CROSS-SPECIES MECHANICAL FINGERPRINTING OF CARDIAC MYOSIN BINDING PROTEIN-C

Supporting Material

Árpád Karsai[1], Miklós S. Z. Kellermayer[2,3], Samantha P. Harris[1]*

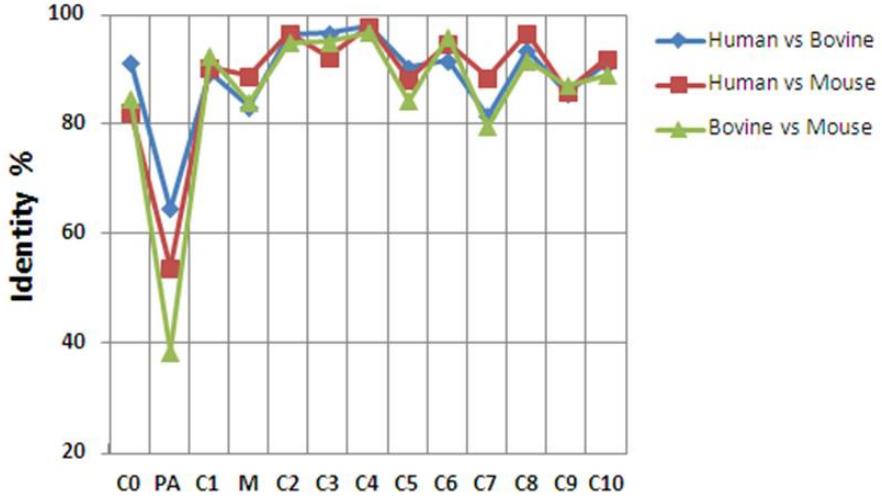
[1]University of California - Davis, Davis, CA, USA,
[2] MTA-SE Molecular Biophysics Research Group and [3]Department of Biophysics and Radiation Biology, Semmelweis University, Budapest, Hungary.

*To Whom Correspondence Should be Addressed.

Department of Neurobiology, Physiology, and Behavior
One Shields Avenue
University of California-Davis
Davis, CA 95616

Supporting Material

A



B

	HUMAN		MOUSE		BOVINE	
	Identity	Similarity	Identity	Similarity	Identity	Similarity
C0 vs C1	-		24.70%	55.60%	-	
C1 vs C2	-		-		-	
C2 vs C3	33.30%	66.70%	32.40%	66.20%	32.40%	66.20%
C3 vs C4	28.40%	63.00%	32.10%	64.20%	29.60%	61.70%
C4 vs C5	-		-		-	
C5 vs C6	-		-		-	
C6 vs C7	22.50%	52.80%	22.50%	55.10%	22.20%	54.40%
C7 vs C8	-		-		-	
C8 vs C9	-		-		-	
C9 vs C10	-		-		-	

Figure S1. A) Sequence comparisons of human, bovine and mouse cMyBP-C by domain. Comparisons were performed using William Pearson's lalign software [1] with human (accession # NM_000256.3), bovine (accession # NP_001070004), and mouse (accession # AF097333) sequences. B) Table showing the percentage of identity and similarity among adjacent domains within human, bovine and mouse cMyBP-C sequences. Similarity was determined with the FASTA sequence comparison software of University of Virginia [2]. Dash indicates that there was no significant similarity between the domains.

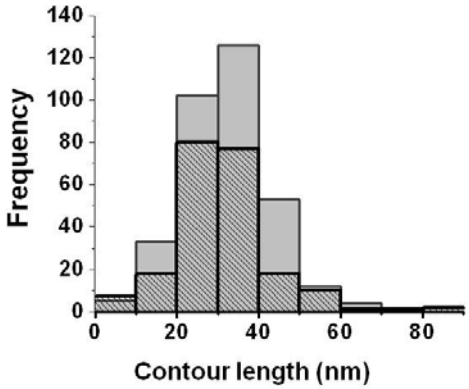


Figure S2. Histogram showing the contour length gain (ΔL) of the unfolded Ig/FNIII domains of human (32.3 ± 11.8 nm, n=340, gray) and bovine (31.7 ± 11.3nm n=171, dark dashed) cMyBP-C.

