinone. The potential required to form the semiquinone state can be determined from the conductivity plot. This technique can also be applied to other molecules where the chemical reaction changes it response to an electric field, such as deprotonation, cation incorporation and radical formation.

3186-Pos Board B616 Modeling of the Liquid Crystal/Lipid Interface for Bio-Sensing Applications Donya Ohadi, Mark Uline, Vitalii Silin, David Vanderah, John P. Marino, 1Corning Inc, Corning, NY, USA, 2RPI, Troy, NY, USA, 3UPENN, Philadelphia, PA, USA.

The control of the orientation of liquid crystal thin films at surfactant-decorated interfaces is of primary importance in the development of liquid crystalline devices as well as many applications in biological systems. Highly detailed molecular level modeling of these interfaces is needed to help us to create liquid crystal-based sensors that respond to specific chemical and biological signals. These liquid crystal/surfactant systems have been studied extensively due, in part, to both their birefringence optical properties and orientational sensitivity to surface interactions. It is therefore critical to understand the interplay between the conformational entropy of the surfactants, the rotational entropy of the liquid crystals, the intermolecular and molecule-surface interactions, and the packing at the interfaces to be able to create design platforms for sensing applications using these systems.

In the absence of liquid crystal molecules, binary DPPC/DOPC lipid monolayers undergo phase transitions from liquid-expanded to liquid-condensed phases as the lipid areal density decreases. DPPC has two fully saturated fatty acid tails, and DOPC has two monounsaturated fatty acid tails. The area per molecule of this phase transition is highly dependent on the temperature and the composition of the monolayer. In this work, we present the effect of liquid crystal nematic elasticity on liquid-expanded/liquid-condensed phase diagram. We use theoretical model predictions for the phase behavior of liquid crystal thin films in the presence of various lipid monolayer mixtures to better understand the fundamental interactions that control molecular reorganization. These results shed light on the interplay between the conformational entropy of the lipids, the penetration of the liquid crystal into the lipid region, the propagation of the interfacial orientation to the bulk phase behavior of the liquid crystal film and the effects of liquid crystal orientation on the phase transitions of the lipids themselves.

3187-Pos Board B617 Surface Modification of Solid-State Nanopores for Sticky-Free Translocation of Single-Stranded DNA Zhipeng Tang, Peking University, Beijing, China.

Nanotechnology is one of the most promising approaches for fast and low-cost DNA sequencing application. Single-stranded DNA detection is primary objective in such device, while solid-state nanopores remain less explored than their biological counterparts due to bio-molecule clogging issue caused by surface interaction between DNA and nanopore wall. By surface coating a layer of polyethylene glycol (PEG), solid-state nanopore can achieve long lifetime for single-stranded DNA sticky-free translocation at pH 11.5. Associating with elimination of non-specific binding of molecule, PEG coated nanopore presents new surface characteristic as less hydrophlicity, lower 1/f noise and passivated surface charge responsiveness on pH. Meanwhile, conductance blockage of single-stranded DNA is found to be deeper than double-stranded DNA, which can be well described by a string of blobs model for a quasi-equilibrium state polymer in constraint space.

Biosurface Interactions

3188-Pos Board B618 Predicting Adhesion of Functionalized Nanocarriers for Specific Peptide Sequences using Atomic Potentials of Mean Force Matt McKenzie1, Aravind Rammohan2, Jacob Miner2, Natesan Ramakrishnan1, Ravi Radhakrishnan1, 1Corning Inc, Corning, NY, USA, 2RPI, Troy, NY, USA, 3UPENN, Philadelphia, PA, USA.

In this work we use atomistically computed potentials of mean force (PMF) between peptide sequences and cell surface receptors as inputs to a Monte Carlo based code for predicting adhesion of nanocarriers onto surfaces functionalized with peptides. Here we demonstrate the validity of this approach to capture adhesion equilibrium constants by implementing experimentally measured interaction potentials for the ICAM-1/ICAM system as a look-up table. This methodology was then propagated to predict adhesion for two different peptide sequences: KGEGPRGDYTR and GEGDSFFAFLRSPF. From ligand-docking studies, we derived the binding free energy, and estimated the PMFs and obtained the differences in adhesion equilibrium constants. This work showcases a method for incorporating sequence specificity in predicting adhesion equilibrium constants for nanocarriers onto functionalized surfaces.

3189-Pos Board B619 Activated Membrane Surfaces by Functionalized Peptides Daniel R. Scott1, Vitalii Silin, David Vanderah, John P. Marino, Susan Krueger1, Hirsh Nanda1, 1National Institute of Standards and Technology, Gaithersburg, MD, USA, 2Institute for Bioscience and Biotechnology Research, UMD, Rockville, MD, USA, 3Institute for Bioscience and Biotechnology Research, NIST, Rockville, MD, USA.

