



Supplementary Figure 8. Overlay of the wild type and the a4 mutant BAR domains (stereo views). (A) Four monomers of the a4 mutant (dark to pale blue) are superimposed on the wild type monomer (red) and viewed from the outside. The surface representation of the wild type dimer is also shown. All these monomer structures are almost completely the same in the core domain while they start to diverge at the kinks in helix II and III. (B) When four mutant monomers are superimposed as they fit in the arm, they are converged into one arm structure. These four mutant conformers differ only around the kinks. (C) Overlay of the wild type (blue trace) and the a4 mutant (orange) in the arm viewed from the concave surface. The inserted four amino acids segment in the mutant helix II is shown in red. Side chains of basic and hydrophobic residues on the concave surface are shown. The spatial positions of these residues are well conserved. The helix 0 is omitted.