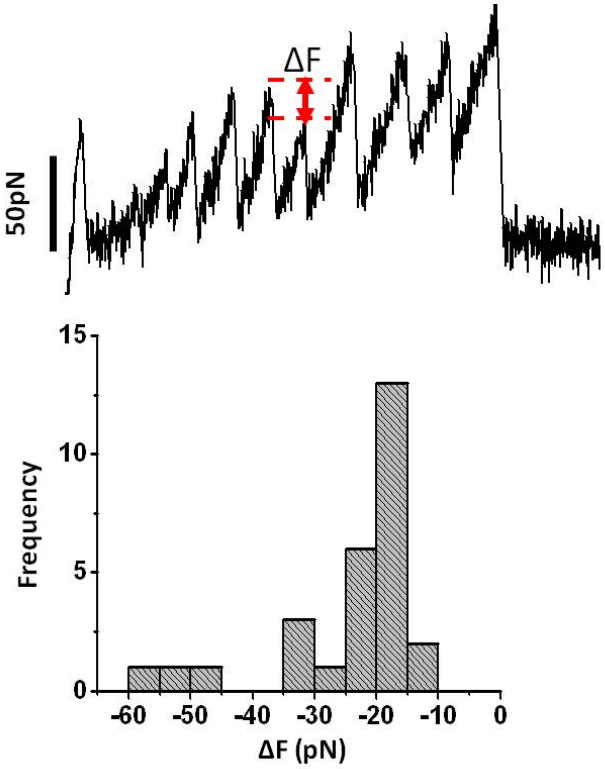


Figure S3. Histogram of the magnitude of all force drops of human cMyBP-C. The red arrow on the example force extension curve above the histogram indicates the magnitude of the force drop (ΔF). ΔF was measured as the force difference (pN) between the two peaks.

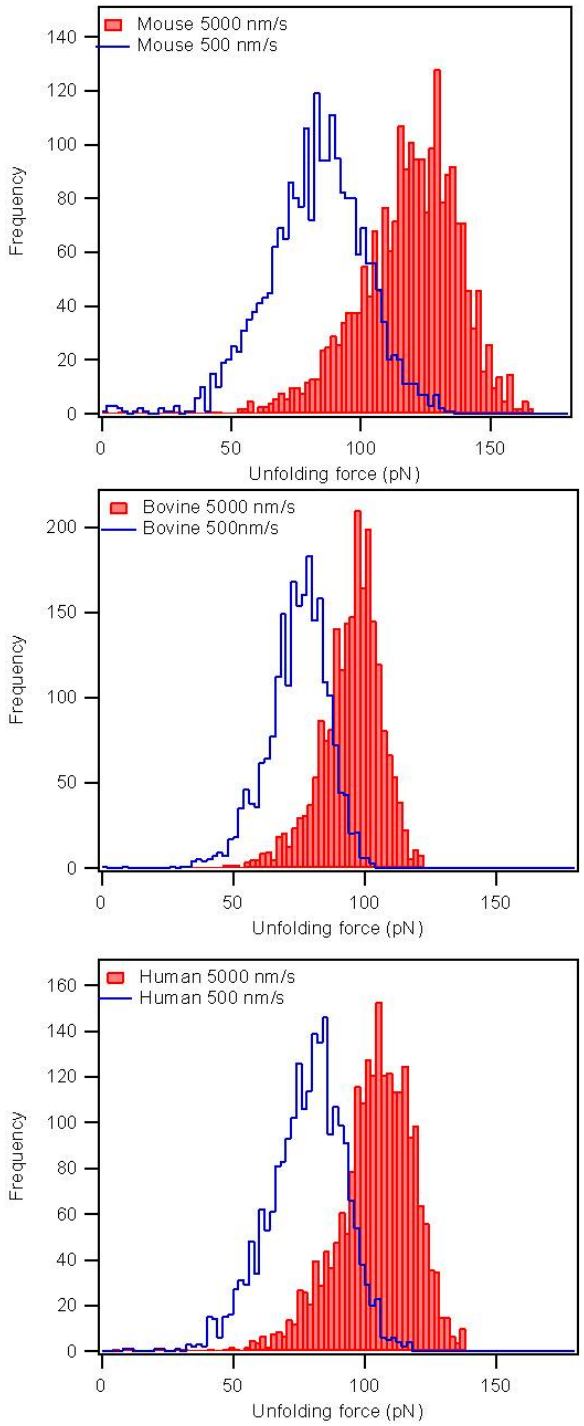


Figure S4. Histograms of simulated unfolding force values for bovine, human and mouse cMyBP-C obtained from Monte-Carlo simulations.