For integral membrane proteins (IMP), an assessment of their structures and interactions with other membrane proteins within a bio-mimetic lipid bilayer environment is critical for determining their cellular function. Hydrophobic sequences prevalent within the transmembrane domain(s) of IMPs, however, make these proteins susceptible to aggregation, and thus create difficulties in examining their structural and functional properties via canonical techniques. Working exclusively with transmembrane (TM) segments of polytopic membrane proteins - in the form of soluble peptides - bypasses many of the pitfalls of full-length protein preparations, while allowing for the opportunity to examine the properties of TM domains within bio-mimetic membrane environments. In this study, peptides mimicking the TM domains of the epidermal growth factor (EGFR) and CD4 receptors, both cell-signaling membrane proteins, have been reconstituted into POPC lipid bilayers. The formation of their native alpha-helical structure within vesicle membranes was observed from CD spectra, and proper orientation of the peptides passing through the membrane was demonstrated by tryptophan fluorescence using brominated lids. Functionalized with an N-terminal biotin tag, and utilizing an engineered planar lipid bilayer system ideally set up for surface plasmon resonance measurements, the TM peptides demonstrated capabilities of “activating” a membrane surface by the capture of streptavidin. Prospectively, these peptides
reconstituted as near-native membrane proteins within artificial bilayer systems could be utilized in formulating bioactive surfaces for powerful biomedical and biosensor applications. Novel techniques for re-forming the full-length IMP construct will be discussed.

3190-Pos Board B620
Characterization of Peptides Designed to Control Crystal Nucleation and Growth
Shourya Sonkar Roy Burman1, Michael S. Pacella1, James J. De Yoreo1, Jeffrey J. Gray1,2
1Chemical and Biomolecular Engineering, Johns Hopkins University, Baltimore, MD, USA; 2Biomedical Engineering, Johns Hopkins University, Baltimore, MD, USA.

Organisms, from algae to humans are known to mold complex, hierarchical hard tissues from minerals using biomolecular templates and additives. Molecular-level mechanistic understanding of how these biomolecules, particularly proteins, participate in the nucleation and growth of these inorganic crystals has been a longstanding goal. We design peptides with transformative abilities over calcite crystals using Rosetta. Based on the theory of how additives alter crystal nucleation and growth, we employ four modification strategies to modify the morphology of the crystal, viz. a peptide binding to a face, an array of peptides binding to a face, peptides pinning steps and peptides blocking kinks. To test the designs, we employ a variety of techniques ranging from measurements at the atomic scale to full crystal observations. We also investigate alternative mechanisms of modification by comparing the interactions predicted by Rosetta in other select states to those in the target state. For each design, we obtain the solution-state structure of the peptide by circular dichroism. To test peptides designed against a non-native face of calcite, we artificially stabilize the face for binding measurements. The overall crystal morphology change is then tested by incubating supersaturated precursor solutions with the design peptides. To confirm the predicted mechanism of growth alternation, we observe the change in kinetics of calcite step growth with peptide doping using in situ AFM, and report calcite step velocities. Finally, by nucleating calcite on a monolayer of the designed peptides, we examine the face on which calcite nucleated and compare it to our target face. These experimental results provide a feedback loop to the next generation of designs and enable the rational design of bio-surface interactions.

3191-Pos Board B621
Examining Bacterial Cell Interactions using Atomic Force Micorscopy
Ronald Aucapina, Nadia Ouedraogo, Megan A. Ferguson.
SUNY New Paltz, New Paltz, NY, USA.

Given the prevalence of bacterial biofilms in both native and engineered environments, our understanding of their interactions with both other bacteria and abiotic surfaces is quite limited. In this research we use an AFM to analyze the interactions of bacteria such as E. coli and a saprophytic, biofilm forming variant of B. bacteriovorus with other bacteria and chemically characterized surfaces. Tipless AFM cantilevers were left unmodified (Si3N4), or coated with a monolayer of E. coli. These cantilevers were then used to collect force curves on biofilms of B. bacteriovorus and E. coli as well as chemically characterized surfaces such as mica, silicon, and poly-L-lysine-coated glass. The greater the cantilever’s contact time with the surface, the more force and energy was required to retract from the surface. E. coli-coated cantilevers had more adhesion to B. bacteriovorus biofilms than to E. coli biofilms, but even E. coli - B. bacteriovorus interaction paled in comparison to adhesion between E. coli biofilms and abiotic surfaces. Further results probing biofilms with cantilevers that have been chemically modified with acid or amine groups will be presented.

3192-Pos Board B622
A Self-Consistent Multiscale Methodology for Predicting Adhesion of Mammalian Cells onto Functionalized Surfaces
Aravind R. Rammohan1, Matthew McKenzie1, Jacob Miner2, Natesan Ramakrishnan3, Ravi Radhakrishnan1
1Corning Inc., Corning, NY, USA; 2RPI, Troy, NY, USA; 3UPENN, Philadelphia, PA, USA.

