

## Folding Propensity of Intrinsically Disordered Proteins by Osmotic Stress

### Supporting Information

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# A

PPRSISPSALQDLLRTLKSPSSPQQQQOVLNILKSNPOLMAAFIKQRTAKYVANQPQGMQ 59  
-----HHHHHHHHHHH-----HHHHHHHHH---HHHHHHHHHHHHHH----- 59

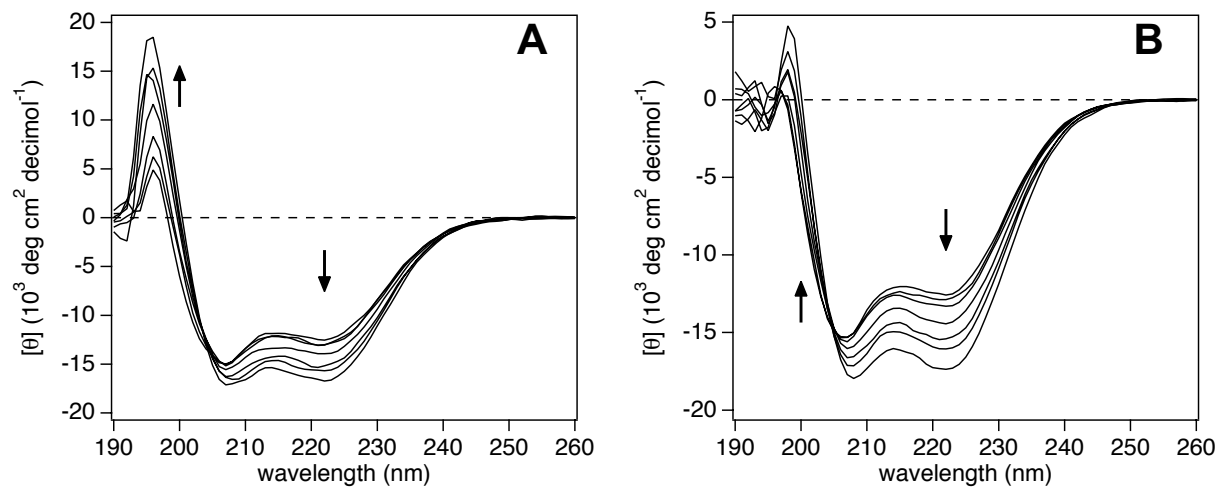
Total Residues: H: 34    E: 0    T: 0  
                  Percent: H: 57.6    E: 0    T: 0

