Supplementary Information

Similarities between Protein Folding and Granular Jamming

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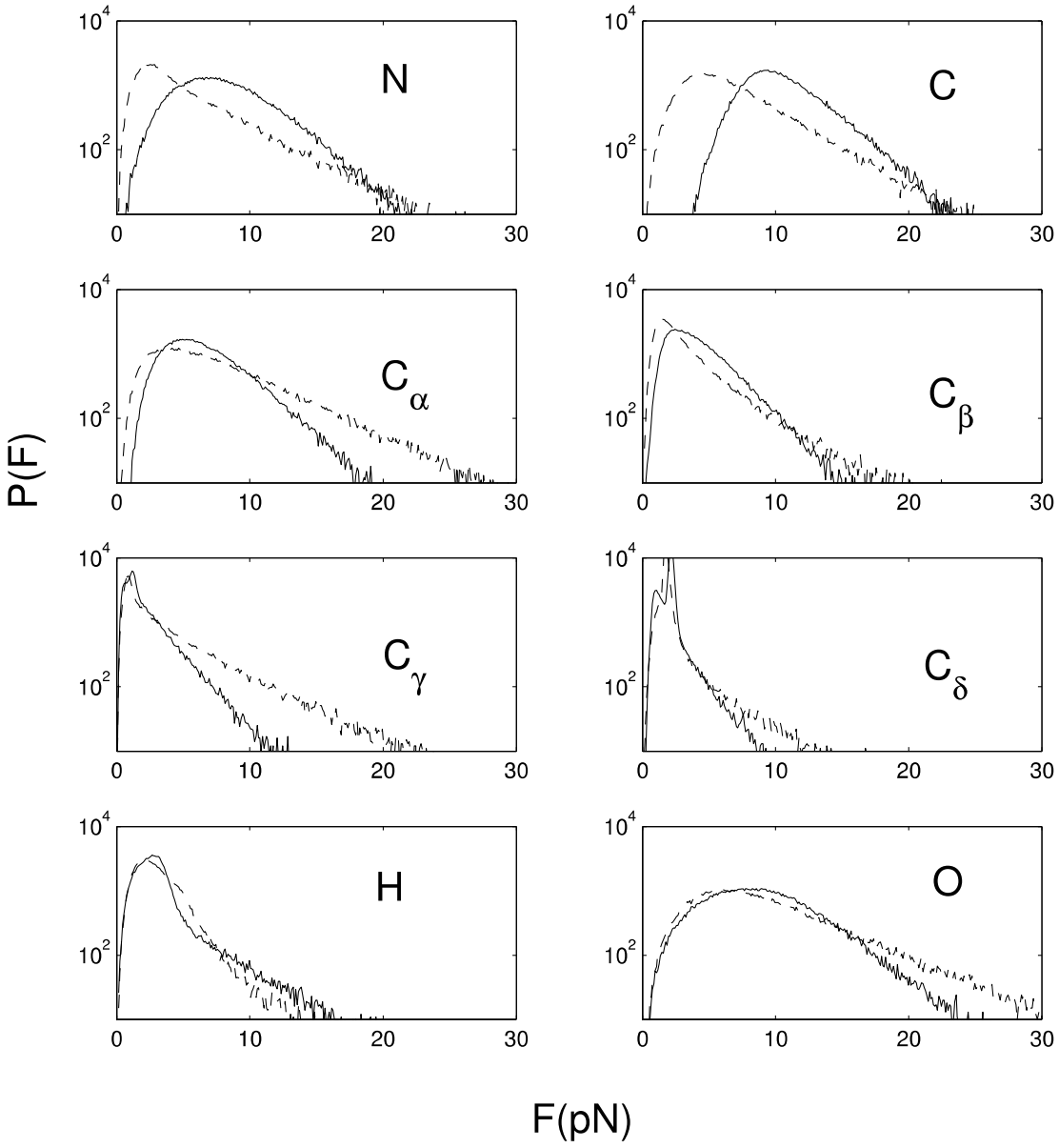
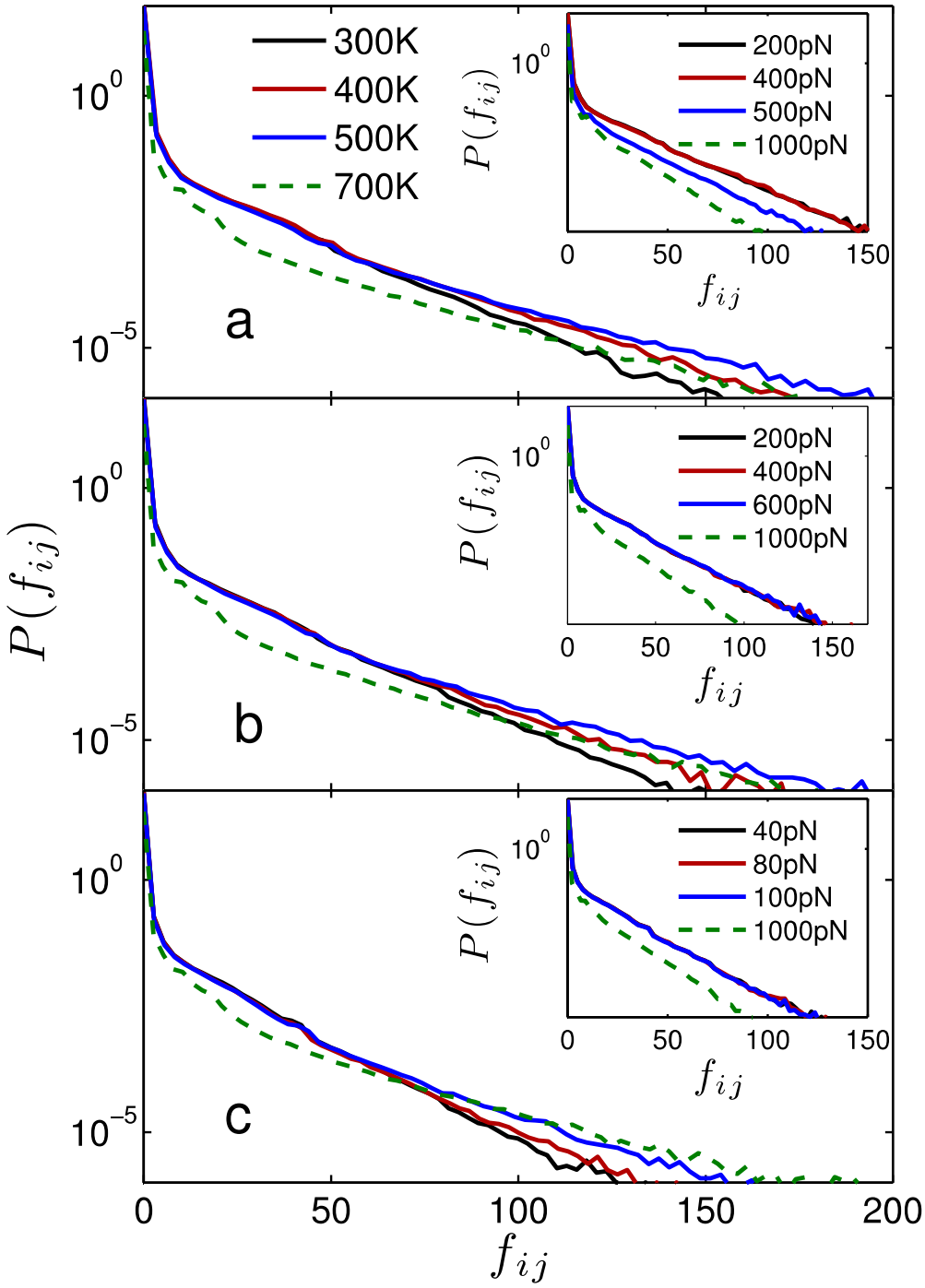
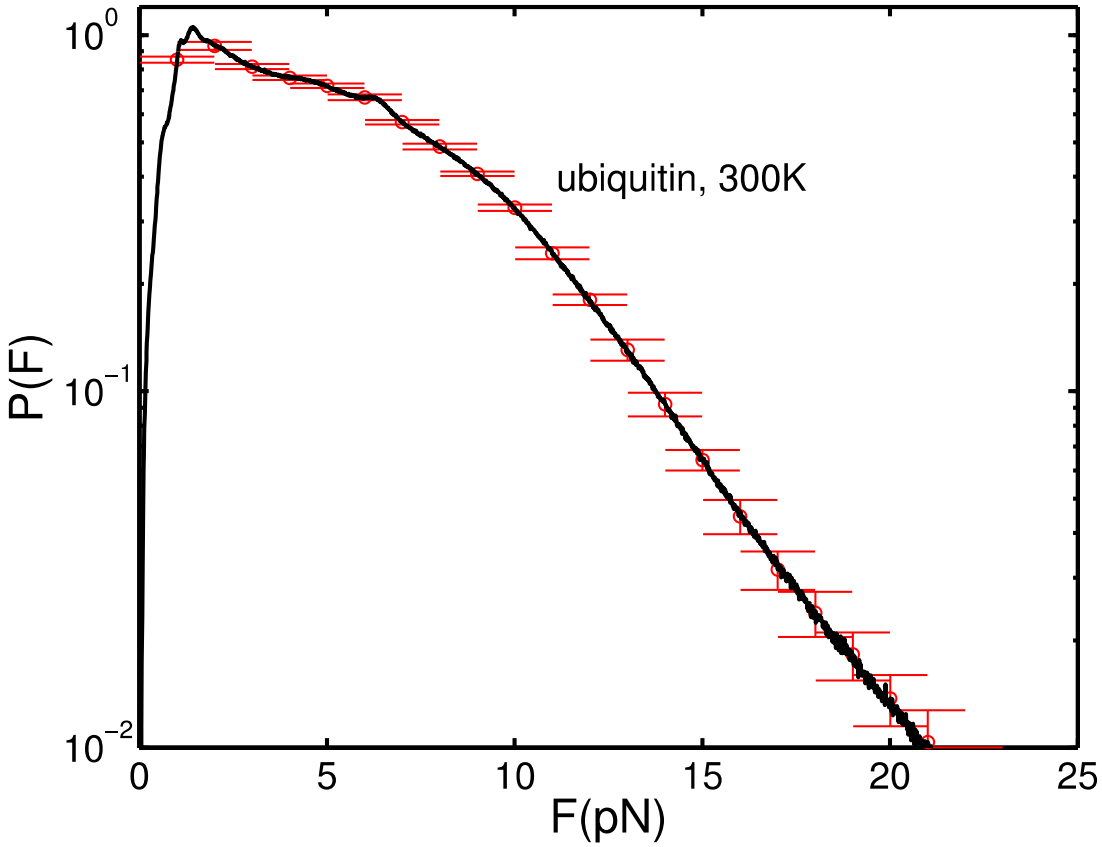
Supplementary Figures



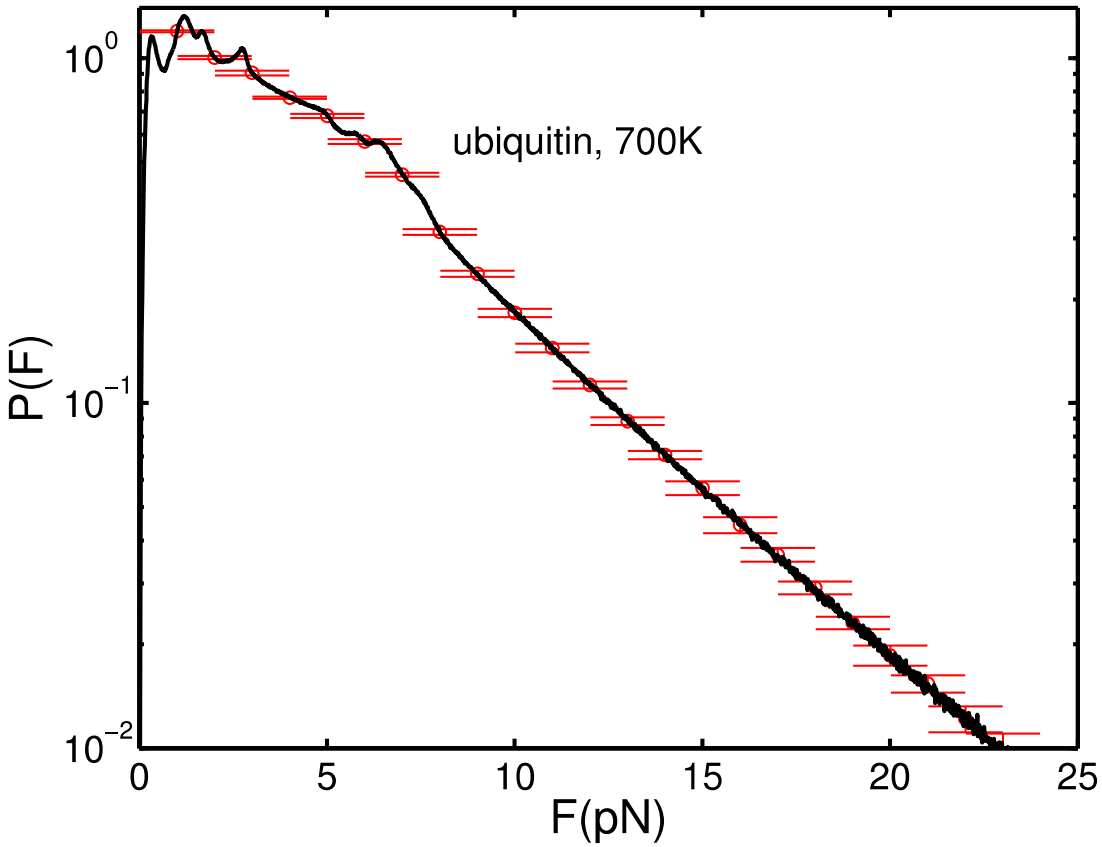
