**Supplementary Figure 5**: Comparison of thermodynamic stabilities of the PHₙ-PDZ-PHₐ tandem and its mutants. (a) Urea-denaturation curves of the PHₙ-PDZ-PHₐ tandem and its mutants measured by circular dichroism at 222 nm. The denaturation equilibrium data were each fit to a two-state model for a direct transition between unfolded and folded protein. CD spectra were acquired on a Jasco J-720 spectropolarimeter at 25°C. The samples contained 50 μM proteins in 20 mM phosphate buffer, pH 7.0. (b) Temperature-dependent denaturation profiles of the PHₙ-PDZ-PHₐ tandem and its mutants measured by ¹H NMR spectroscopy. Proteins (0.1–0.2 mM) were dissolved in 100 mM potassium phosphate pH 7.0. Only the upfield-shifted methyl region of each spectrum was plotted for comparison. The assignments for two methyl protons from the split PH domain of the proteins are labeled.