SUPPLEMENTARY DATA FOR

Nonadditivity in Conformational Entropy Upon Molecular Rigidification Reveals a Universal Mechanism Affecting Folding Cooperativity

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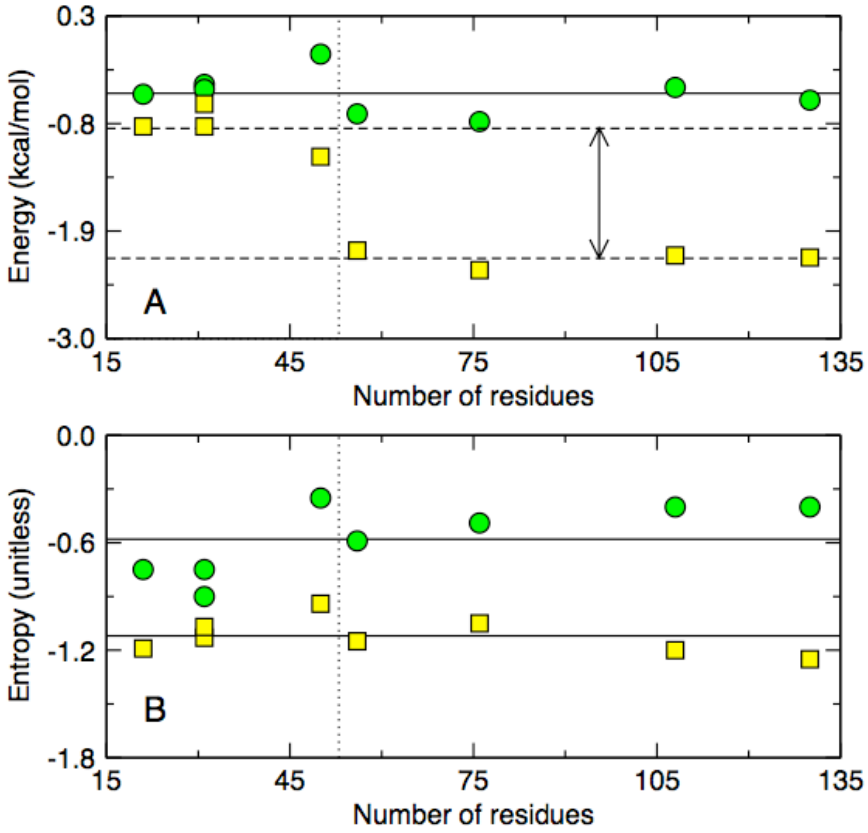

Supp. Fig. S1. Model parameters are physically realistic. Energy parameters are plotted in (a), and entropy parameters plotted in (b). Squares indicate H-bond parameters and circles indicate torsion parameters. Values to the left of the vertical dashed line are from our previously published results on polypeptides (26). The straight horizontal lines are average values that guide the eye. The variability within ε_{hb}, indicated by the vertical arrow, is consistent with expected differences from solvent H-bonding. In this case, the average over the four polypeptides is significantly greater than the average the four considered protein structures.