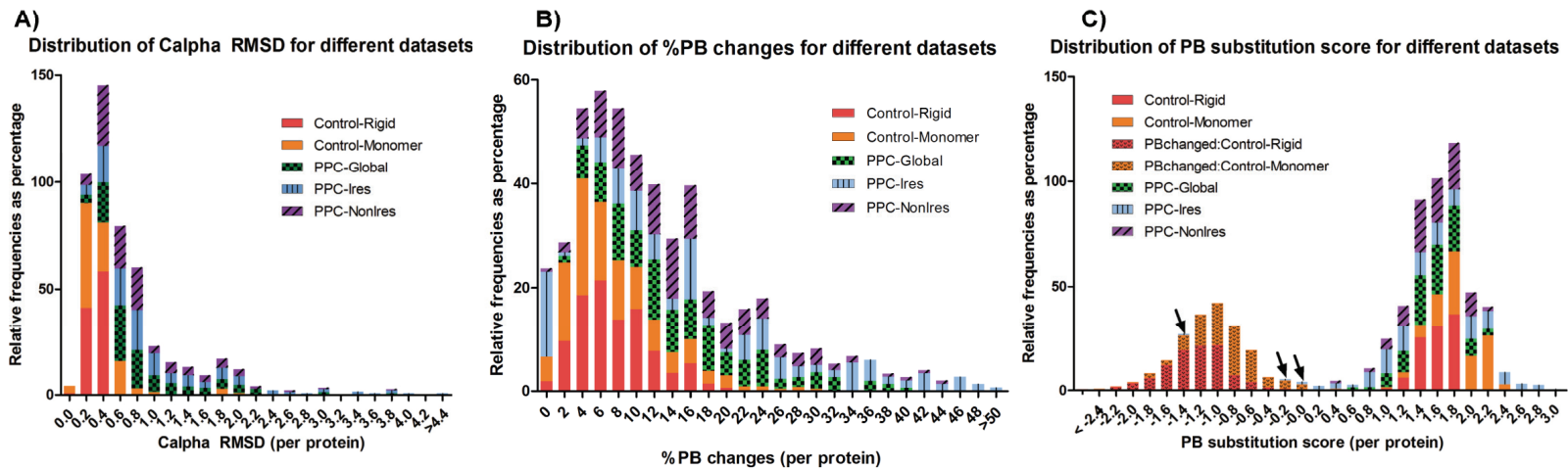


**Figure S1: Distribution of parameters capturing structural change for Control and Test datasets**



Distribution of values for the three parameters a).  $C\alpha$  RMSD b). %PB changes and c). PB substitution score, which quantify structural change for the following datasets: Changes in all residues (global) for Rigid, Monomeric and PPC datasets; Changes in interacting residues (Ires) for PPC dataset; Changes in Non-interacting residues (NonIres) for PPC dataset. The values plotted are calculated on a per-protein basis. In c), the arrows indicate proteins having negative PB substitution scores for PPI-Ires. The total number of pairwise comparisons used for different datasets are: Control-Rigid (n=1328), Control-Monomer (n=2286), PPC (n=154).