SUPPLEMENTARY FIGURE S1: **Contributions from different atom types.** Peak details in the force distributions are shown to be due to a convolution of different atom-type distributions, i.e., to individual peaks that belong to specific types of atoms. Panels show these peaks computed separately for a range of atom types. Continuous line corresponds to folded states, dotted line to unfolded state. When the systems undergo folding transitions, the position of the peaks shifts. However, the shape remains the same (for example, see, most notably, the force distribution of C_δ atoms).



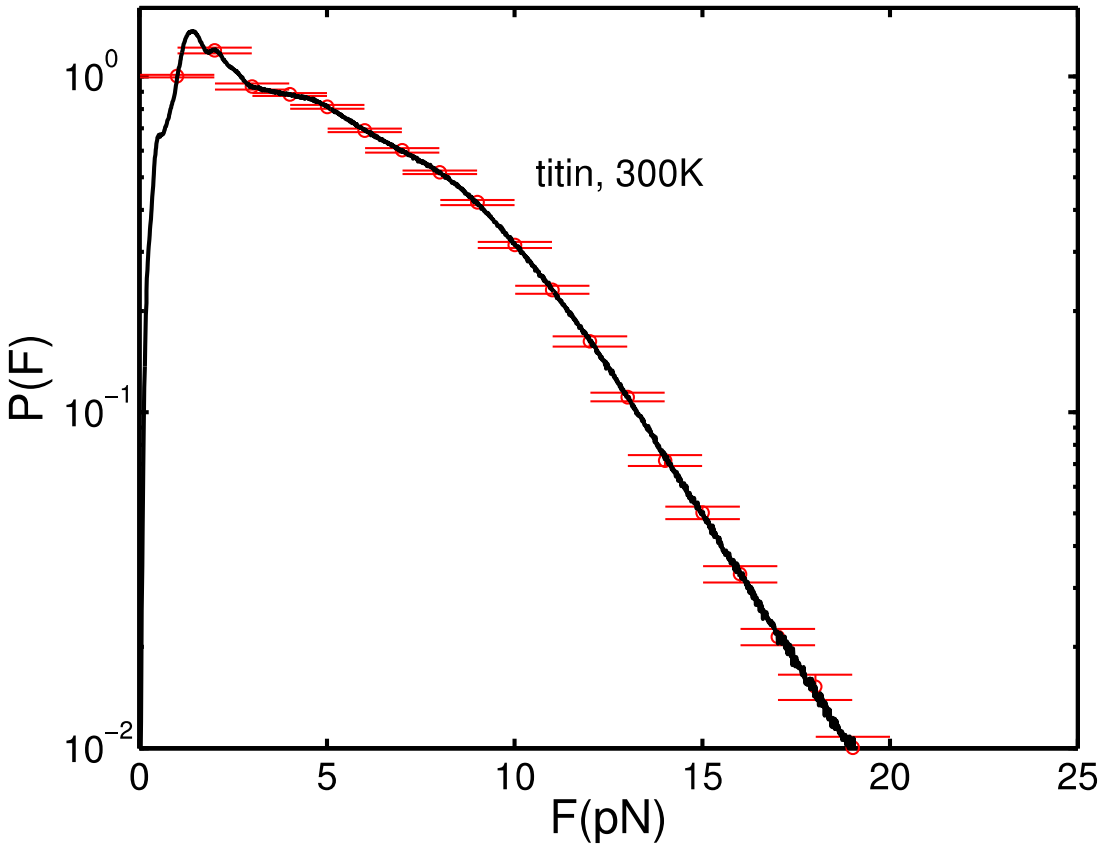
