a backshift in the activation pathway [3]. Additionally, recent ^{2}H nuclear magnetic resonance (NMR) studies on retinal bound to rhodopsin hint towards a much lower methyl rotation activation barrier than observed in previous MD simulations [4]. Here we report quantum chemical calculations of torsional surfaces of model compounds and molecular dynamics (MD) simulations of the proteolipid complex in full atomic detail, to aid in the interpretation of the body of experimental data. Specifically, by using larger retinal fragments and a higher level of theory (MP2/cc-pVDZ), we are able to accurately reproduce the rotational behavior observed from ^{2}H NMR relaxation data [4]. For example, the relaxation data indicate an unusually low activation energy (E_a) for C9-methyl rotation, due to intraretinal interactions with H7 and H11 of the retinal polyene chain. These results in turn should lead to the ability to begin to simulate the coupling of small- to large-scale motions in rhodopsin activation. Ultimately, these efforts are aimed towards modeling more accurate comparisons to other GPCR proteins. [1] P.-W. Lau *et al.* (2007) *J. Mol. Biol.* 372(4) 906-917. [2] K. Martínez-Mayorga *et al.* (2006) *J. Amer. Chem. Soc.* 128(51) 16502-16503. [3] R. Vogel *et al.* (2006) *Biochemistry* 45(6), 1640-1652. [4] M.F. Brown *et al.* (2009) *Biochim. Biophys. Acta*, in press.

2924-Pos
Towards a Computational Model of Lignocellulose: Molecular Simulation of Lignin
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Atomic-detailed computational models of lignocellulose can complement experiments in understanding its structure and dynamics. Here, we present results of Molecular Dynamics simulation of the plant cell wall polymer lignin. Polymer theory is employed to interpret these results. Finally the steps towards a realistic model of lignocellulose are discussed.
1. L. Petridis and J.C. Smith (2009); A molecular mechanics force field for lignin; Journal of Computational Chemistry 30 457-467
2. R. Shulz, B. Lindner, L. Petridis and J.C. Smith (in print); Scaling of Multimillion-atom Biological Molecular Dynamics Simulation on a Petascale Supercomputer; DOI: 10.1021/ct900292r

2925-Pos
Molecular Simulations of Dodecyl-D-Maltoside Micelles in Water: Influence of the Headgroup Conformation and the Force Field Parameters
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Dodecyl-D-maltoside (DDM) is a non-ionic glycolipid detergent with a maltose headgoup and a dodecan chain. It is used for the extraction and purification of membrane proteins from their natural environment. DDM has two anomers: one with a linear conformation (beta) and one with a right angle bend between the headgoup and the alkyl tail (alpha). Experiments show that the headgroup conformations change the micelle properties. However, little is known about the influence of the surfactant conformation on the micelle internal structure and hydration properties. To examine these aspects, we have used molecular dynamics (MD). MD was performed with micelles containing 75 and 132 alpha-DDM and beta-DDM monomers, respectively, at ambient conditions with different parameters (CHARMM22 and a newly developed force field (ff) compatible with GLYCAM06). We analyse the simulations in terms of the aggregate structure, surfactant conformations and interfacial water dynamic properties. Our results show that micelle properties vary with the force field used and that the simulations performed with the GLYCAM reproduce better the experimental findings from SANS or NMR. The micelles are slightly ellipsoidal with dimensions around 20.0 and 26.4 Å. The structures of the aggregate do not change significantly with the ff. Surfactant and the headgroup conformations show similar behaviour with an exception for the ether link between the headgroup and the tail. The dynamics of the interfacial water are 7-10 times slower than that of bulk water and seem, surprisingly, to be independent of the headgroup conformation. Finally, to evaluate the robustness of the simulations, we also performed additional runs with a new release of the CHARMM ff for disaccharide with new optimized parameters for the ether link. Comparison of these runs with the preceding simulations will be presented.

