**Table S1.** Two larger protein domains

Length	PDB code	CATH code	Class(C)
104	1K79(333:436)	1.10.10.10	Mainly-α
105	1FMT(209:313)	3.10.25.10	α-β

**Figure S1.** The average and the standard deviation of RMSD of the structural ensembles subject to 10%, 30%, 50%, 70%, 90% randomly-selected constraints for (a) 1FMT (209-313) and (b) 1K79 (333-436). For each fraction of constraints, we only show the largest (◊) and the smallest (•) average RMSD and their corresponding standard deviations (out of five ensembles).

