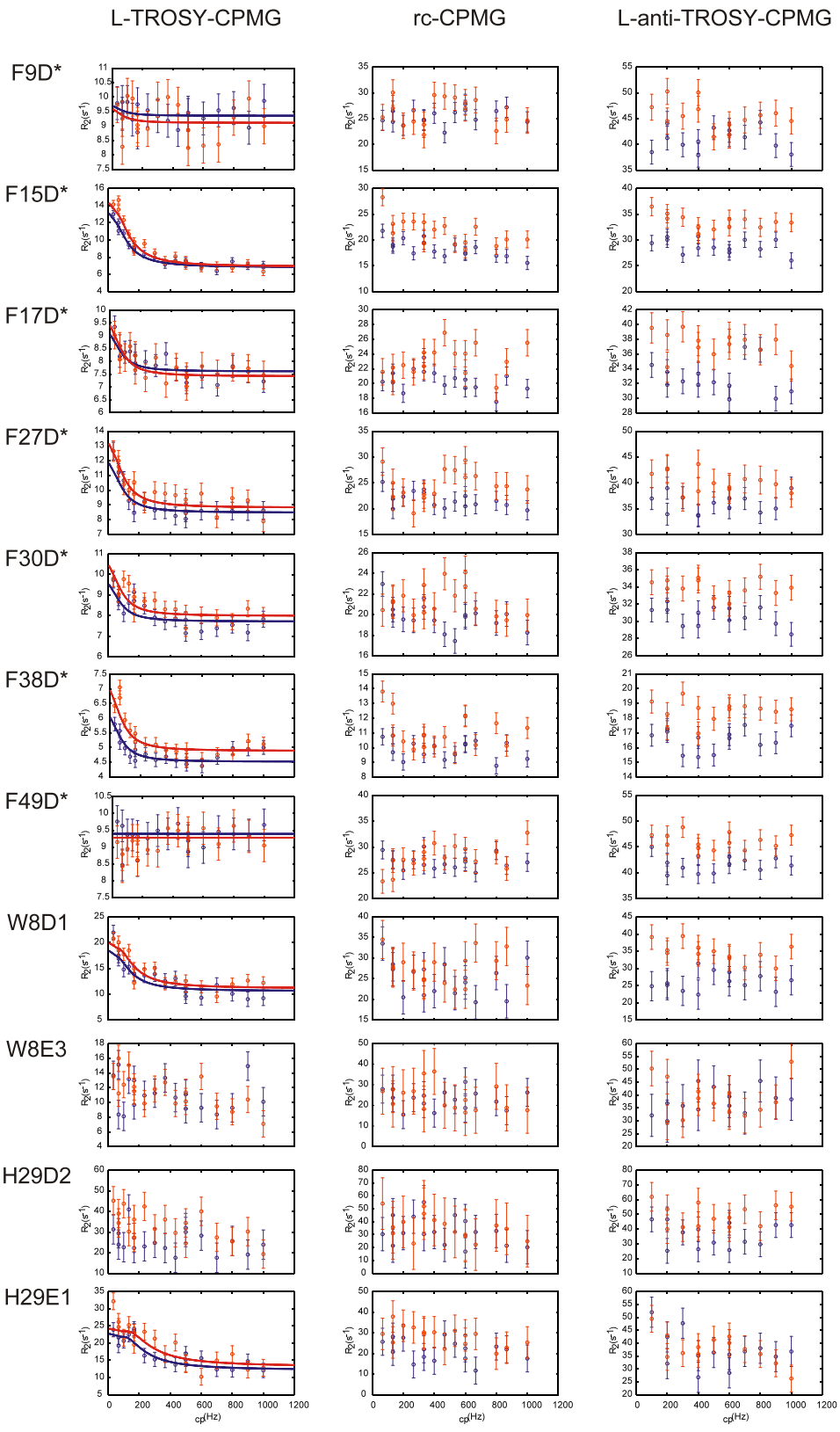
Supporting Information

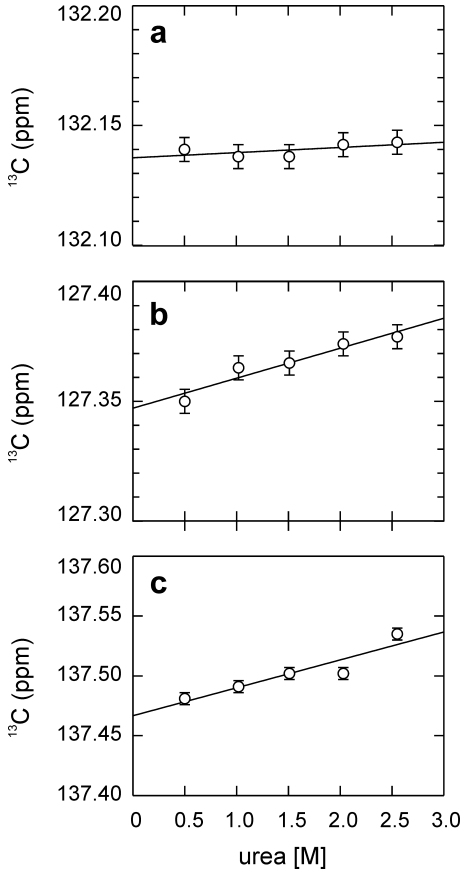
Conformational Exchange of Aromatic Side Chains Characterized by L-optimized TROSY-Selected ^{13}C CPMG Relaxation Dispersion

Ulrich Weininger, Michal Respondek, and Mikael Akke*

Department of Biophysical Chemistry, Center for Molecular Protein Science, Lund University, P.O. Box 124, SE-22100 Lund, Sweden



SI Figure 1. All obtained ^{13}C aromatic CPMG relaxation dispersion profiles in three different versions acquired on a 0.4 mM sample of CspB in 10 mM HEPES pH 7.0 at 25 °C and static magnetic field strengths of 11.7 T (blue) and 14.1 T (red). The solid lines in the L-TROSY variant represent global fits of the folding–unfolding model to the experimental data.



SI Figure 2. Urea dependence of the ^{13}C chemical shifts of the unfolded state of CspB at 25°C monitored by ^{1}H-^{13}C HSQC. (a) Phe D*, (b) Trp D1, (c) His E1.