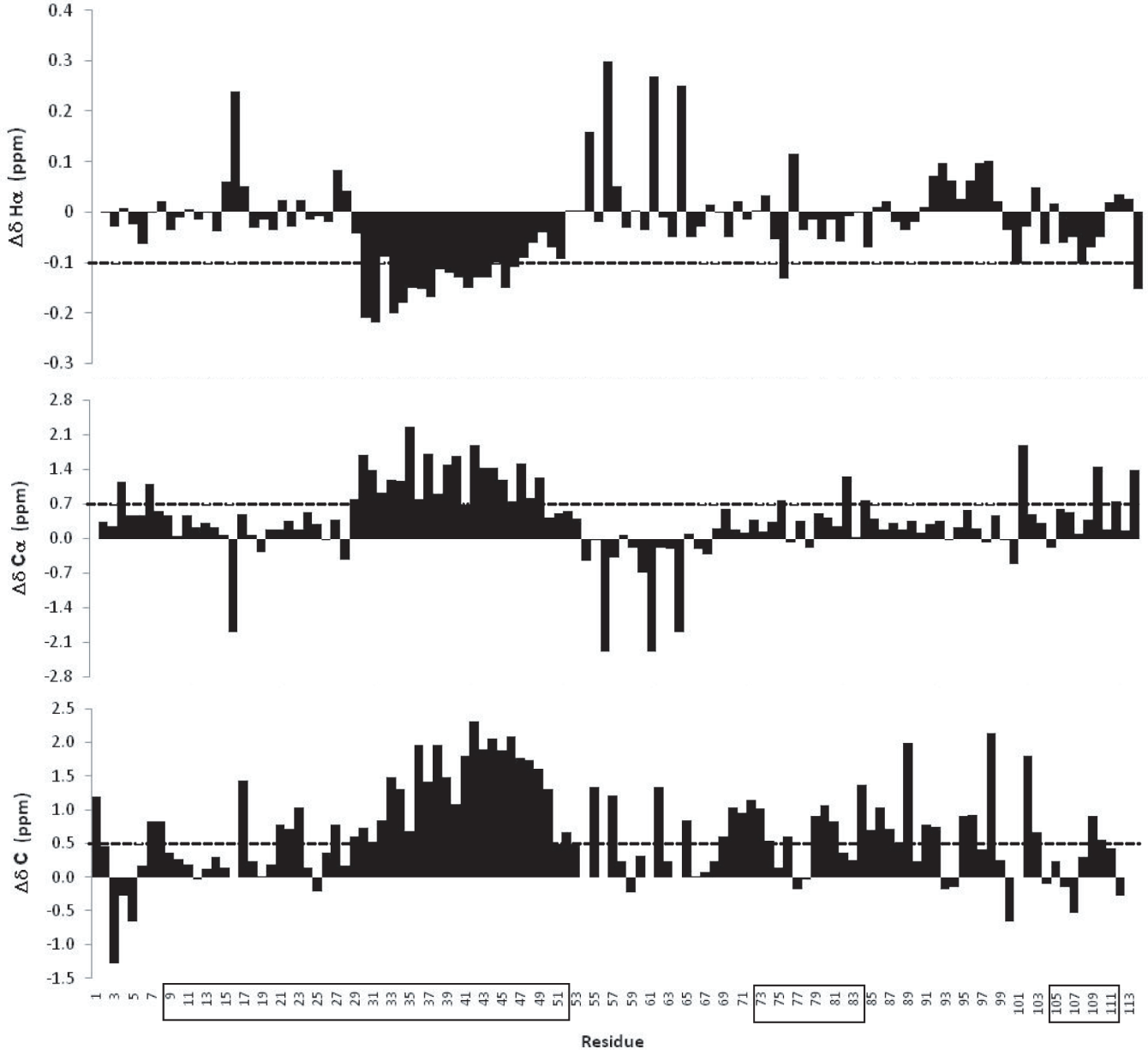
Supplementary Figure 1: Secondary structure of PN2-3. (A) Chemical shift deviations (CSD) from random coil values of Hα, Cα and C (carbonyl) of PN2-3 residues. Residues 29 to 51 present CSD characteristic of α-helical conformation, i.e. ^{1}Hα CSD < -0.1 ppm, ^{13}Cα CSD > 0.7 ppm and carbonyl CSD > 0.5 ppm. In the PN2-3 sequence, boxed residues are predicted to be α-helical by two secondary structure prediction algorithms or more. (B) Ribbon representation of 7 calculated "best" structures of PN2-3 based on TALOS-derived torsion angle constraints. The helical regions (F29-E51) of the backbones of these structures are superimposed (rmsd = 0.8 Å). The tubulin-binding domain (V10-K85) is colored in red.

Supplementary figure 1

A



B