# B

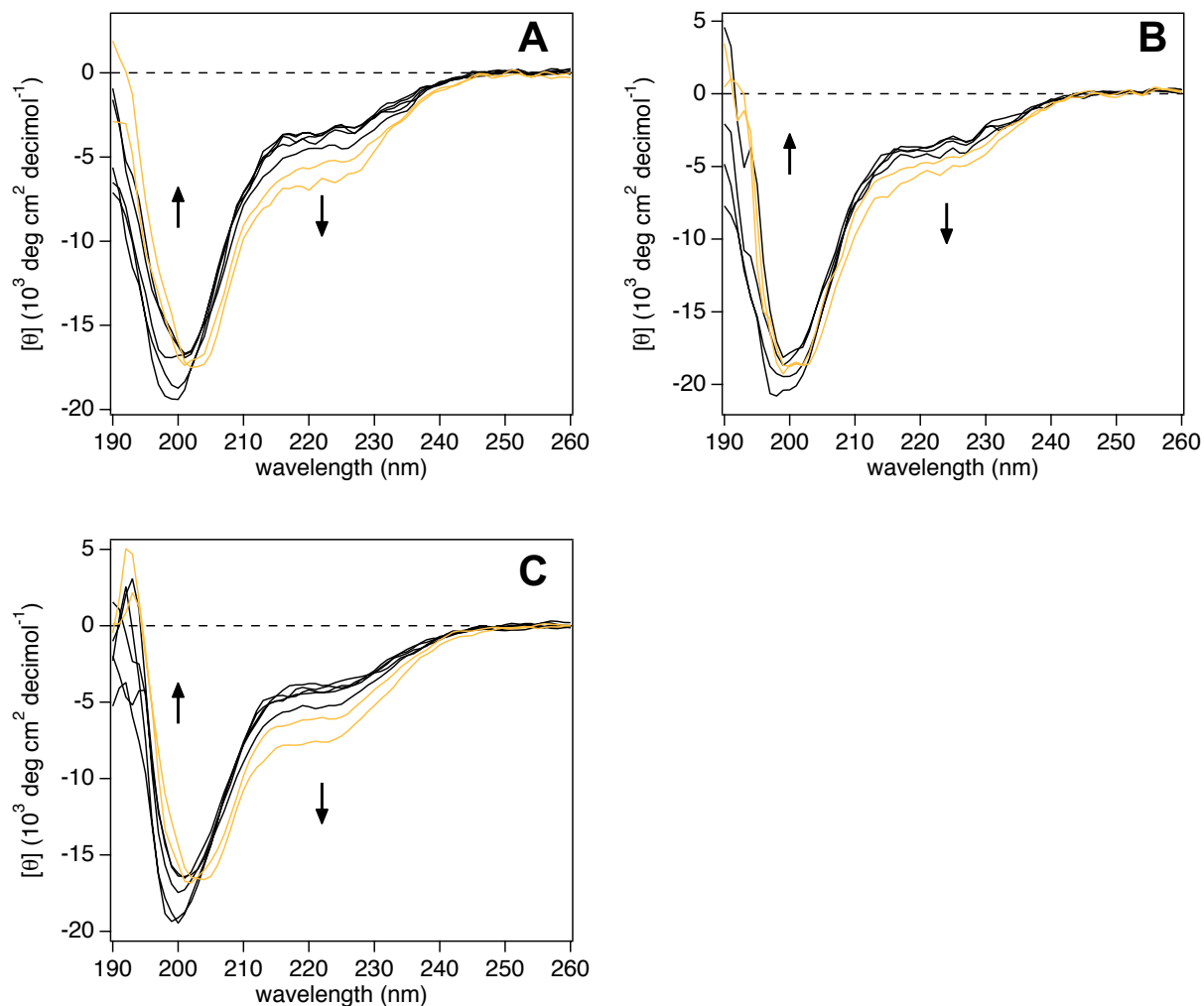
EQGPHGSQNRPLLNRSLDDLLGPPSNAEGQSDERALLDQLHTFLSNTDATGLEEIDRALGIPELVNQGQALESK 74  
-----E-----HHHHHHHHHHHH---HHHHHHHHHH---HHHHH----- 74

Total Residues: H: 28    E: 1    T: 0  
                  Percent: H: 37.8    E: 1.4    T: 0

