

Modulation of folding kinetics of repeat proteins: Interplay between intra- and interdomain interactions

Supporting Information

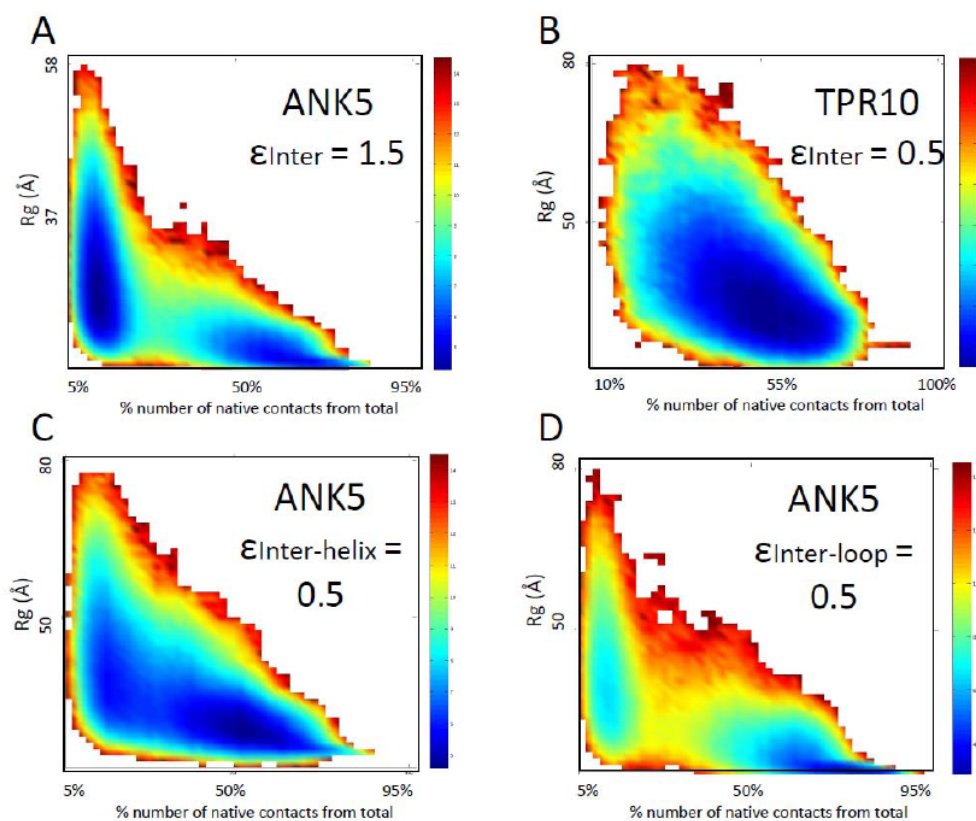


Figure S1.

The free energy landscapes of various ANK and TPR systems projected along R_g and Q . The free energy of the system in a given R_g (radius of gyration) and a given number of contacts (Q). Dark blue regions indicate relatively populated conformations. (A) ANK5 system with inter-contacts with increased strength. (B) TPR10 system with reduced inter-contact strength. (C) ANK5 system with reduced inter-contacts between helices (D) ANK5 system with reduced inter-contacts between loops.

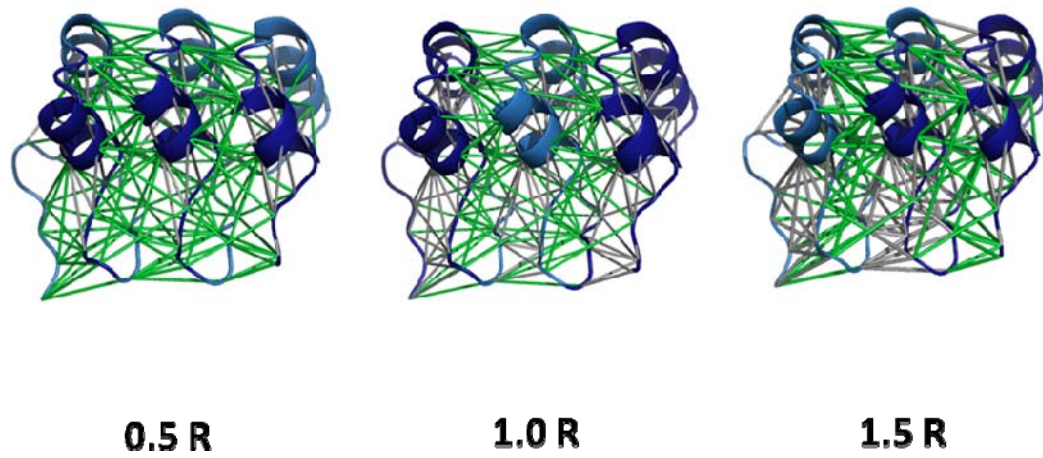


Figure S2.

Definition of repeat boundaries in ANK proteins.

The interface contacts (in green) and the intra-contacts (in grey) in ANK3 where the repeating unit definition was altered. The boundaries are defined by half a repeat (a single helix) (left), a repeat unit (34 residues) (middle), and repeat and a half (right)