Structure *16*
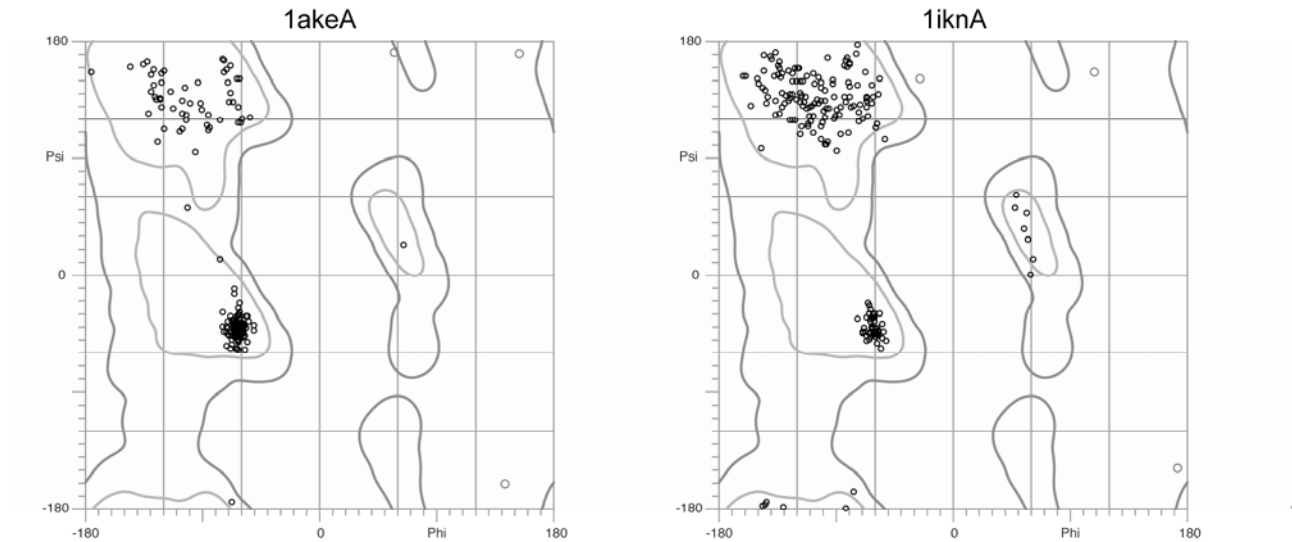
Supplemental Data

Protein Structure Fitting and Refinement

Guided by Cryo-EM Density

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Figure S1. Ramachandran Plots of the Final Structures of the Single-Domain Protein 1akeA and the Two-Domain Protein 1iknA (Calculated with MOLprobity [Lovell, et al., 2003])

The average numbers of residues in the allowed regions for the (Φ,Ψ) dihedral angles are 98.6% and 98.8%, respectively, and in the favored regions are 96.7% and 96.8%, respectively.