

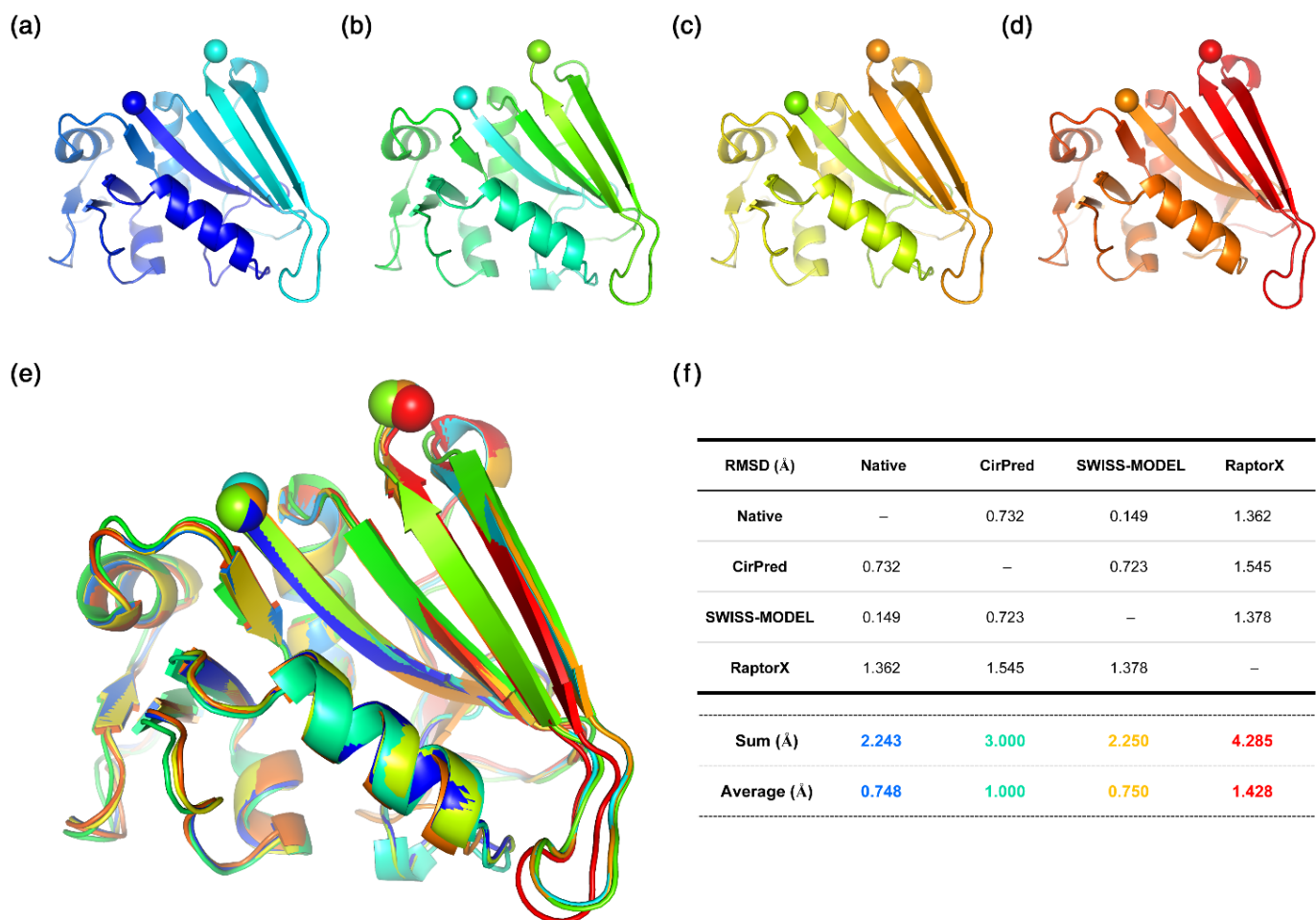


Fig. S1. Co-linear modeling quality of the CirPred and several state-of-the-art modeling methods. Although the CirPred is designed for circularly-permuted proteins, it can be applied to traditional co-linear structure modeling, simply by setting the CP site of the query template protein as residue 1. Here the dihydrofolate reductase (DHFR) was used as the template to construct models of the DHFR itself by CirPred and two widely-used comparative structure modeling methods, SWISS-MODEL [18] and RaptorX [19]. **(a)** Crystal structure of the native DHFR protein (PDB 1rx4). **(b)** Model constructed by CirPred. **(c)** Model constructed by SWISS-MODEL. **(d)** Model constructed by RaptorX. **(e)** Superimposition of all the above structures. **(f)** Root-mean-square distances (RMSD) between all pairs of the above structures. In this example, on average, the co-linear model made by CirPred showed only 1 Å difference from the native structure or models made by other methods.