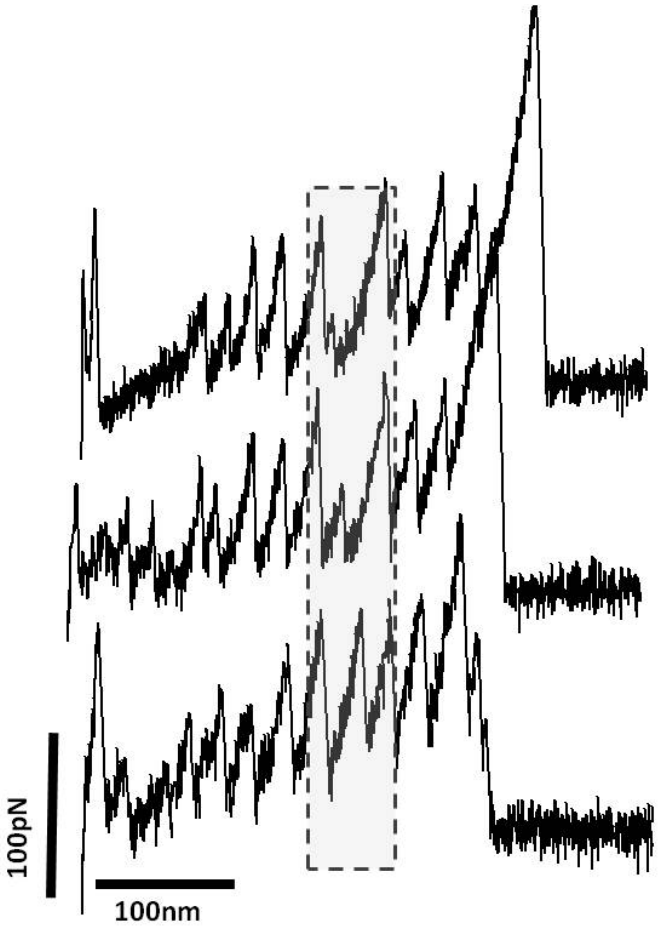


Figure S5. Force extension curves of human cMyBP-C with (top, middle) and without (bottom) force drops. The length gain before and after the force drops (≈ 60 nm which is equal to the unfolded length of two domains) is indicated with a dashed box.

