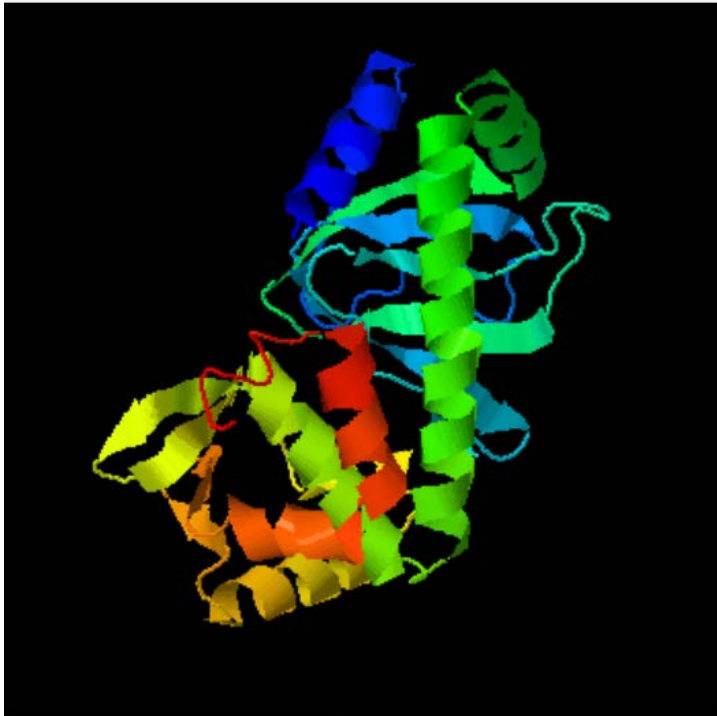


Figure S5: Predicted 3D protein structure of PrfA using I-TASSER



PrfA_EGDe
C-score= 1.07



PrfA_CDL65 (ST155)
C-score= -1.62

C-score is calculated based on the significance of threading template alignments and the convergence parameters of the structure assembly simulations. C-score is typically in the range of $[-5, 2]$, where a C-score of a higher value signifies a model with a higher confidence and vice-versa.