Molecular Basis of the Mechanical Hierarchy in Myomesin Dimers for Sarcomere Integrity

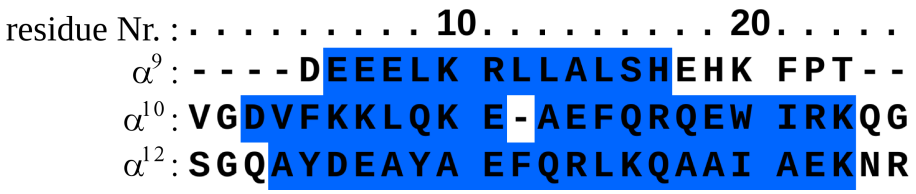
Senbo Xiao[1] and Frauke Gräter[1,2,*]

Heidelberg Institute for Theoretical Studies, Heidelberg, Germany; and [2]Chinese Academy of Sciences-Max-Planck-Society Partner Institute and Key Laboratory for Computational Biology, Shanghai, China

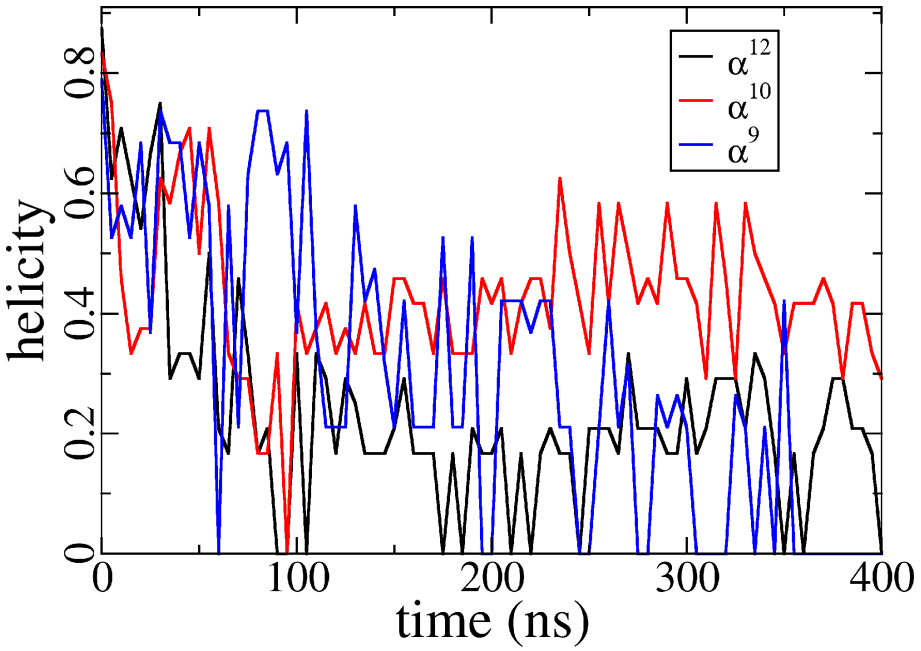
Supplementary Material

	helicity	end-to-end distance (nm)
0 pN :	0.23±0.06	1.452±0.008
5 pN :	0.31±0.08	1.870±0.008

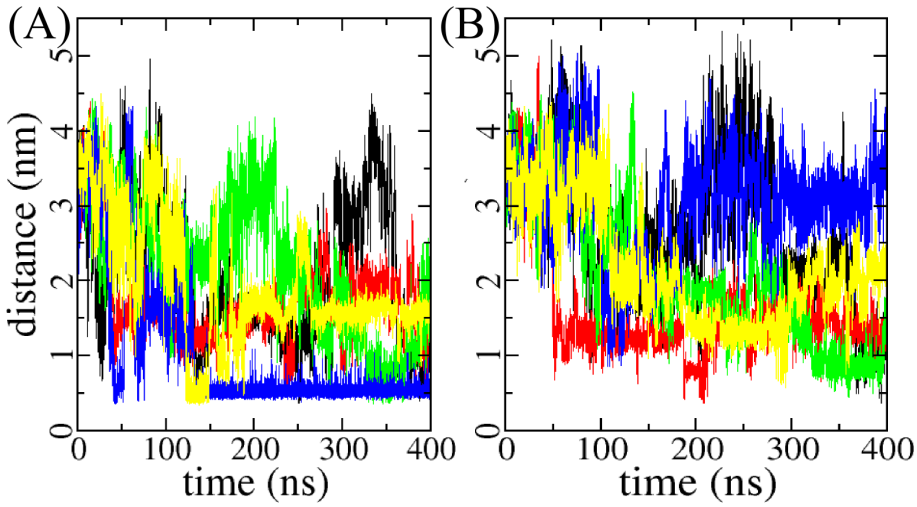
Supplementary Table S1: Helicity and End-to-end distance of α^{12} in equilibrium and under constant holding force of 5 pN. Helicity data is collected at all second half of 5 independent runs of each state. End-to-end distances are from the last 100 ns of each run. Standard errors are shown here.



