Proteins and protein domains that lack unique folds are essential participants in a variety of biological processes. How these disordered structures function such as the assembly of multiprotein complexes and cellular signaling are emerging themes in structural biology. Some disordered domains gain structure upon binding to another protein or a nucleic acid and lead to highly specific interactions with low affinity. In other cases, disordered domains are linkers. Here the degree of disorder affects the flexibility and effective length of the linker sequence. While typically grouped under the name of intrinsically disordered proteins, there is a wide range of disorderness among these proteins and an important goal in each case is to obtain a quantitative and functionally useful understanding of the interplay between structure and disorder in these proteins. Many proteins that are important to muscle function have disordered regions that are known to behave at least in part as elastic elements and are directly involved in the mechanical properties of this complex protein system. We have been studying the mechanical properties of many of these disordered proteins through both single molecule nanomechanical measurements with the atomic force microscope and steered molecular dynamics simulations. Full atom simulations of the stretching of these intrinsically disordered proteins provide insights into how they respond to force that cannot be gleaned from the experimental measurements by themselves. A thorough understanding of the nanomechanics of protein systems requires the close integration of both experiment and simulation. The insights gained from these studies on muscle proteins are applicable to the nanomechanics of other protein systems and also open up the possibility of engineering new protein based biomaterials with novel mechanical properties.