Electronic Supplementary Material (ESI) for Molecular BioSystems

Insights in the (un)structural organization of *Bacillus pasteurii* UreG, an intrinsically disordered GTPase enzyme

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Table ESI-1. Free energy of unfolding calculated from the fluorescence data for the conformational transitions of *Bp*UreG at different temperatures, with a fixed denaturant concentration index (m = 1.57 kcal $mol^{-1}M^{-1}$).

Temperature (°C)	$\Delta G_{0,un}$ (kcal mol^{-1})
10	0.610 ± 0.23
20	1.012 ± 0.16
25	1.148 ± 0.12
30	1.092 ± 0.08
40	1.043 ± 0.09
50	0.644 ± 0.28

Figure ESI-1. Thermal denaturation of *Bp*UreG followed by far-UV circular dichroism in the presence or absence of 1mM TCEP. All the spectra refer to equal protein concentrations.

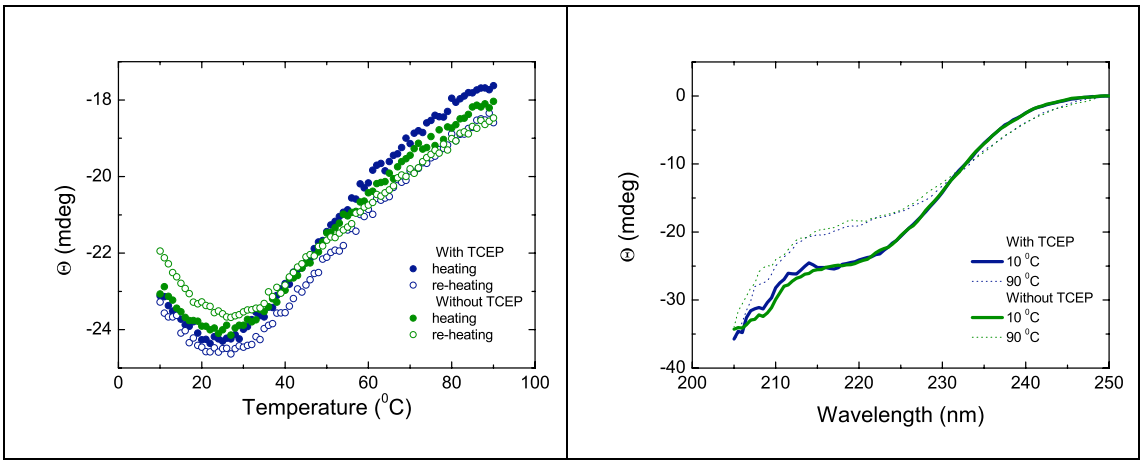

Figure ESI-2. Temperature-induced denaturation of *Bp*UreG at different GuHCl concentrations. The four thermal curves show the expected behaviour according to the phase diagram presented in Figure 6. The complete far-UV CD spectra of the temperature-induced denaturation of the protein at 0 M (top left), 0.92 M (top right), and 2 M (bottom left) are shown in the bottom panels. All the spectra refer to equal protein concentrations.

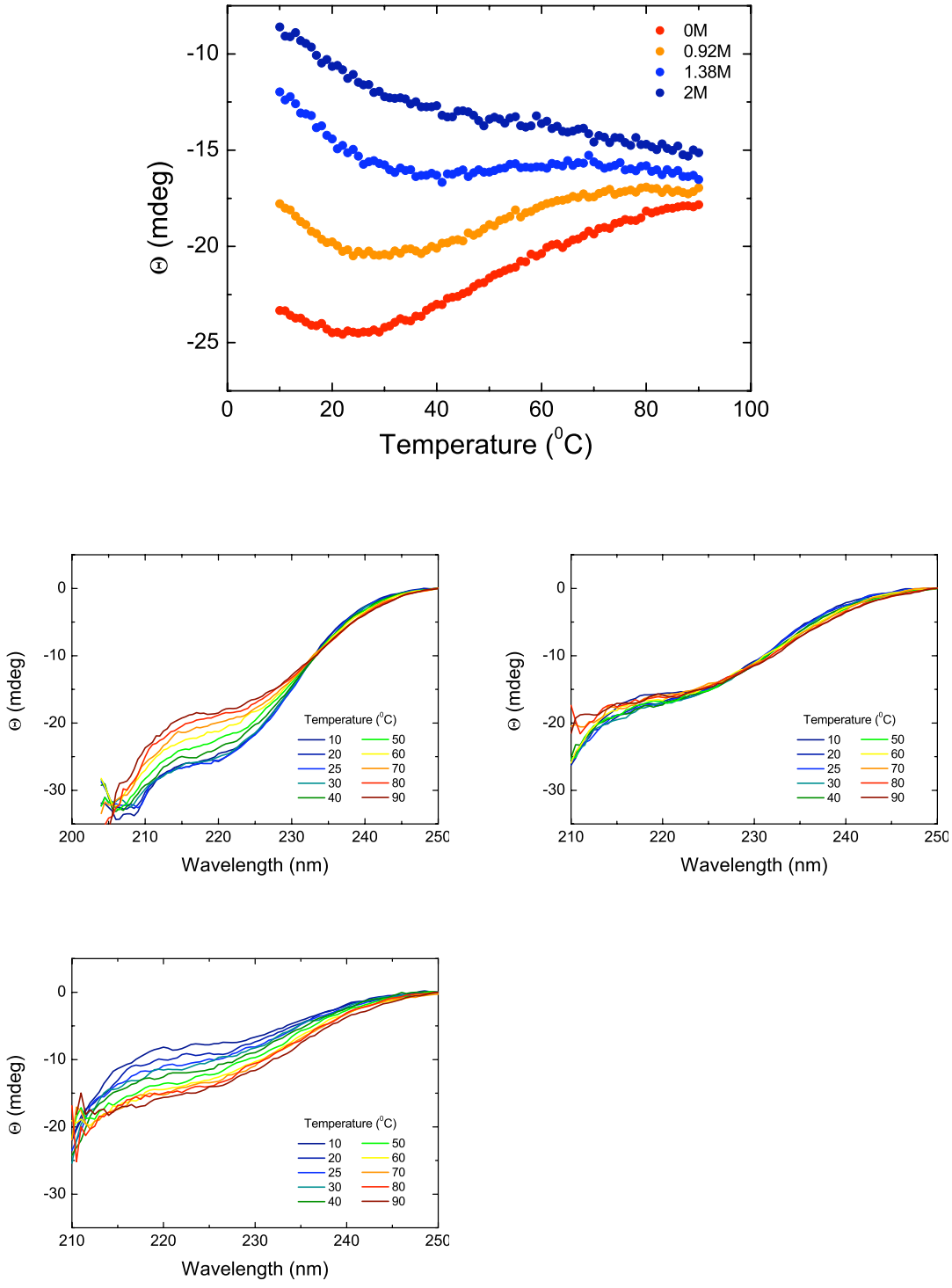

Figure ESI-3. Far-UV CD spectra of *Bp*UreG and protein buffer at 10 °C, in the absence and in the presence of 2.5 M GuHCl. All the protein spectra were recorded at the same *Bp*UreG concentration.