individual repeats or their alpha-helical subunits. We also present evidence for the capture of unfolding/refolding transient events while stretching or relaxing by AFM and analyze differences in refolding lengths and forces for each repeat. This class of stacked helical-repeats behave as molecular nanosprings, are likely important for cellular mechanosensation, and can be used as platforms for structural elements of nanomechanical systems based on proteins. Supported by the NIH (PEM) and HHMI (VB).

3077-Pos

High Force Elastic Profiles of Single and Double Stranded Polynucleotides Probed with AFM Force Spectroscopy

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Elasticity is an important property of nucleic acids. During cellular processes, DNA and RNA are subjected to various mechanical forces which greatly deform their original structure. Also, in the field of DNA nanotechnology, an understanding of how DNA will react to mechanical loading will allow for the design of novel nanostructures with different forms and functions. The elastic response of nucleic acids subjected to very high loadings on the order of 1 nN has not been previously studied. We use AFM-based single-molecule force spectroscopy to, for the first time, compare and contrast the elasticity of different sequences of double and single stranded polynucleotides, including single stranded poly(A), poly(dA), poly(dT), poly(C), and poly(dC); and double stranded poly(dA)poly(dT), poly(dA-dT), poly(dG)poly(dC), and poly(dG-dC). We found that even up to forces as high as 800 pN poly(dA) is stiffer than the other single stranded structures. We have also observed marked differences in the behavior of double stranded poly(dA)poly(dT) and poly(dG)poly(dC) with poly(dA-dT) and poly(dG-dC), respectively. Despite their different elasticities, these double stranded polynucleotides exhibit striking features similar to those exhibited by poly(dA) when stretched. We investigate the origin of these differences and similarities in terms of base-base and base-backbone interactions.

3078-Pos

Adhesion Mechanisms of the Mussel Foot Proteins mfp-1 and mfp-3

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Mussels adhere to a variety of surfaces by depositing a highly specific ensemble of 3,4-dihydroxyphenyl-L-alanine (DOPA) containing proteins. The adhesive properties of Mytilus edulis foot proteins mfp-1 and mfp-3 on mica (a common alumino-silicate clay mineral) and TiO2 surfaces were directly measured at the nano-scale by using a surface forces apparatus (SFA). The adhesion energy between mfp-3 and mica was on the order of W=3×10-4 J/m2 which corresponds to an approximate force per plaque of ~100 gm - more than enough to hold a mussel in place if no peeling occurs. In contrast, no adhesion was detected between mica surfaces bridged by mfp-1. AFM imaging and SFA experiments showed that mfp-1 can adhere well to a single mica surface, but in order for bridging to occur between two mica surfaces the protein must be sheared or allowed extended contact time with the opposing surface. On TiO2 surfaces the mfp-1 interaction is 10-fold stronger than with mica, presumably due to capability of DOPA to form coordination bonds with the TiO2 surface. The results are consistent with the apparent function of the proteins, i.e., mfp-1 is disposed as a "protective" coating and mfp-3 as the adhesive or ''glue'' that binds mussels to surfaces. While mussel foot protein is capable of making strong adhesive bonds with TiO2, the adhesion to mica is actually weak and likely due to weak physical interactions rather than chemical bonding. However, strong adhesion forces of mussel plaques can arise as a consequence of plaque geometry (i.e., their inability to be peeled off) even on surfaces such as mica that do not have a high intrinsic surface or adhesion energy, W.

3079-Pos

Motor-Substrate Interactions in a Ring ATPase

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Many processes in biology, including DNA recombination, prokaryotic cell-segregation, gene transposition, and viral DNA packaging, involve the translocation of DNA or RNA by ATP-driven ring motors belonging to the ASCE/AAA superfamily. While the mechanism by which these motors convert the chemical energy from ATP hydrolysis to mechanical work is beginning to be understood, little is known about how these motors engage their nucleic acid substrates. Do motors contact a single DNA element, such as a phosphate or a base, or are contacts distributed over multiple parts of the DNA? In addition, what role do these contacts play in the mechanochemical cycle? Here we use a single-molecule assay for the genome packaging motor of the *Bacillus subtilis* bacteriophage phi-29 to address these questions. The full mechanochemical cycle of the motor involves two phases–an ATP loading dwell followed by a translocation burst of four 2.5-bp steps. By challenging the motor with a variety of modified DNA substrates, we show that during the dwell phase important contacts are made with adjacent phosphates every 10-bp on the 5'-3' strand in the direction of packaging. In addition to providing stable, long-lived contacts, these phosphate interactions also regulate the chemical cycle. In contrast, during the burst phase, we find that DNA translocation is driven against large forces by extensive contacts, some of which are not specific to the chemical moieties of DNA. Such promiscuous, non-specific contacts may reflect common translocase-substrate interactions for both the nucleic acid and protein translocases of the ASCE superfamily.

