To combat the deleterious effects of radiation and other stresses on long-term human space exploration, it is critical to better understand cardiovascular cell function. The correlation of molecular activities and mechanic-electro performance of muscle cells will provide us with complete dynamic data to develop adequate countermeasures to combat these adverse effects. Unlike the conventional measurements techniques, we have created a novel method capable of in situ characterization of the mechanical properties of muscle at both tissue and single-cell levels using a self-assembly system. This system has shown the capability of spatially and selectively directed growth and differentiation of myocytes into single muscle bundles in situ, attachment of these functional bundles to MEMS structures, and the controlled release of the resultant hybrid devices without any manual assistance. The mechanical properties of the neonatal ventricular myocytes 1-3-day-old Sprague-Dawley rats (NRVMs), such as substrate-induced stress and Young's modulus, have been measured using this force transducer and were found to be 2-2.5 kPa and 40 kPA respectively. Here we expand this system to dynamically monitor the cellular activities in response to the external applied stresses. It has been noted that intracellular calcium concentrations of cardiac myocytes fluctuate between 10-5M - 10-7M upon contraction and relaxation respectively. Using an intracellular fluorescent calcium indicator we can correlate fluorescent density with cellular function. By monitoring the fluorescent signal, we can visualize calcium fluxes and in turn determine what state a particular cell is in. In addition to detecting cellular activity, the effect of UV radiation and mechanic stresses on the cells are also under investigation. Further study of genetically engineered cells will enable us to in situ monitor the molecular and genetic information and simultaneously investigate the correlation of their activities with the external applied stresses. The self-assembly system established is not only suitable for studying dynamic mechanics of muscle cells, including the correlation of intracellular activities with external factors, but also applied to the studies of other cells.

SESSION K10: Biomaterials: Theory and Experiment
Chair: Elaine DiMasi
Friday Morning, April 1, 2005
Room 2007 (Moscone West)

8:30 AM K10.1
Simulations and Design of a New Green Fluorescence Protein Mutant. Murat Cetinkaya[1], Ahmet Zeytun[2], Andrew Bradbury[2] and Melik C. Demirel[1]; [1]Engineering Science and Mechanics, The Pennsylvania State University, University Park, Pennsylvania; [2]Bioscience Division, Los Alamos National Laboratory, Los Alamos, New Mexico.

A set of new green fluorescence protein (GFP) mutants are experimentally created by modifying four loop regions of GFP. The excitation / emission spectra of a number of different GFP mutants were determined and some GFPs showed a reduction in both the absorption and emission at each wavelength. We have performed molecular dynamics simulations of these mutants using the AMBER force field. We especially concentrated on loop3 (residues 171-175) modifications since new residue insertions to this region cause drastic changes in fluorescence intensity properties. A possible explanation is the quenching of the chromophore located at the center of the structure due to local unfolding. A 10 ns molecular dynamics simulation showed that insertion in the loop3 region creates local unfolding of the "beta-can" structure of GFP, confirming our hypothesis for the change in fluorescence intensity of the protein. We have also performed simulations regarding other loop regions and compared with the corresponding experimental data.

8:45 AM K10.2
Nano-Phononics in Biological Systems. Alexander A. Balandin and Vladimir A. Fonoberov; Nano-Device Laboratory, Department of Electrical Engineering, University of California, Riverside, California.

Viruses have recently attracted attention as biological templates for assembly of nanostructures and nanoelectronic circuits [1]. They can be coated with metals, silica or semiconductor materials and form end-to-end nanorod assemblies. Such viruses as tobacco mosaic virus (TMV) and M13 bacteriophage have appropriate cylindrical shape and particularly suitable dimensions: M13 is 860 nm long and 6.5 nm in diameter, while TMV is 300 nm long, 18 nm in diameter and with a 4 nm in diameter axial channel. The knowledge of the phonon, i.e. vibrational, modes of these viruses is important for material and structural characterization of the virus-based nano-templates, for in-situ monitoring of the nanostructure self-assembly, and for understanding properties of the biological-inorganic interfaces. In this paper we review our recent theoretical and experimental results on phonon spectra of TMV and M13 bacteriophage immersed in air and water. The low-frequency phonon dispersion has been rigorously calculated using the complex-frequency approach. The radial breathing modes of TMV and M13 viruses in air are found to be 1.85 cm-1 and 6.42 cm-1, respectively. If the viruses are in water, the above frequencies become 2.10 cm-1 and 6.12 cm-1, respectively [2]. The quality factor Re(w)/Im(w) for radial vibrations of TMV in water is about 3.6 for the radial breathing mode and about 10 for the second radial mode. Structurally informative bands of the vibrational spectrum have been studied experimentally by means of the non-resonant micro-Raman spectroscopy. We analysed the damping of vibrations in water and discussed the application of the micro-Raman spectroscopy for monitoring of the virus-based self-assembly processes [3]. The authors acknowledge the financial and program support of the Microelectronics Advanced Research Corporation (MARCO) and its Focus Center on Functional Engineered Nano Architectonics (FENA). [1]. W. Shenton, et al., Adv. Mater. 11, 253-256 (1999); C.E. Flynn, et. al., Acta Materialia 51, 5867-5880 (2003). [2]. V.A. Fonoberov and A.A. Balandin, Phys. Stat. Sol. B 241, R67-R69 (2004); A.A. Balandin and A.V. Fonoberov, Vibrational modes of the nano-template viruses, J. Biomedical Nanotechnology, in press, 2005. [3] see details at http://ndl.ee.ucr.edu/

