Figure 4 – figure supplement 3

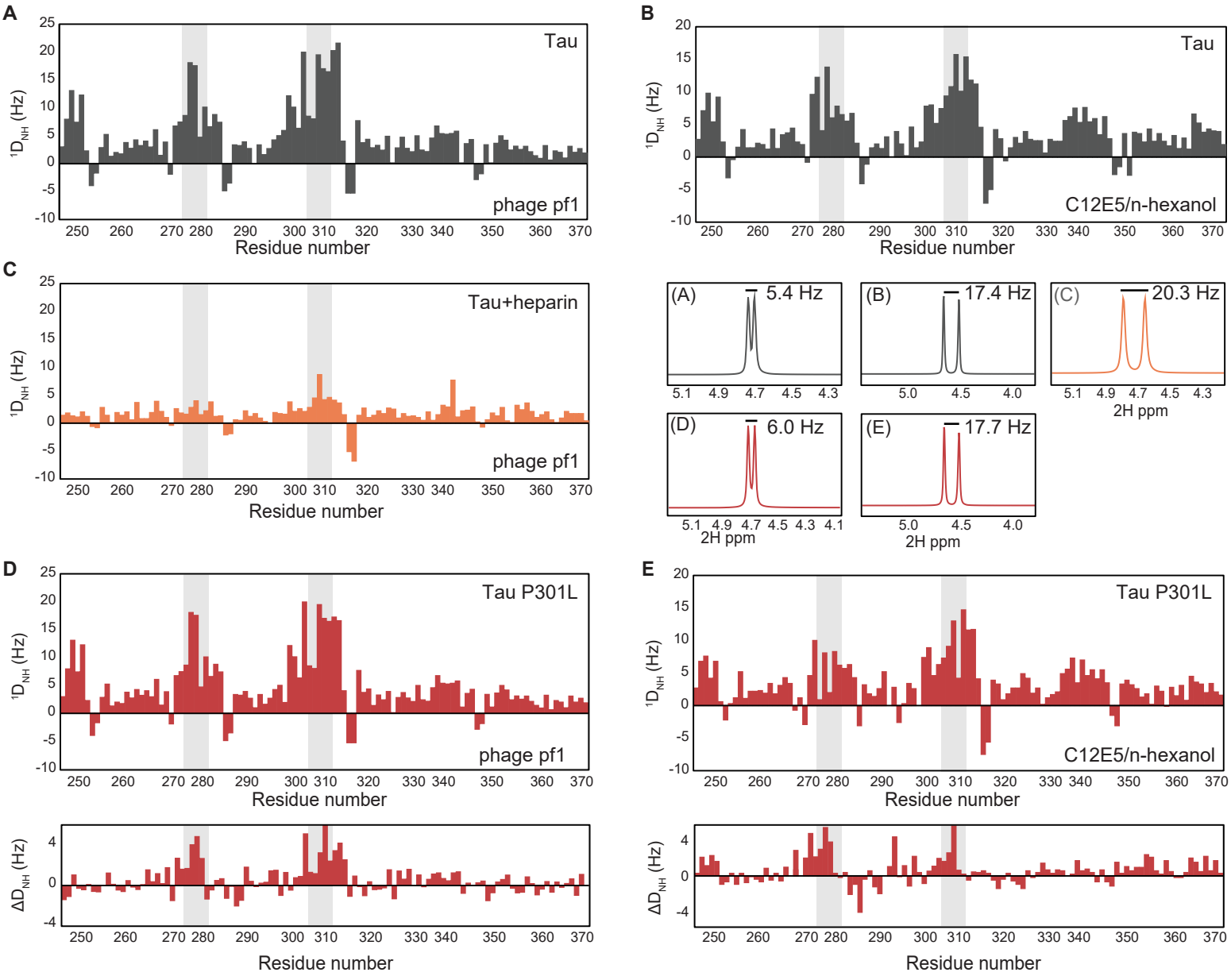

Figure 4 – figure supplement 3

Conformations of the various tau species measured through RDCs. (A-B) Backbone amide RDCs ($^1D_{NH}$), collected in 5 mg/ml phage pf1(70) (A) or 4.5% (vol/vol) C12E5/n-hexanol(71) (B) alignment media, showing a compaction in the PHF6* and PHF6 repeat regions (highlighted in grey). The 1D ^2H spectra, recorded on the 1000 MHz spectrometer (middle, right) show splitting of 5.4Hz (A) and 17.4 Hz (B), respectively. In both alignment media, large RDCs were observed for residues in the PHF6 aggregation-prone repeats, indicating the presence of a compaction of this region. **(C)** $^1D_{NH}$ RDCs measured for 1:1 tau:heparin complex aligned with 16 mg/ml phage pf1. The RDCs show highly decreased values in the PHF6* and PHF6 repeat regions compared to tau alone, indicating an expansion in this region. The 1D ^2H spectra, recorded on the 1000 MHz spectrometer (middle, right, C), shows splitting of 20.3 Hz, indicating a higher degree of alignment compared to tau alone. **(D-E)** $^1D_{NH}$ RDCs measured for tau^{4R} P301L mutant collected in 5 mg/ml phage pf1 (D) or 4.5% (vov/vol) C12E5/n-hexanol (E) alignment media. Both conditions show lower RDC values in the PHF6* and PHF6 repeat regions compared to wild-type tau^{4R} (differences in RDCs between WT tau and the P301L sample are shown underneath each plot), indicating a slightly increased tendency toward an extended structure in this tauopathy-associated mutant. The degree of alignment for the two samples was slightly higher than that of tau^{4R}, as indicated by the ^2H splitting (middle, right) of 6.0 Hz (D) and 17.7 Hz (E).