Figure S1. Quality assessment of the three-dimensional models. Quality of the generated models along with that of the template structure was evaluated using PsoSA-web at https://prosa.services.came.sbg.ac.at/prosa.php. The calculated quality (Z) scores (closed circles) are displayed in the context of the Z-scores of all experimentally determined protein structures available in the Protein Data Bank. Every dot represents a distinct structure solved by X-ray crystallography (light blue) or NMR (dark blue). PBCV-1, *Paramecium bursaria Chlorella* virus 1 (Z-score: -6.09); P1-DR, Polinton 1 from *Danio rerio* (Z-score: -6.84); Tlr, Tlr element from *Tetrahymena thermophila* (Z-score: -6.05).