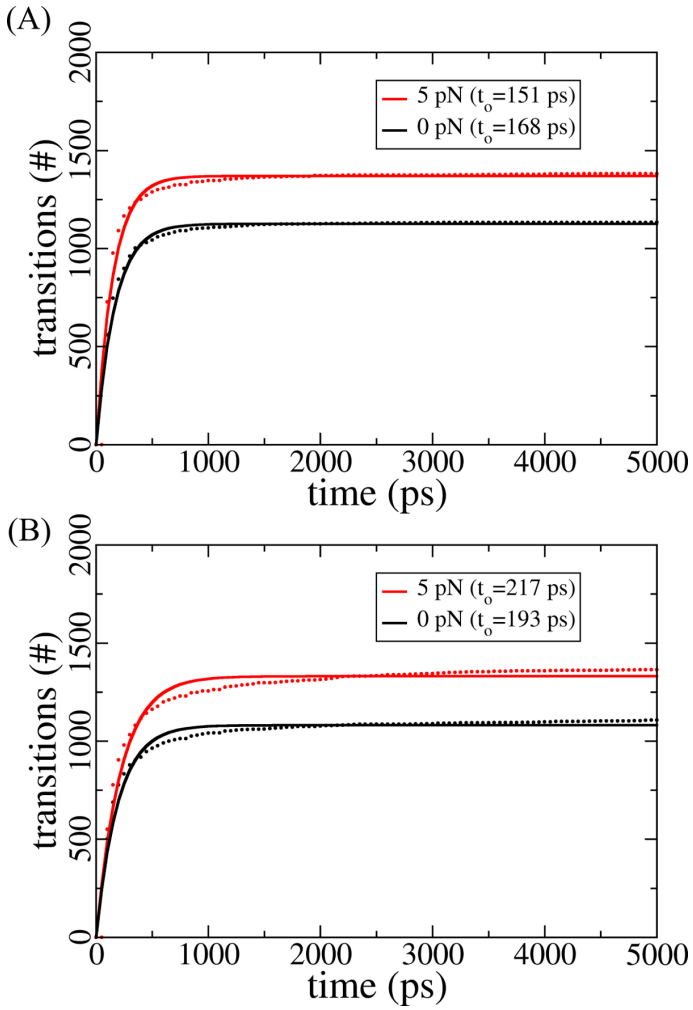
Supplementary Figure S1: Sequence alignment of the three structurally known myomesin helices considered here. Predicted helical residues are highlighted in blue. We used the PRALINE server (1, 2) for the secondary structure prediction.



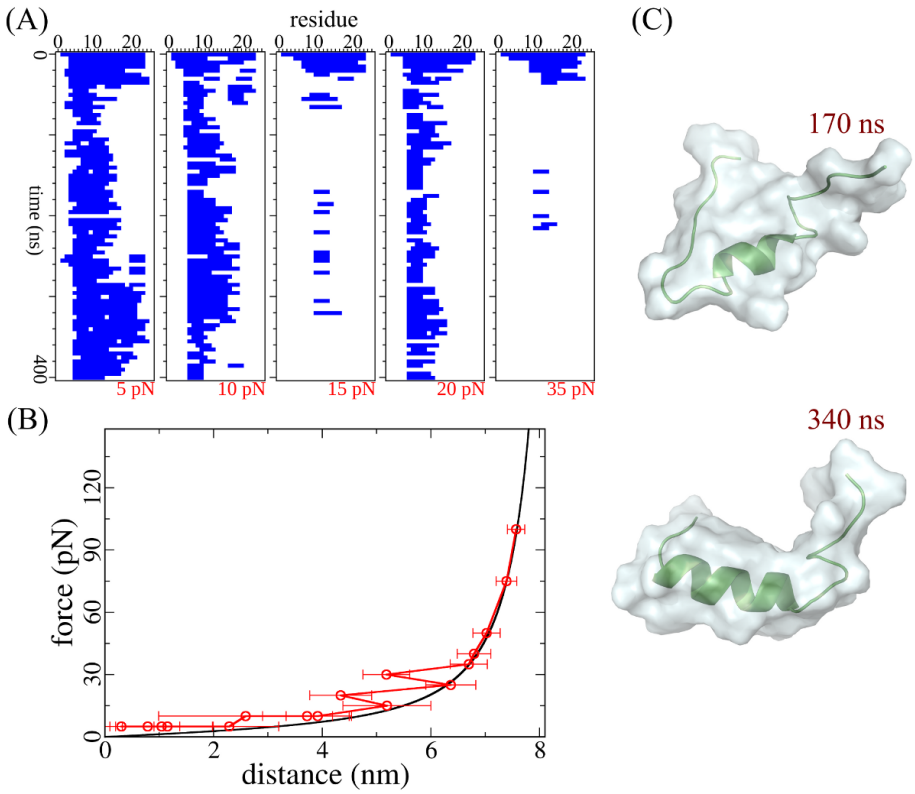
Supplementary Figure S2: Helicity of three myomesin helices in the absence of their adjacent Ig domains. Helical residue number normalized by the helix sequence length is taken as helicity here. All three example simulation trajectories start from full helices in the PDB structures.