SUPPLEMENTARY FIG. S2**: Similarity across protein folds.** The distributions $P(f_{ij})$ of normalized force of pairwise forces f_{ij} for: (a) ubiquitin, (b) titin, and (c) calmodulin are similar. A peak in $P(f_{ij})$ appears when the proteins have most of the native contacts; the location of the peak is around the same force value for all the proteins, which may be a universal feature for all proteins.



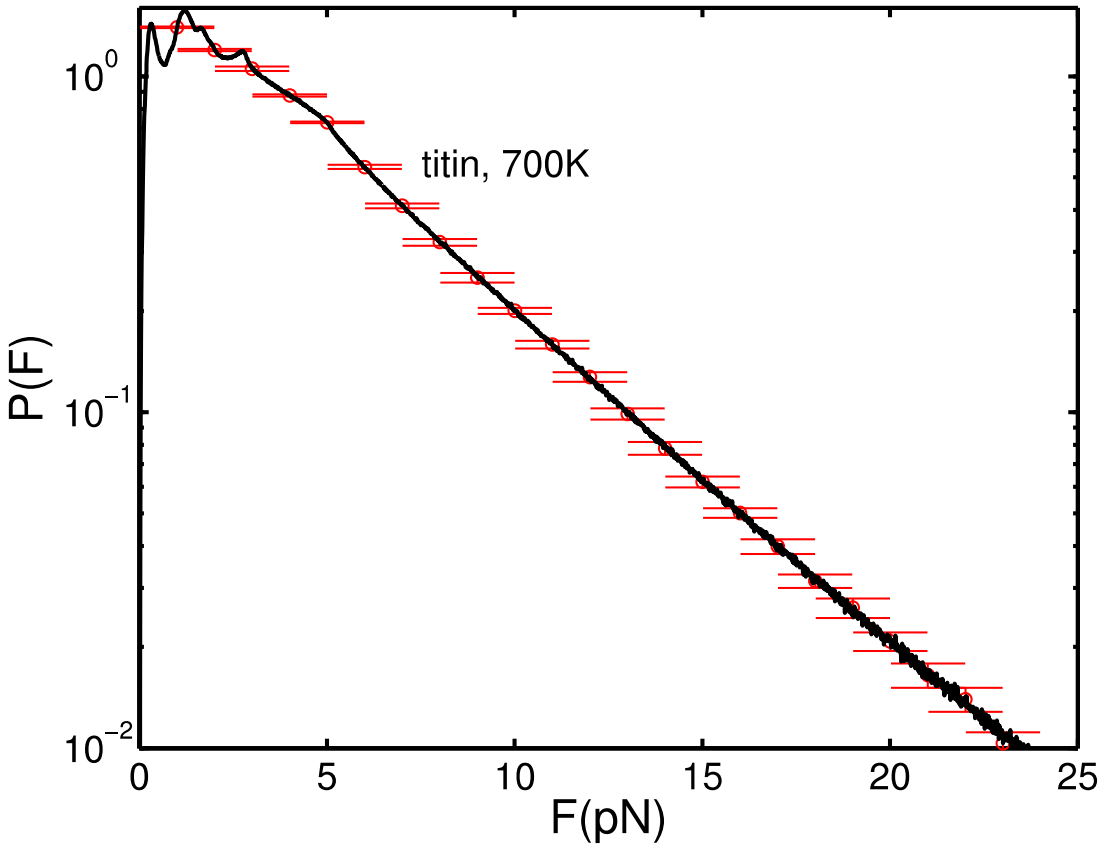
SUPPLEMENTARY FIGURE S3: **Error bars for folded state of ubiquitin.** The relatively small errors (estimated by the standard deviation form the mean, see Methods section in