Predicting cell adhesion onto surfaces functionalized with peptides is inherently a multiscale problem since the adhesion interface is mediated largely by interactions of specific peptides with surface receptors. This interaction occurs over length scales on the order of nanometers, while typical mammalian cells are on the order of microns. In this work, we showcase a self-consistent approach for obtaining specific of interactions between peptide sequences and receptors, and then applying this chemical information to describe these interactions for cells that are decorated with these receptors. Using this approach we present adhesion equilibrium behavior for 3 different receptor-peptide sequences across a range of length scales, from 50 nm, to 500 nm. We believe this approach offers a clear path to scaling up to mammalian cells (5-20 microns).

3193-Pos Board B623
Mapping Interactions between Silver Nanoparticles and Biomolecules at the Atomic Level
Jeffrey Comer1, Horacio Pobleto2, Emilio I. Alarcon3
1Nanotechnology Innovation Center of Kansas State and Institute of Computational Comparative Medicine, Kansas State University, Manhattan, KS, USA; 2Center for Bioinformatics and Molecular Simulations, Universidad de Talca, Talca, Chile; 3Bio-nanomaterials Chemistry and Engineering Laboratory, University of Ottawa Heart Institute, Ottawa, ON, Canada.

The association of biomolecules with silver nanoparticles (AgNPs) has been shown to modify the nanoparticles’ stability as well as their behavior in the physiological environment. However, the details of how silver nanoparticle surfaces – replete with heterogeneities – interact with the equally heterogeneous surfaces of biomolecules remain elusive, yet essential to understanding the origin of the biological activity of AgNPs. Leveraging molecular dynamics simulation and free-energy/kinetics calculations, we have constructed maps detailing interactions of bare and functionalized AgNPs with peptides, proteins, and lipid bilayer membranes.

3194-Pos Board B624
Protein Corona and Secondary Structure in Response to Nanoparticle Pegylation
Sabina Runa1, Alexandra Hill1, Victoria Cochran2, Christine Payne1
1School of Chemistry and Biochemistry and Petit Institute for Bioengineering and Bioscience, Georgia Institute of Technology, Atlanta, GA, USA; 2Department of Chemistry and Chemical Biology, Harvard College, Cambridge, MA, USA.

Nanoparticles are versatile tools for biophysical applications. Using these particles requires a close examination of the protein corona: the layer of proteins that adsorbs onto the particle surface. Modifying nanoparticle surfaces with polyethylene glycol (PEG) has been shown to reduce corona formation. Because tightly bound ‘hard’ corona proteins can block surface ligands that could be used in targeting applications, a reduction in corona is desirable and can enhance our ability to effectively utilize nanoparticle surface modifications. First, gold nanoparticles were PEGylated and characterized with dynamic light scattering. Using gel electrophoresis, a three-fold decrease in corona formation was found for PEGylated nanoparticles compared to bare nanoparticles. With a reduction of corona confirmed, we next investigated the secondary structure of the corona proteins. PEGylated and bare nanoparticles were incubated with bovine serum albumin, the most prevalent serum protein. Using CD spectroscopy, we probed the secondary structure of the adsorbed albumin. Significant structural changes were not detected. In addition, bovine serum albumin, α2-macroglobulin, and transferrin were each incubated with free PEG. Once again, no alteration of protein secondary structures were found, even in the presence of a one hundred molar excess of free PEG. These results conclude that PEG can quantitatively reduce corona formation without altering structural aspects of corona proteins.

3195-Pos Board B625
A Theoretical Study of Polymer-Based Drug Delivery Systems
Ebitisam A. Alداا3, Mark J. Uline3
1Biomedical Engineering, University of South Carolina, Columbia, SC, USA; 2Biomedical Engineering, University of Dammam, Dammam, Saudi Arabia; 3Chemical Engineering, University of South Carolina, Columbia, SC, USA.

A variety of interactions between drug delivery devices and local cells and tissues impact clinical outcomes in terms of both therapeutic action and biological response. Understanding the competition of interactions in highly inhomogeneous environments such as those relevant in tissue engineering, nanotechnology, and those responsible for biological cell function is critical to the further development of design platforms for delivery systems. We use a three dimensional mean-field theory to study the competition between electrostatic, van der Waals and steric interactions in determining the molecular organization of micelles made of amphiphilic diblock polypeptides designed to carry doxorubicin to cancer cells. The micelles are assumed to target cancer cells primarily through electrostatic binding as several cancers are known to flip negatively charged lipids to the outer-leaflet. The polyelectrolyte micelles spontaneously form self-assembled aggregates whose physical properties are manipulated by the composition of the solution in contact with the polymer system. These theoretical calculations show that chemical equilibrium and the relevant physical interactions present in responsive polymer micelle couple in such