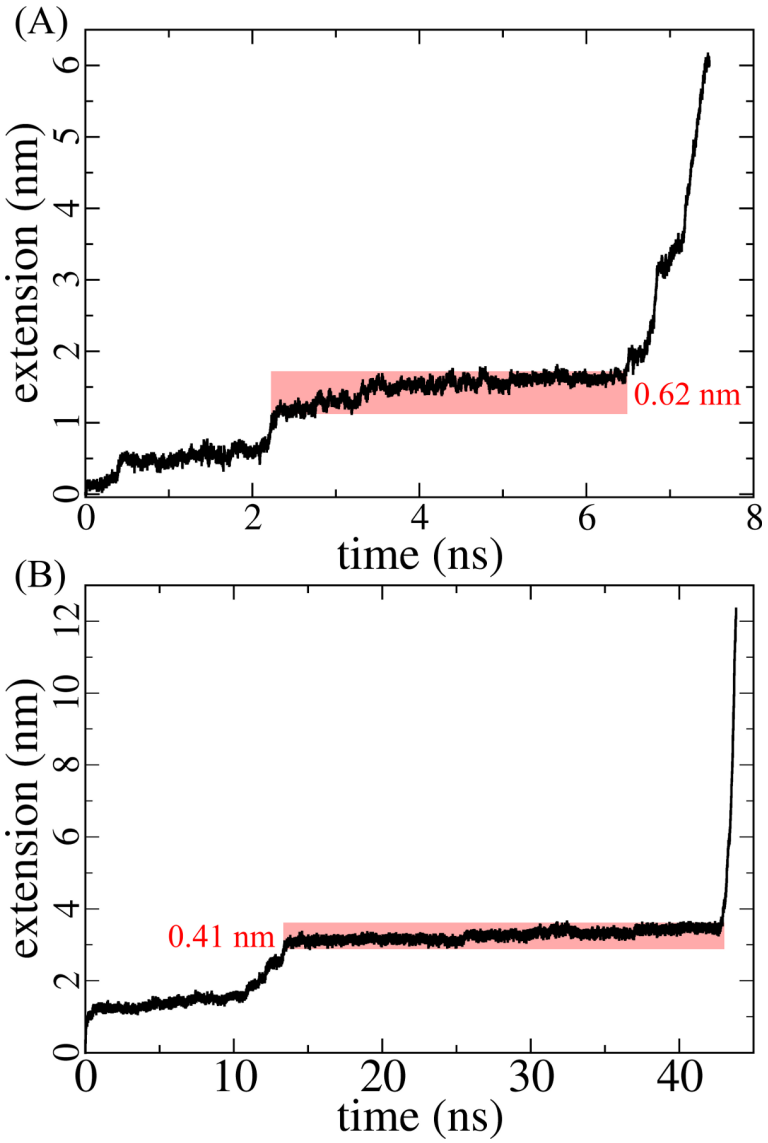
Supplementary Figure S3: End-to-end distances of α^{12} without (A) and with (B) constant quenching force of 5 pN. 5 independent FCMD simulations of 400 ns are indicated by different colors in both plots.