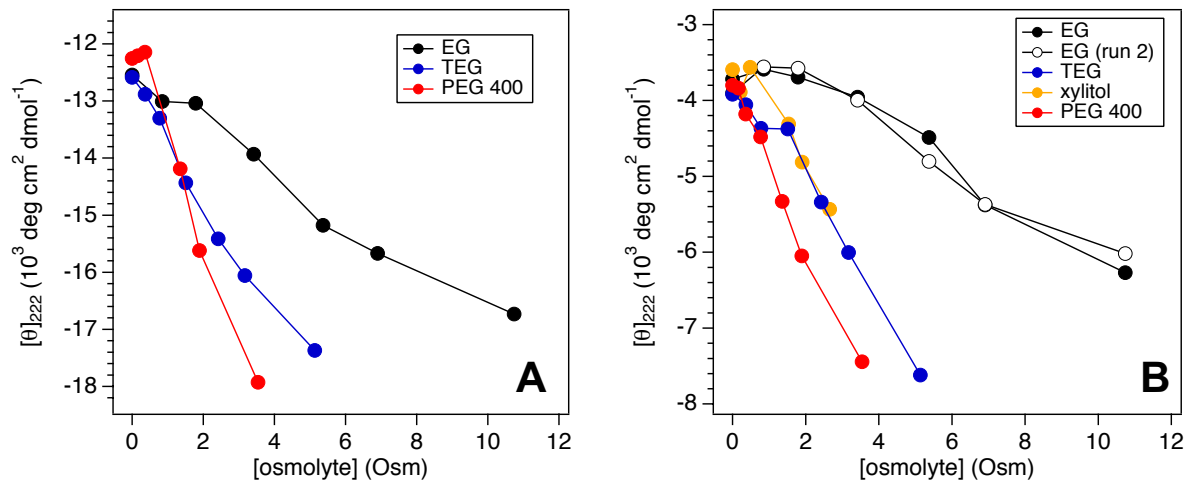
**Figure S1.** The JPred4 secondary structure predictions for (A) NCBD and (B) ACTR, where H = helix, S = sheet, and T = turn.



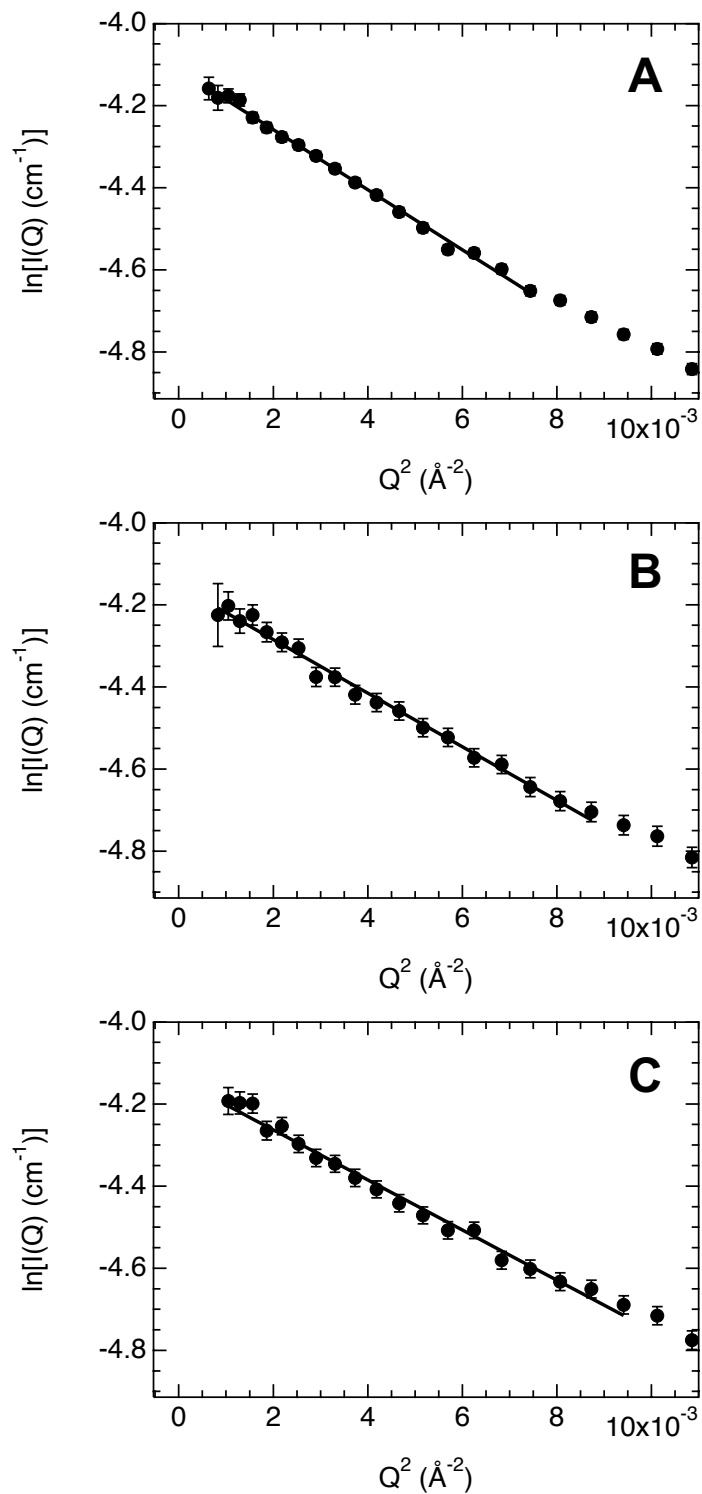
**Figure S2.** CD spectra for NCBD with (A) EG added from 0 to 40% (v/v) and (B) TEG added from 0 to 40% (v/v). The arrows indicate the CD spectral changes that occur with increasing osmolyte concentration.



