

Figure S1. Modeling Mutation Effect on RAD51 Protein Stability

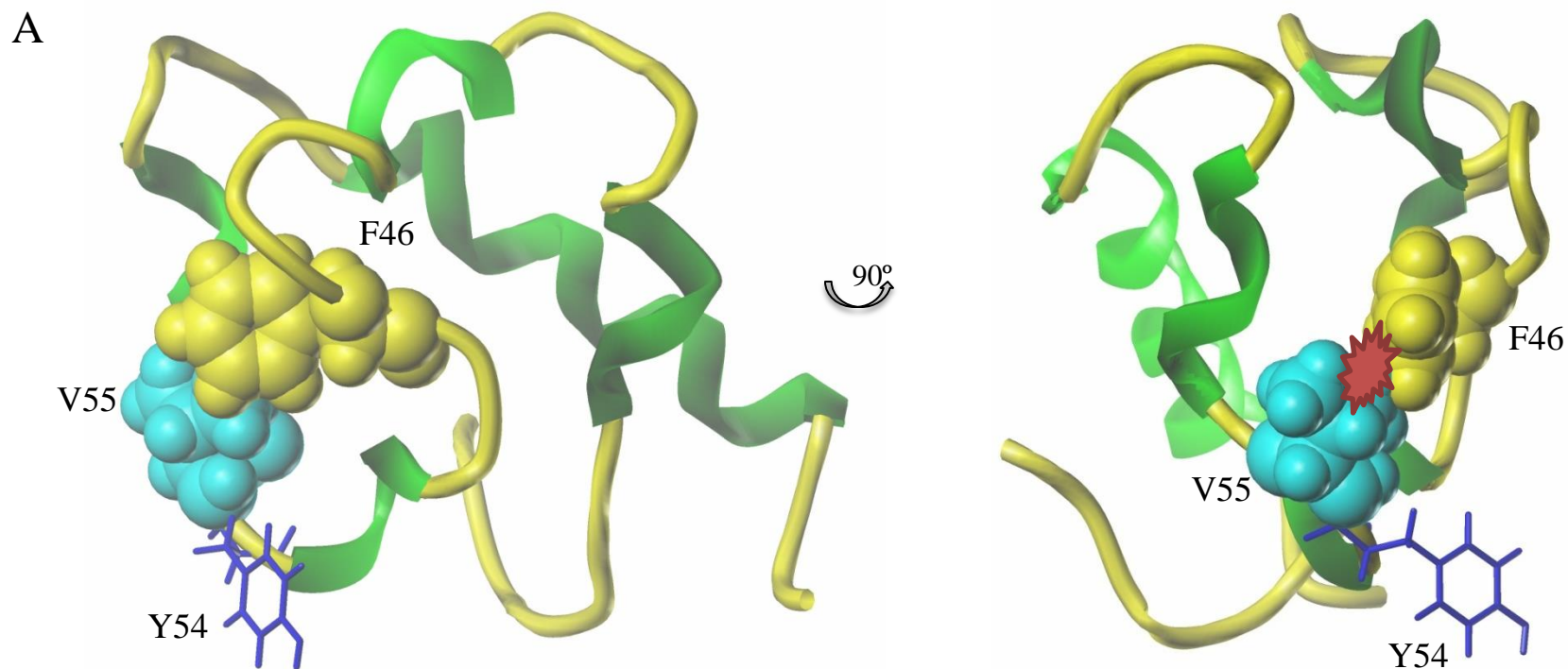


Figure S1 (A): A55V in RAD51 - Orthographic view of human RAD51 A55V mutation based on the human RAD51 structure (PDB 1B22, Aihara et al., 1999). Ribbon representation of RAD51 structure is colored by its secondary structures, α -helices in green, and loops in yellow. Residues Val55 and Phe46 are highlighted with space fill rendering colored in cyan and yellow, respectively, showing the steric clash between the two residues. Tyr54 is highlighted in stick rendering and colored blue, which neighbors the mutated Val55 and is located in a loop. Left, front view; Right, side view.

