Undergraduate Research Symposium May 17, 2013 Mary Gates Hall

Online Proceedings

POSTER SESSION 3

MGH 241, Easel 131

2:30 PM to 4:00 PM

Quantification of Quantum Dots in Solution using Surface Plasmon Resonance and Analytical Ultracentrifugation

Chinonso C (Chinonso) Opara, Junior, Biochemistry
Amgen Scholar, McNair Scholar
Mentor: William Atkins, Medicinal Chemistry
Mentor: John Sumida, Medicinal Chemistry

Quantum dots are nanoparticles with several applications including cellular imaging and drug delivery. Because of quantum confinement, their ability to fluoresce under ultraviolet light is size dependent. However, quantum confinement not only plays a role in emissive properties, but is also a factor in the absorbance spectrum of quantum dots. As a result, there is not a simple relationship between the concentration of quantum dots and optical density. It is the goal of this project to craft a new approach in accurately measuring the concentration of quantum dots in solution. We have determined a correction factor relating response units as measured by surface plasmon resonance (SPR) to values of refractive index. With this, we further use SPR in conjunction with analytical ultracentrifugation (AUC) to determine the concentration dependence of the refractive index, dn/dc, for TOPO-PMAT quantum dots. The measurement of dn/dc for the quantum dots allows us to use an interferometric determination of their total fringe increment observed by AUC synthetic boundary to measure the concentration of quantum dots in solution. We have estimated a dn/dc for 565 TOPO-PMAT CdSe quantum dots. In addition, we have used AUC to show that total fringe increments scale with concentration. Furthermore, we have estimated mass extinction coefficients for all wavelengths at which absorbance is observed for these quantum dost. This allows for UV-vis determination of concentration. Our results indicate that our strategy holds promise for providing a new method for measuring the concentration of quantum dots in solution.

POSTER SESSION 3

Commons East, Easel 54

2:30 PM to 4:00 PM

Understanding the Function of the gpFI Protein in Bacteriophage Lambda Virus Assembly

Angelo Esquivel (Angelo) Condulle, Fifth Year, Postbaccalaureate Study
Mentor: Carlos Enrique Catalano, Medicinal Chemistry

Double stranded DNA (dsDNA) viruses such as herpesviruses, adenoviruses, and many bacteriophages, have common development pathways. In these cases, a packaging motor (the terminase enzyme) inserts the viral genome into a capsid shell. We study the DNA packaging motor from phage lambda as a model system. Lambda terminase plays four critical roles in virus assembly: (1) It has a site specific DNA binding activity where it binds to the cos sequence in the lambda genome, (2) it has an endonuclease activity where it symmetrically nicks the duplex at the cosN site, (3) it has a strand-separation activity that separates the cleaved DNA strands, and (4) it has "packaging" activity where it translocates the "matured" viral genome into a capsid shell through a portal ring structure. The lambda gpFI protein is required for virus assembly in vivo but the function remains unknown. In this study, we use a defined in vitro system to study the effects of gpFI on the endonuclease, strand-separation, and DNA packaging activities of lambda terminase as our first steps towards an understanding the function of gpFI in virus assembly. Our data demonstrate that gpFI affects the cos-cleavage and strand-separation activities of terminase. In contrast, the protein significantly increases the efficiency of DNA packaging in vitro. In addition, we demonstrate a direct interaction between gpFI and the procapsid shell. The significance of these results with respect to the biological role of gpFI in virus assembly is discussed. The information obtained from these experiments will be useful in understanding similar processes in the eukaryotic herpesviruses and adenoviruses.

POSTER SESSION 4

MGH 241, Easel 136

4:15 PM to 5:45 PM

Isolation and Biophysical Studies of the Influenza M1 Viral Protein

Chloe Anne Goolsby, Senior, Dance: Creative Studies, Biology (Molecular, Cellular & Developmental)
Howard Hughes Scholar, Mary Gates Scholar
Mentor: Kelly Lee, Medicinal Chemistry

Influenza has long plagued the human population, and continues to cause sickness throughout the world. As an enveloped virus that utilizes the process of endocytosis to enter and infect cells, it must fuse its membrane with the host's endosomal membrane in order to deliver its genetic material to the cell. This specific process is mediated by the viral glycoprotein hemagglutinin. Through my research, I hope to determine the underlying mechanisms of the HA-mediated fusion process. One aspect of the membrane fusion process that remains poorly understood involves the association between HA and the internal structural protein M1 or matrix protein. It has been hypothesized that these work together to keep the virus intact while the host membrane is remodeled. The M1 protein is located between the viral envelope and ribonuclear core, and is believed to be a bridge between these two layers. We hypothesize that the interactions between the cytoplasmic tail of HA and the M1 protein layer in the virus interior are disrupted in a low pH environment. To test this hypothesis, I have isolated and purifyed the influenza matrix protein from whole virus particles. Having obtained a pure matrix protein, I can further study the oligomerization process and start to determine the behavior of the M1 protein in solution. I hope to be able to use dynamic light scattering and gel filtration chromatography to observe the M1-M1 complexes. I will also examine how M1 interacts with membranes of different compositions using lipid flotation gradients and electron microscopy. By understanding the dynamics of M1 secondary structure and HA membrane fusion, my research could help to generate information for rational drug and vaccine targets against the influenza virus.