9:00 AM K10.3
Guanine Quartet Networks Stabilized by Cooperative Hydrogen Bonds. Roberto Otero Martin, Maya Schoeck, Luis M. Molina, Erik Laegsgaard, Ivan Stensgaard, Bjork Hammer and Flemming Besenbacher; Department of Physics and Astronomy, University of Aarhus, Aarhus, Denmark.

Hydrogen bonding between DNA or RNA bases is one of the main interactions that determine the conformation and biochemical interactions of nucleic acid (NA) molecules. Apart from the Watson-Crick model for base pairing, NA bases can form other hydrogen-bonded aggregates that lead to different DNA structures, like G-quadruplexes or i-motifs. In spite of the increasing evidence for the in vivo existence and function of these structures, the exact physico-chemical nature of the hydrogen bonds and the importance of charge transfer contribution to the stabilization energy associated to hydrogen bonding in these structures is still under debate. Here we show, by high-resolution, variable-temperature Scanning Tunnelling Microscopy (STM), that the NA base guanine (G), deposited under ultra-clean conditions onto the inert Au(111) substrate, self-assembles into a hydrogen-bonded network of G-quartets with the same structure as that found in quadruplex telomeric DNA. Comparison with our Density Functional Theory (DFT) calculations shows that the strong preference of G molecules to form quartets arises from a cooperative effect that strengthens the hydrogen bonds within the G-quartet network relative to those in isolated G dimers.

9:15 AM K10.4
Molecular Recognition in 2D Binary Mixtures of DNA Bases Studied by STM. Maya Schoeck, Eva Rauls, Roberto Otero Martin, Wei Xu, Erik Laegsgaard, Ivan Stensgard, Bjork Hammer and Flemming Besenbacher; Department of Physics and Astronomy, University of Aarhus, Aarhus, Denmark.

Molecular recognition events between complementary nucleic acid bases are fundamental for many biological processes, like DNA replication. These processes have found an application in the field of Nanotechnology, and strands of complementary DNA sequences have been used to direct the self-assembly of nanostructures. In principle, the complementarity in hydrogen-donors and acceptors groups in single DNA bases might as well lead to molecular recognition processes, that could be used to control 2D molecular assemblies as well. However, the existence of "wobble" or "deviant" base pairs, and a possible disturbing effect of the substrate on the hydrogen bonds made this possibility more difficult to explore. In this contribution we compare the 2D molecular networks formed on Au(111) upon deposition of the binary mixtures G-C (purine-pyrimidine pair of complementary bases) and A-C (purine-pyrimidine pair of non-complementary bases) by means of a combination of STM experiments and DFT calculations. We show that, after a gentle annealing to 80 C the non-complementary bases segregate into islands of pure A and a network of pure C, whereas the complementary bases G and C form a network that cannot be separated by annealing up to the desorption temperature for C. High-resolution STM images allow us to identify structures that contain G-C bonds, possibly with the a structure similar to the Watson-Crick pairs in DNA molecules. The stronger bond between G and C molecules with respect to G-G or G-C pairs explain the enhanced thermal stability of the combined G-C mixture. This result shows that the hydrogen-bonding interaction alone can steer the processes necessary for molecular recognition to take place in 2D networks, thereby opening new avenues to design molecular self-assemblies with desired geometries.

9:30 AM K10.5
A Solution to the Streptavidin-Biotin Paradox? Frederic Pincet and Julien Husson; Laboratoire de Physique Statistique, Ecole