individual repeats or their alpha-helical subunits. We also present evidence for the capture of unfolding/refolding transient events while stretching or releasing by AFM and analyze differences in refolding lengths and forces for each repeat. This class of stacked helical-repeats behave as molecular sprays, 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
Mahir Rabbi1, Michal Sarna2, Laura Manson1, Yong Jiang1, Piotr E. Marszałek2
1Duke University, Durham, NC, USA, 2AGH University of Science and Technology, Krakow, Poland.

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 that 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
Travers Anderson, Jacob Israelachvili
University of California, Santa Barbara, Santa Barbara, CA, USA.

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 aluminosilicate clay mineral) and TiO2 surfaces were directly measured at the nano-scale by using a surface forces apparatus (SFA). The adhesion energy between mfp-1 and mica was on the order of W~3×10^2 J/m^2 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 capa-
ility 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 mus-

3079-Pos
Motor-Substrate Interactions in a Ring ATPase
 Ariel Kaplan1, K. Aathavan2, Adam Politzer3, Jeffrey Moffitt1, Yann R. Chemla1, Shelley Grimes1, Paul J. Jardine2, Dwight L. Anderson2, Carlos J. Bustamante1
1University of California, Berkeley, Berkeley, CA, USA, 2Department of Microbiology, University of Minnesota, Minneapolis, MN, USA.

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/Mia 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 phosphatase or a base, or are contacts distributed over multiple parts of the DNA? In addition, what role do these contacts play in the mechnanochemical 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 mechnanochemical 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 translocate-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
Graham K. Helen, Riaz Akhtar, Constantinos Kridiotis, Brian Derby, Andrew W. Trafford, Michael J. Sherratt
The University of Manchester, Manchester, United Kingdom.

In elderly individuals, arterial compliance (arteriosclerosis) is critically dependent on the biome-

3081-Pos
Integrating Dynamic Force Spectroscopy and Surface Plasmon Resonance to Define the Energy Landscape for Integrin:Ligand Binding
Samrat Dutta1, Martin Guthold2, Roy R. Hantgan3
1Wake Forest University, Winston-Salem, NC, USA, 2Wake Forest University School of Medicine, Winston-Salem, NC, USA.

Background: Blood clots, aggregates of platelets trapped in a mesh of fibrin fibers, can impede normal blood flow, causing heart attacks and strokes. Therapeu-
tic interventions use drugs with Arg-Gly-Asp (RGD) sequences to disrupt integrin antagonists. We focused on cHARGD, a cyclic peptide structurally similar to eptipitabide, a cardiovascular disease drug, as well as to fibrinogen's KQAGDV integrin-

Methods: DFS determined single bond rupture forces, the dissociation constant \( k_{off} \), and the rupture distance \( x_{r} \) for zlBb3: cHARGD interactions. SPR determined the kinetic and thermodynamic parameters for zlBb3: 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 \( k_{off} \approx 0.03 \text{ sec}^{-1} \) and rupture distance \( x_{r} \approx 0.6 \text{ nm} \). Excess cHARGD in solution dramatically reduced the rupture