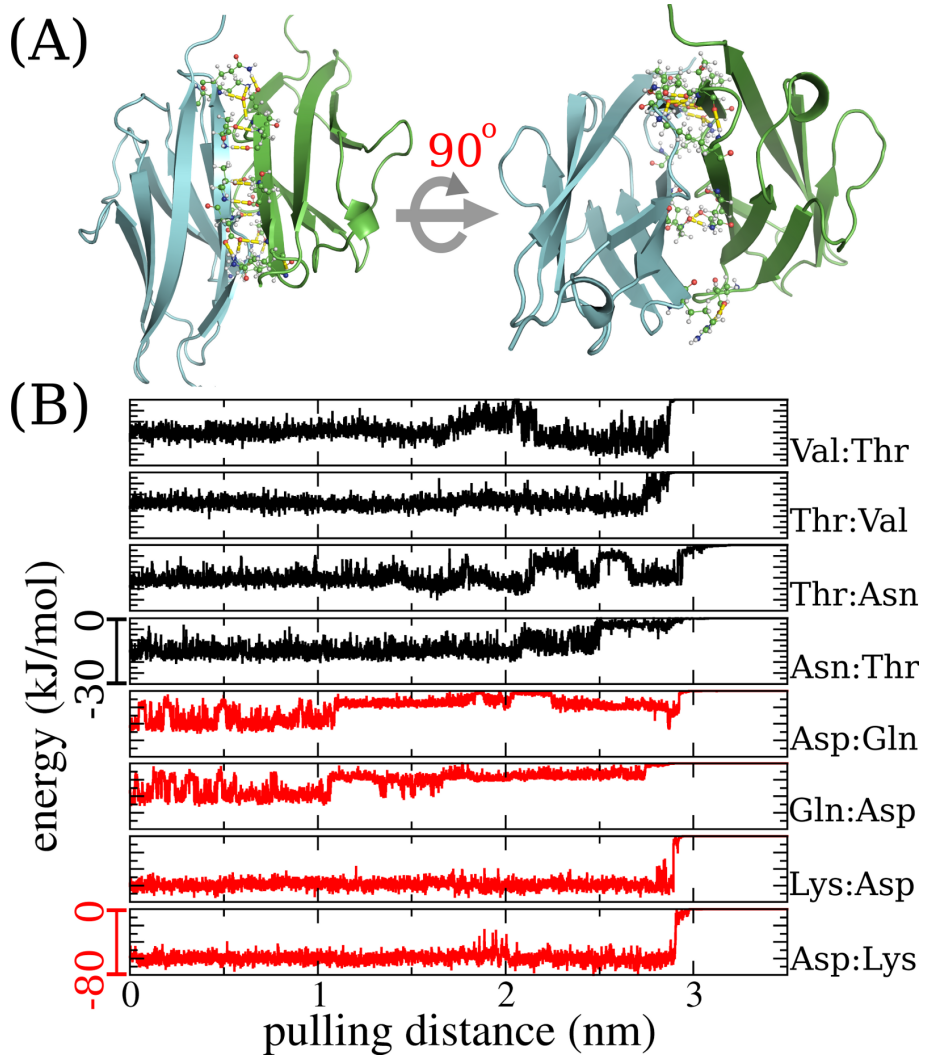
Supplementary Figure S4: Cumulation of α^{12} transitions in equilibrium and under force. (A) Transitions from state 1 (less than 50% helicity) to state 2 (not less than 50% helicity). (B) transitions from state 2 to state 1. The cumulative distributions are fitted with $N_{transition} = N_{max} \times (1 - e^{-t/t_o})$, with N_{max} is the total tansitions number and t_o the transition time (shown in the legends). The data is collected in the second half of 5 independent simulations in both equilibrium and under force.



Supplementary Figure S5: Secondary structure and force-extension curve of α^{12} under increasing constant forces. (A) Helical structure (blue) of α^{12} during simulations at different constant forces as indicated. (B) End-to-end distance of α^{12} under force (red) compared to a worm-like chain model using the same parameters as in previous experiments: a persistence length of 0.5 nm for coiled coil peptide and contour length of 0.365 nm for each residue in the peptide. (3) (C) Two conformations of α^{12} under a pulling force of 5 pN at different simulation times, exemplifying the nanosecond scale refolding of helical structure.



Supplementary Figure S6: Extension of my12 (A) and my13 dimer (B) under pulling force in FCMD simulations. The extension depths of both molecular structures before rupture are highlighted and labeled in the figure, which are approximately equal to their transition state distances.



Supplementary Figure S7: Polar contacts between two dimerized my13 domains. (A) Molecular structure of the myomesin dimer. Two my13 domains are shown in cartoon presentations and differently colored, with contact residues shown in all-atom representation. Hydrogen bonds and salt bridges are shown as yellow dashes. (B) Interaction energies between contacting residue pairs as observed in one representative rupture simulation. Detachment of the dimer is reflected by a drop of the interaction energy to zero. Black, top: backbone-mediated contacts; red, bottom: sidechian-mediated contacts.

References

1. Simossis, V. A., and J. Heringa, 2003. The PRALINE online server: optimising progressive multiple alignment on the web. *Comp Biol Chem* 27:511–519. http://view.ncbi.nlm.nih.gov/pubmed/14642759.

2. Simossis, V. A., and J. Heringa, 2005. PRALINE: a multiple sequence alignment toolbox that integrates homology-extended and secondary structure information. *Nucleic Acids Res* 33:W289–W294. http://dx.doi.org/10.1093/nar/gki390.

3. Berkemeier, F., M. Bertz, S. Xiao, N. Pinotsis, M. Wilmanns, F. Gräter, and M. Rief, 2011. Fast-folding *alpha*-helices as reversible strain absorbers in the muscle protein myomesin. *Proc Natl Acad Sci USA* 108:14139–14144. http://dx.doi.org/10.1073/pnas.1105734108.