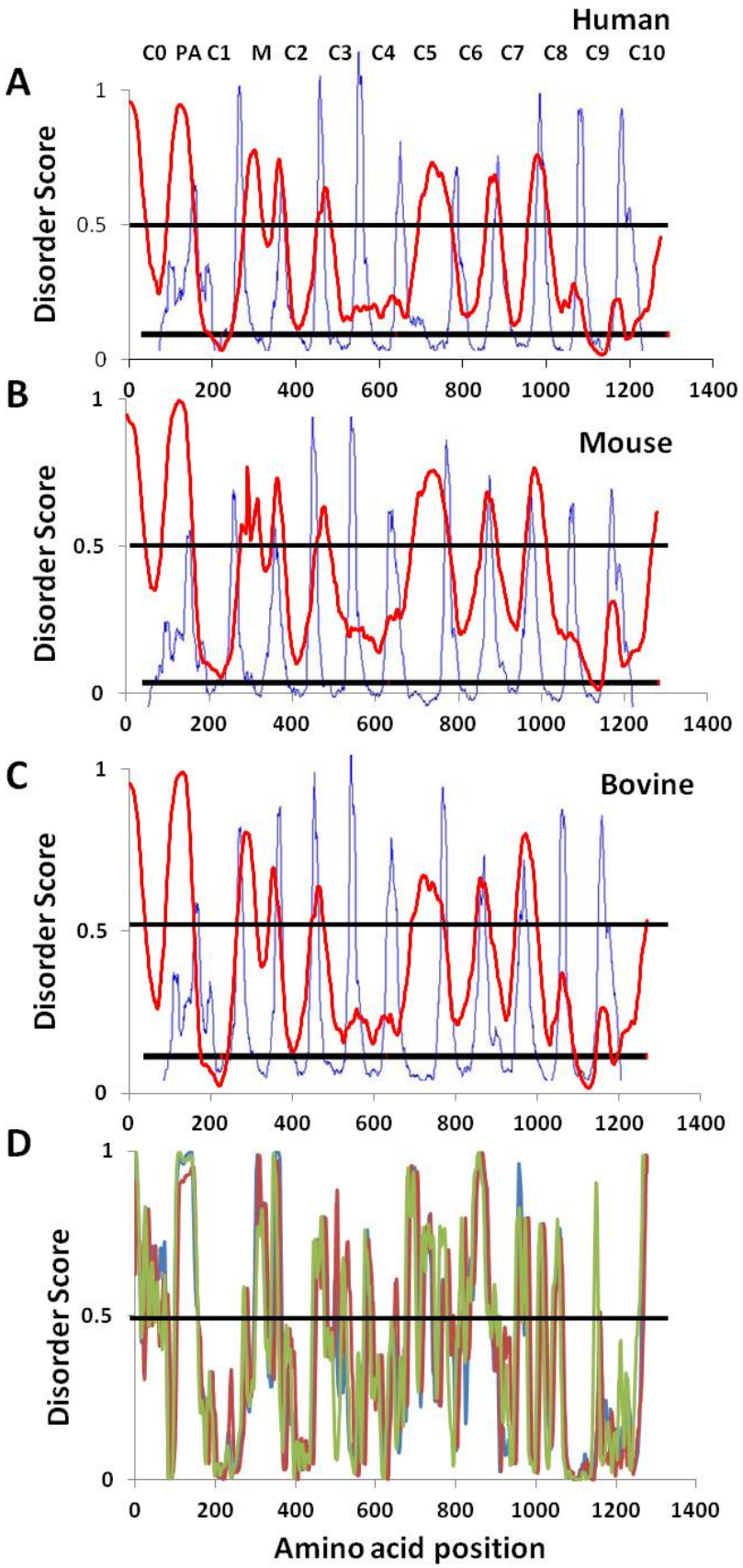

Human
C0 PA C1 M C2 C3 C4 C5 C6 C7 C8 C9 C10
A
B
Mouse
C
Bovine
D
Disorder Score
1
0.5
0
0 200 400 600 800 1000 1200 1400
Amino acid position

Figure S6. Computational predictions of intrinsically disordered segments (IDRs) within cMyBP-C. The VL3 PONDR algorithm [3] was used to predicted IDRs (red lines) for cMyBP-C from A) human, B) bovine and C) mouse.. A disorder score greater than 0.5 indicates increased propensity towards disorder. Blue peaks are the predicted domain boundaries obtained from DomPred [4]. D. Results of VLXT PONDR [5] predictions superimposed for each of the three cMyBP-C proteins showing that the P/A region, the M-domain and C2-C3 C6-C7 regions could contains IDRs as well as the CD loop within the C5 domain.

References for Supporting Material

1. Huang, X., and W. Miller, *A time-efficient, linear-space local similarity algorithm.* Adv. Appl. Math. 1991 **12**: p. 337-357.
2. Pearson, W.R. and D.J. Lipman, *Improved tools for biological sequence comparison.* Proc Natl Acad Sci U S A, 1988. **85**(8): p. 2444-8.
3. Radivojac, P., et al., *Prediction of boundaries between intrinsically ordered and disordered protein regions.* Pac Symp Biocomput, 2003: p. 216-27.
4. Bryson, K., et al., *Protein structure prediction servers at University College London.* Nucleic Acids Res, 2005. **33**(Web Server issue): p. W36-8.
5. Romero, P., et al., *Sequence complexity of disordered protein.* Proteins, 2001. **42**(1): p. 38-48.