the main text) for low force values show that the fine details of the distribution in the low-force range are, for this and the other two proteins below, statistically significant.



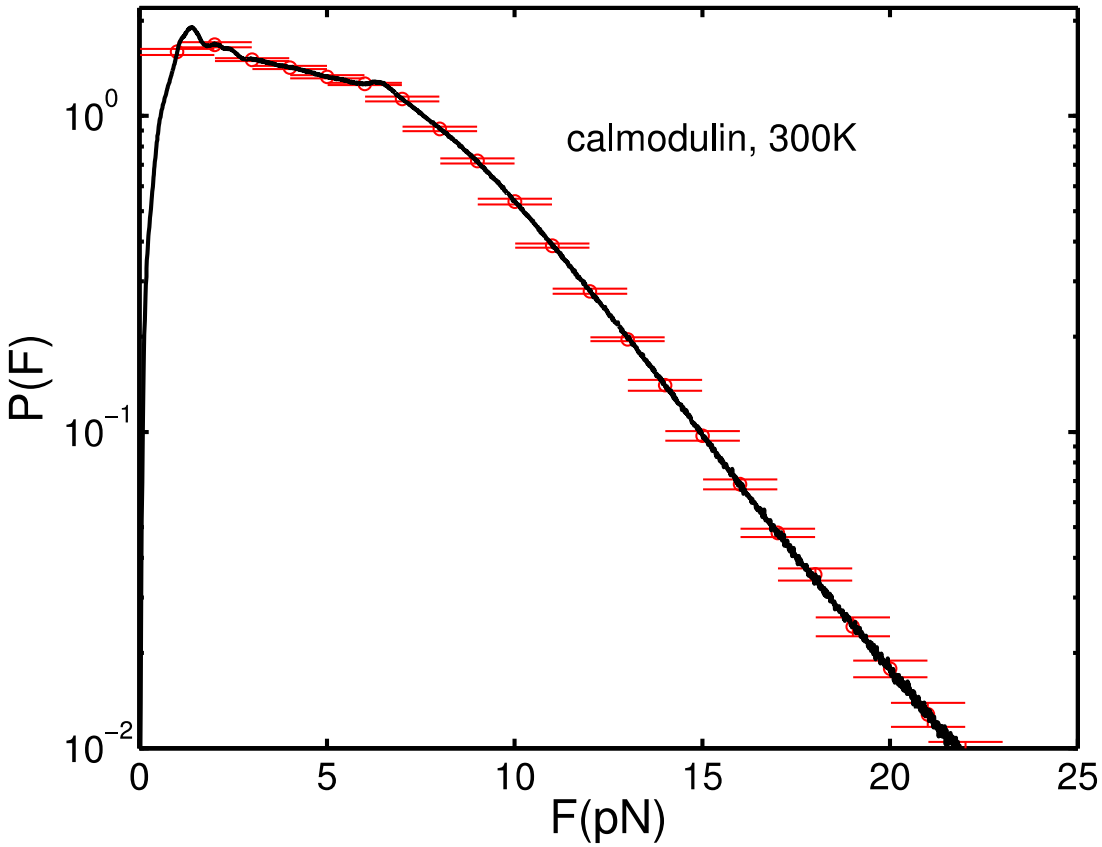
SUPPLEMENTARY FIGURE S4: **Error bars for unfolded states of ubiquitin.**