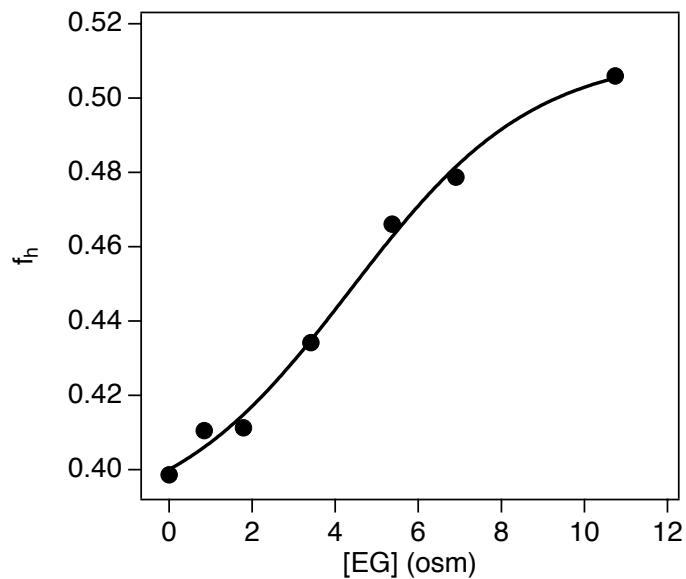
**Figure S3.** CD spectra for ACTR with (A) EG added from 0 to 40% (v/v), (B) xylitol added from 0 to 4 molal, and (C) TEG added from 0 to 40% (v/v). The arrows indicate the CD spectral changes that occur with increasing osmolyte concentration. Spectra in orange are the two highest osmolyte concentrations and that begin to show deviations from the 205 nm isodichroic point.



**Figure S4.** Change in CD mean residue ellipticity ( $[\theta]_{222}$ ) with osmolality for (A) NCBD and (B) ACTR.



**Figure S5.** Guinier plots and fits (solid lines) of the SANS data for NCBD with (A) 0, (B) 1.63, and (C) 3.67 osmolal d6-EG.



**Figure S6.** NCBD fraction helicity,  $f_h$ , as a function of EG osmolality. Here,  $f_h$  is calculated as absolute using Equation 1 in the main text with  $[\theta]_{222,h} = -36,000 \text{ deg cm}^2 \text{ dmol}^{-1}$ . The sigmoid fit (solid line),  $f_h = A/(1 + \exp[(\text{[EG]}_{1/2} - \text{[EG]})/\tau]) + f_{h,0}$  yielded  $A = 0.13 \pm 0.02$ ,  $[\text{EG}]_{1/2} = 4.4 \pm 0.5$ ,  $\tau = 2.2 \pm 0.6$ , and  $f_{h,0} = 0.38 \pm 0.01$ . The fit was used to interpolate  $f_h$  vs.  $[\text{EG}]$  for the Figure 5 inset.