

Captions for Supplementary Figures

Figure S1. ^{15}N relaxation data acquired at 500 MHz for CTD-EF. The ^{15}N T_1 (top), T_2 (middle) and NOE (bottom) values are plotted versus sequence.

Figure S2. Comparative structural analysis of CTD-EF. (A) Comparison of the structure of CTD-EF with (from left to right) EF-hand 3 calpain domain VI (PDB 1KFU), troponin-C (PDB 1TOP), N lobe of Zn bound CaM (2PQ3) and N lobe of apo CaM (1F70). CTD-EF is in gray and related proteins are in black. Structures are aligned by superimposition of all common backbone atoms. The termini of CTD-EF are labeled. (B,C) Comparisons of the structures of CTD-EF and calpain. (B) Best-fit superposition of CTD-EF and EF-hand 3 of domain VI. (C) Best-fit superposition of CTD-EF and the EF-hand 5 of domain IV. CTD-EF is in gray and calpain is in black. Residues and helices numbers of CTD-EF are labeled.

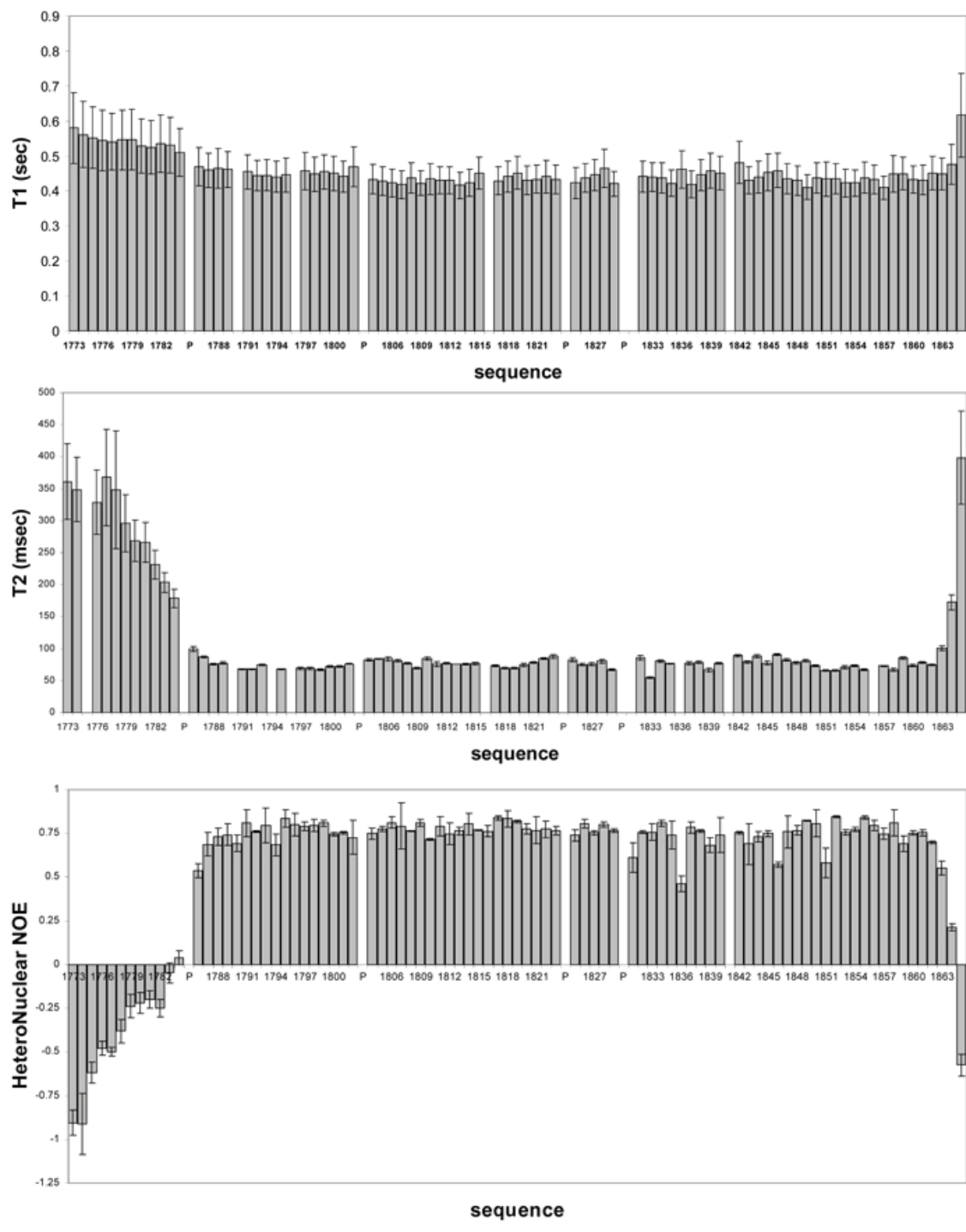


Figure S1

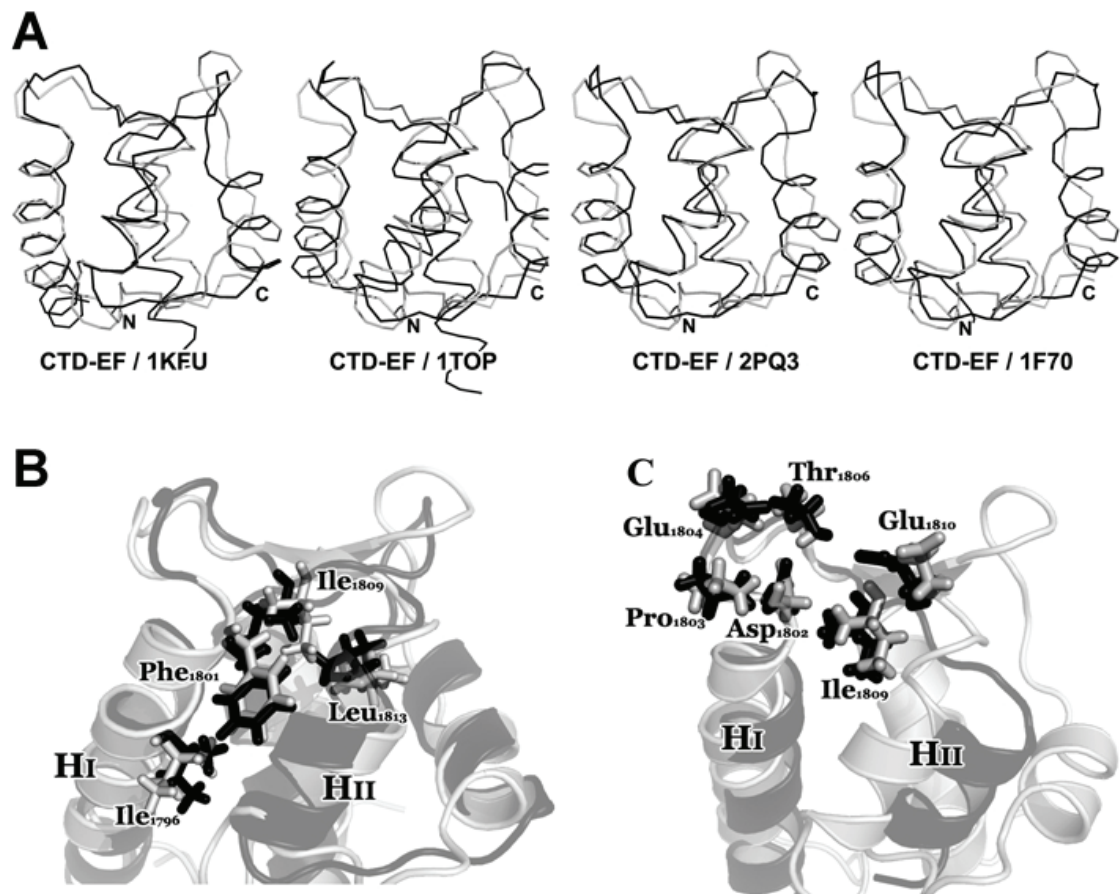


Figure S2