3080-Pos

Mapping Micro-Mechanical and Micro-Structural Changes in the Ageing Aorta

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In healthy individuals, arterial function is critically dependent on the biomechanical properties of stiff fibrillar collagens, resilient elastic fibre proteins and contractile smooth muscle cells. Although age-related reductions in arterial compliance (arteriosclerosis) are associated with chronic hypertension and hence with the development of aortic aneurysms, heart failure and stroke, the differential role played by each of these vascular components in the progression of disease remains unclear.

The scanning acoustic microscope (SAM), when operated at frequencies close to 1GHz, is capable of measuring acoustic wave speeds (which are related to tissue stiffness) with a spatial resolution of ~1 micrometer. Using unfixed tissue cryo-sections, we mapped variations in wavespeed from the intimal surface of young (less than 1.75years) and old (more than 8.00years) sheep aortas. Whilst there was a significant age-related increase in mean wavespeed, across the tissue (young: 1.847km/s, SEM 0.004km/s; old: 1.882km/s, SEM 0.003km/s; Mann Whitney U test, $p<0.001$) the increase was most pronounced in the inter-lamellar (IL) regions located between large elastic lamellae (EL) (wavespeed increase; IL: 0.047km/s, EL: 0.021km/s). Atomic force microscopy of ovine aorta cryo-sections identified both fine elastic fibres and collagen fibril bundles within this IL space. Collagen and elastin contents of young and old aortas were determined (as a percentage of tissue section area) using light microscopy of picrosirious red and Miller's stained sections respectively. Although collagen content increased significantly in old compared with young sheep (young: 30.97%, SD 2.63%; old: 44.86%, SEM 5.00%; Student's t-test $p<0.05$) there was no significant change in elastin content (young: 49.75%, SD 4.86%; old: 49.98%, SEM 4.27%; Student's t-test $p=0.97$).

These observations suggest, therefore, that gross mechanical stiffening of the ageing aorta, may occur primarily as a result of localised collagen remodelling in the space between elastic lamellae.

3081-Pos

Integrating Dynamic Force Spectroscopy and Surface Plasmon Resonance to Define the Energy Landscape for Integrin:Ligand Binding

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Background: Blood clots, aggregates of platelets trapped in a mesh of fibrin fibers, can impede normal blood flow, causing heart attacks and strokes. Therapeutic interventions use drugs with Arg-Gly-Asp (RGD) sequences to disrupt interactions between platelet αIIbβ3 integrins and the fibrin network's subunits. Determination of the αIIbβ3-ligand energy landscape will elucidate the successes and limitations of integrin antagonists.

Objectives: Integrating surface plasmon resonance (SPR) and dynamic force spectroscopy (DFS), we studied the energetics of αIIbβ3: ligand interactions. We focused on cHArGD, a cyclic peptide structurally similar to eptifibatide, a cardiovascular disease drug, as well as to fibrinogen's KQAGDV integrin-recognition sequence.

Methods: DFS determined single bond rupture forces, the dissociation constant k_{off}, and the rupture distance x_{-1} for αIIbβ3: cHArGD interactions. SPR determined the kinetic and thermodynamic parameters for αIIbβ3: cHArGD binding.

Results: DFS performed at three different pulling rates (14000, 42000, and 70000) pN/s) yielded rupture forces of 77, 86 and 88 pN; Bell model analysis yielded a dissociation constant, k_{off} ~ 0.03 sec^{-1} and rupture distance x_{-1}~ 0.6 nm. Excess cHArGD in solution dramatically reduced the rupture