

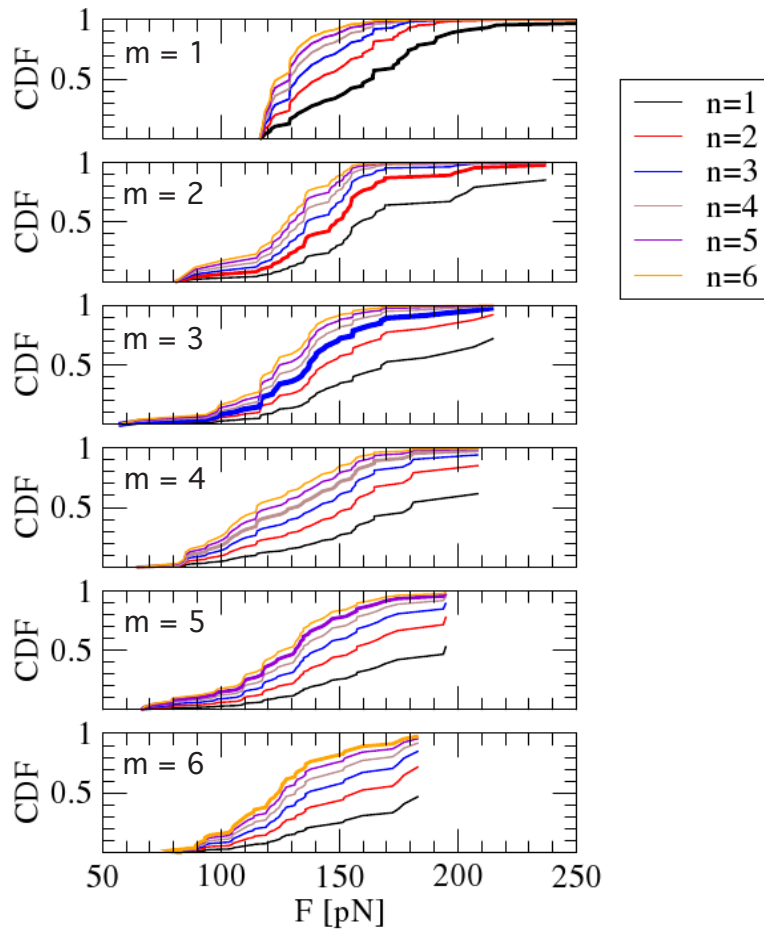
Non-kinetic modeling of the mechanical unfolding of multimodular proteins: theory and experiments

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SUPPORTING INFORMATION

		peak order n	6	5	4	3	2	1
average unfolding force (pN)	Average – experiment		124	128	129	137	146	162
	back-calculation from peak order	$m = 1$	127	129	132	137	144	--
		$m = 2$	123	126	130	136	--	168
		$m = 3$	120	124	129	--	149	170
		$m = 4$	118	123	--	137	150	170
		$m = 5$	123	--	134	142	153	170
		$m = 6$	--	128	134	141	151	164
standard deviation of the mean (pN)	Average – experiment		25	30	31	31	30	31
	back-calculation from peak order	$m = 1$	11	13	15	18	22	--
		$m = 2$	22	23	24	25	--	40
		$m = 3$	25	26	28	--	35	39
		$m = 4$	27	29	--	34	37	38
		$m = 5$	28	--	31	33	34	32
		$m = 6$	--	27	28	30	30	28

SI Table 1: Unfolding forces for GB1. Average and standard deviations of the unfolding forces as obtained from experiments on GB1 (values in bold) and from the back-calculation using data from different peak orders m as indicated. The accuracy in the prediction of the standard deviation is improved when $m \neq 1$ is used. All the data are in units of pN .



SI Figure 1: Cumulated distribution functions (CDF) for the various unfolding peaks (peak order increasing from right to left) obtained using the back-calculation starting from different values of m (different panels as indicated). The experimental CDF are highlighted with a thicker line.