B

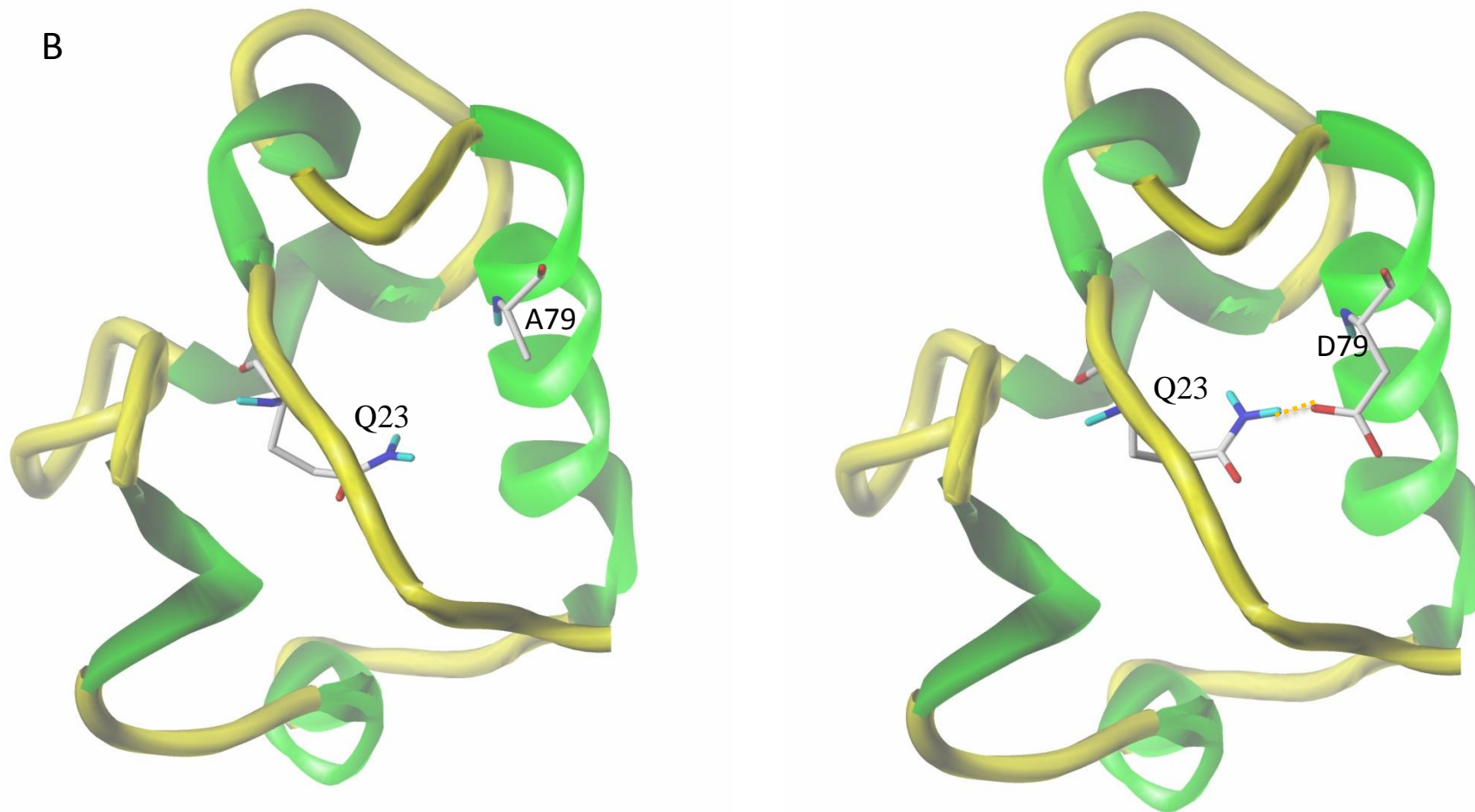


Figure S1 (B): A79D in RAD51 - Structure representation of human RAD51 A79D mutation based on the human RAD51 structure (PDB 1B22, Aihara et al., 1999). Left: Ribbon representation of RAD51 structure is colored by its secondary structures, α -helices in green, and loops in yellow. Residues Gln23 and Asp79 are highlighted with stick rendering colored by atom types. Right: Hydrogen bond was formed between side chains of Gln23 (NH) and Asp79 (C=O) of Rad51 to hold the loop and α -helix together.