1524-Pos Board B368
Synthetic, Protein-Based Molecular Motors
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We present an approach that will lead to an understanding of the operational characteristics of biological molecular motors by designing and modeling synthetic molecular motors that use a combination of natural and designed biological components. One such design is a protein-based rotationally diffusive motor dubbed the Tumbleweed (TW). This is a tri-pedal self-assembling complex in which each foot is able to bind to a unique binding site located periodically on an effective 1D track, and where the binding of each foot is controlled by a unique ligand in solution. The TW motor construct incorporates a combination of biological repressor proteins, a *de-novo* coiled-coil protein structure, and a dsDNA track. We present simulation results of the TW motor that exhibit unidirectional motion and a maximum theoretical speed of 0.01-0.1 mm/s, which is limited by rotational diffusion. Experimental limitations, such as the exchange of ligands in solution, will most likely reduce the motor speed to 10-100 nm/s, which is comparable to biological molecular motors.

1525-Pos Board B369
Theoretical Models of Eumelanin Protomolecule and Its Photoprotection Mechanism
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The molecular structure of melanin, one of the most ubiquitous natural pigments in living organisms, is not known and its multifaceted biological role debated. We examine structural models for eumelanin protomolecules, based on tetramers consisting of four monomer units (hydroquinone, indolequinone and its two tautomers), in arrangements that contain an interior porphyrin ring. These models reproduce convincingly many aspects of eumelanin's experimentally observed behavior. In particular, we present a plausible synthetic pathway of the tetramers and their further complexation through interlayer stacking, or through formation of helical superstructures, into eumelanin macromolecules. The unsaturated nature of C-C bonds in indolequinone units and the finite size of protomolecules introduce covalent bond formation between stacked layers. We employ Time-dependent Density Functional Theory to calculate the optical absorption and the relaxation dynamics of melanin model constituents. The results explain the ability of these molecules to transform photon energy into thermal energy in a remarkably short time scale of ~100 femtoseconds (fs). We find that following electronic excitation by light absorption, ultrafast energy conversion takes place through two novel mechanisms: proton transfer on a timescale of 110 fs and state mixing upon oligomerization on a time scale of $<$50 fs. These results are in good agreement with available experiments and help elucidate melanin's role in photoprotection against ultraviolet radiation.

1526-Pos Board B370
A Brownian Dynamics model of separation-by-partitioning in nanofluidic devices
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We present a Brownian Dynamics model for describing the performance of nanofluidic devices used for biological molecule separation. Our present work focuses on the process of separation of electric-field-driven DNA molecules by partitioning, using periodic nanofilter arrays. Our results show that experimental results for molecules up to 20 persistence lengths can be modeled using the worm-like-chain model, provided free draining behavior is appropriately accounted for in the model.
In particular, our model is able to capture the experimental results of Fu et al. [Phys. Rev. Lett., 97, 018103 (2006)] using realistic values of all physical parameters while being more efficient than explicit molecular dynamics methods.

1527-Pos Board B371
Free Energy Landscape For Biological Systems
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We have investigated methods of constructing free energy landscape of a few biological systems. For simple enzyme kinetics reaction, using a method developed by Ao and coworkers, we have constructed the energy landscape around the stable fixed point. However the landscape resembles that of a saddle point. The discrepancy may come from the slow convergent property of the series used. We also tried solving the master equation for equilibrium statistical distribution, and based on this distribution we can construct the energy landscape which looks qualitatively correct. Following the latter procedure and based on stochastic dynamics we can construct energy landscape of a minimal model for immune response which shows bistability. Finally, a similar procedure is applied to construct the energy landscape for a minimal model of p53 oscillating loops which exhibits limit cycle behavior.

1528-Pos Board B372
Primary Electronic Response In Biomolecules Exposed To X-ray Laser Radiation
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The ultra intense femtosecond X-ray pulses from free electron lasers that are being developed in Hamburg and Stanford hold the promise to obtain X-ray scattering information from single molecules, even from proteins [1]. This technique could enable monitoring ultrafast atomistic dynamics in proteins and other biomolecules at the single molecule level. At such short wavelengths the X-ray photons will eject electrons from the sample. This will lead to a coulomb explosion of the nuclei. Thus it is crucial how much time-resolved structural information can be expected from a single molecule diffraction experiment. To address this question, we have begun to develop a method to simulate the electronic response of biomolecular systems subject to electron emission. Due to their strong binding to the nuclei, the inner shell electrons show significantly larger X-ray cross section than the outer electrons, such that the initial event will be the nearly instantaneous partial removal of the inner shells. The resulting fast re-filling dynamics by electrons of the outer shells will critically determine the atomic dynamics and the pace of the Coulomb explosion.
In our simulations, a stochastic criterion is used to generate an initial open shell system based on the cross sections. We use Hartree-Fock level of theory and gaussian basis sets to treat the initial state. The expansion coefficients of the basis functions are taken to be time-dependent. Thus the expansion coefficients are propagated by the time-dependent Schroedinger equation. This time-dependent approach is currently applied to a one dimensional model system. We plan to apply it to real molecular systems. Our goal is to treat systems up to the size of a peptide.
[1] R. Neutze, et. al., ''Potential for biomolecular imaging with femtosecond X-ray pulses'', Nature, 406, 752 (2000).

1529-Pos Board B373
Revisiting Anomalous Diffusion Due To Molecular Crowding
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Molecular diffusion is called anomalous when the mean-squared displacement of a moving particle does not increase linearly with time. Several simulation works demonstrated anomalous diffusion, as opposed to normal (i.e., Brownian) diffusion, in crowded environments with fixed and/or mobile obstacles. Experimental measurements often report a reduction of molecular diffusion but not necessarily anomalous diffusion in the cytoplasm. Here we propose two possible reasons for the discrepancy between simulations and experiments on diffusion in crowded environments.
First, some of the previously developed algorithms might not accurately simulate three-body or higher order molecular collisions in the crowded environment. To this end, we have developed an event-driven, exact collision detection algorithmic scheme and systematically studied the impact of crowding on molecular diffusion. When these higher-order collisions are explicitly taken into account, the anomalous diffusion in 3D seen with the previously developed algorithms becomes less prominent or disappears.
Second, experimental analyses that suggested anomalous diffusion might have been problematic. This is particularly relevant to fluorescence correlation spectroscopy (FSC). Unlike single-particle tracking (SPT), FCS does not provide direct information about trajectories of individual molecules. It relies on the analysis of fluctuations in the number of fluorescent particles in a focused laser spot. The diffusion of molecule is inferred from the shape of the autocorrelated fluorescent signals fitted to a mathematical formula purportedly representing anomalous diffusion. However, the latter formula was derived from a modified diffusion equation, which may not have physical basis, thus leading to potentially erroneous data analysis. We propose a new FCS autocorrelation formula based on continuous time random walk theory and fractional diffusion equation.
Finally, we use this new FCS formula and the novel event-driven algorithm to simulate diffusion in crowded environments and discuss possible reconciliation of discrepancies between previous simulations and experimental data.