



S3 Figure. *A model with a large unbound/bound conformational change.* The target (protein 1xpi chain A, and RNA 2i82 chain E) is modeled on the template 2ab4 chains A and B) by PRIME. The ligand RMSD between the model and the native complex 2i82 chains A and E is 5.7 Å. Free docking RPDock did not model the target successfully due to the large conformational change.