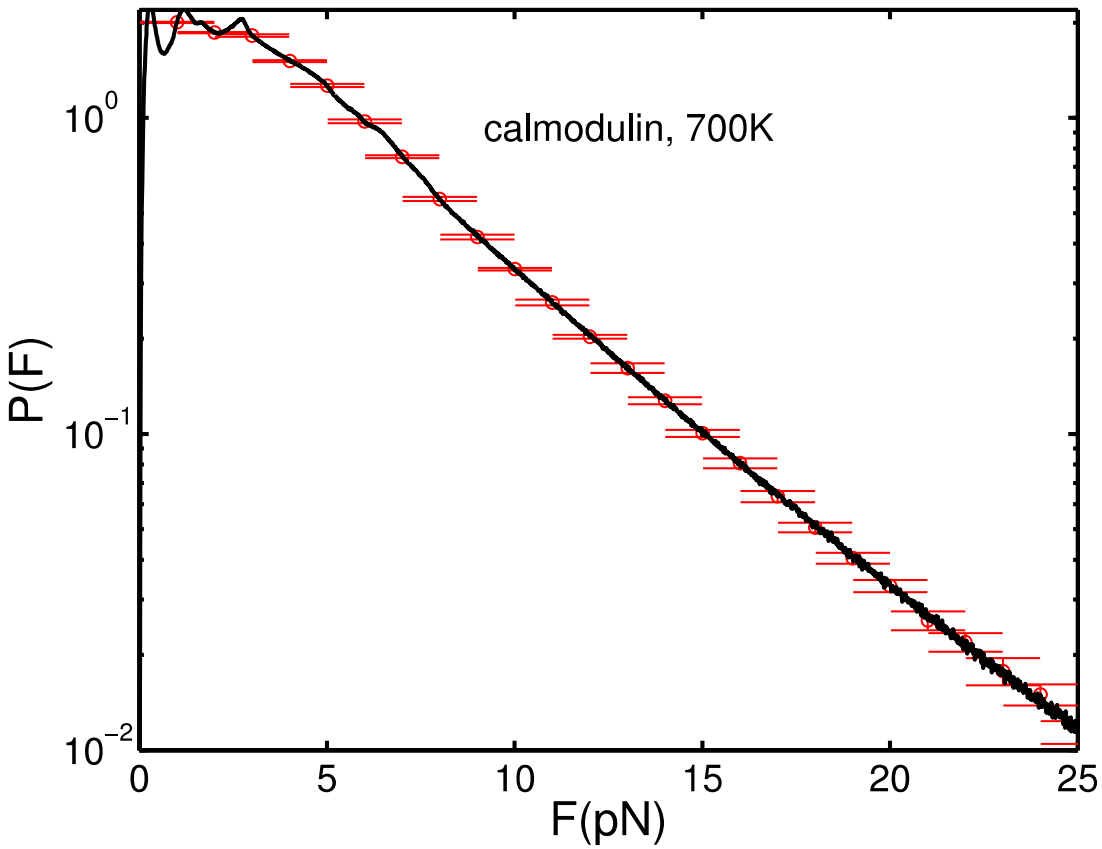
SUPPLEMENTARY FIGURE S5: **Error bars for folded state of titin.**



SUPPLEMENTARY FIGURE S6: **Error bars for unfolded state of titin.**



SUPPLEMENTARY FIGURE S7: **Error bars for folded state of calmodulin.**



SUPPLEMENTARY FIGURE S8: **Error bars for unfolded state of calmodulin.**