Figure S4. Reduced $\Delta C_p$ up-shifts and broadens the protein stability curve. The protein stability curve of a hypothetical protein with $\Delta C_p = 7.3$ kJ mol$^{-1}$ K$^{-1}$, $T_m = 356$ K, $\Delta H_m = 382$ kJ mol$^{-1}$ was simulated using the Gibbs-Helmholtz equation (dashed line). Keeping $\Delta H_m$ and $T_s$ (temperature for maximum stability) constant, the protein stability curve with a reduced value of $\Delta C_p = 5.3$ kJ mol$^{-1}$ K$^{-1}$ was simulated as the solid line.