2926-Pos
Dynamics in Tethered Particle Motion: Interpreting the Observations
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Tethered Particle Motion (TPM) enables the researcher to examine the properties of semi-flexible polymers at the single molecule level. In TPM, a small reporter particle is tethered to a substrate using the polymer of interest. The particle motion reflects the mechanical properties of the tethering polymer.
We will present a framework in which the influence of the different experimental aspects on the measurement outcome are quantified. The key elements are tether length, particle size, exposure time, fluid properties and frame rate.
Here, we use 80 nanometer diameter gold particles, tethered to a glass slide by double stranded DNA, that are visualized by dark field microscopy. The recorded images of these highly scattering particles have a high contrast and signal-to-noise ratio; therefore the particle can be tracked with high spatial resolution (5-20 nm).
High temporal resolution is necessary to distinguish between different diffusion regimes. At very short time scales the particle is freely diffusing and on longer time scales its motion is influenced and eventually restricted by the retracting harmonic force of the tether. We will show that the diffusion coefficient of the free motion on short time scales is composed of the diffusion properties of both the particle and tether and that the harmonic potential stems from the entropic elasticity of the tether molecule. Motion blur caused by the finite exposure time has to be considered for computing the diffusion constant. Lastly, the choice of tether length and particle size play an important role as well. They determine how often the particle will be in proximity of the substrate where particle-substrate interactions such as van-der-Waals and electrostatic forces play a bigger role.

2927-Pos
Md-Based Method for Computing Configuration Integrals Provides Ability to Test Force Fields
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Modern force fields allow the study of biological molecules in atomistic detail. However, too often computational limitations prohibit one from computing many biologically relevant measures such as folding energies and rates, differential population of alternate biological states, and binding affinities. This makes it difficult to test and improve upon the accuracy of force fields for such thermodynamic applications. In this work, new methods are presented for computing the configuration integral of biological molecules both around specific structural states as well as over all of phase space. These methods are based on Molecular Dynamics simulations and can be applied with any force field, including ones with explicit solvent. The methods are applied to study several problems. First, as a proxy for the random-coil state, free energies of hexa- and hepta- peptides are studied as a function of their sequence. Surprisingly, it is demonstrated that the Random Energy Model describes quite well the relationship between sequence and energy, indicating that individual amino acids contribute to the overall free energy largely in a context-independent manner. Second, the ability of EEF1 force field to reproduce experimental helix propensities is studied by computing relative helix folding energies of short peptides. Values computed for polar and non-polar amino acids, separately, show moderate correlation with experimental data. However, the two groups are out of scale with one another, indicating an imbalance between polar and hydrophobic interactions in the force field. Further, each group has two clear outliers - Val/Ile for non-polar amino acids and Lys/Arg for polar ones, suggesting additional avenues for improvement of EEF1. The success of the presented methods has far reaching implications not only for force field development and validation, but also for such areas as computational protein design and drug discovery.

2928-Pos
Molecular Dynamics Simulations of the AAA Protein P97
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The mechanocoupling of energy stored in triphosphate nucleosides provide the power necessary for many fundamental *in vivo* processes. The highly abundant protein p97 (also known as valosin-containing protein) is one of the most widely studied members of the AAA protein family (ATPases Associated with various cellular Activities), and is involved in numerous cellular functions such as nuclear envelope assembly, retrotranslocation of misfolded proteins from the endoplasmic reticulum to the cytosol, reformation of the Golgi following mitosis, and the IκBα pathway. Structurally, each monomer is composed of two hydrolysis domains (D1 and D2 with only D2 being catalytically active under standard cellular conditions), an N-terminal domain that interacts with effector proteins, a C-terminal domain, and linker regions between them. In solution, proteins hexamerize into stacked-ring shaped complexes with rings formed by each of the hydrolysis domains. Here, we present results from molecular dynamics simulations on each of the four predominant hydrolysis states