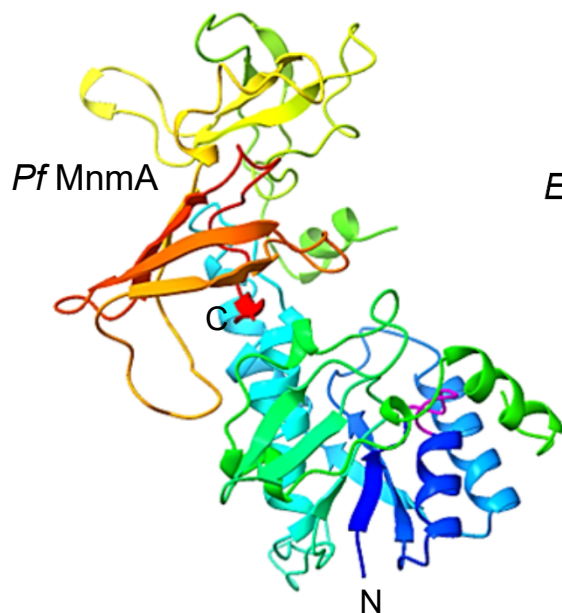
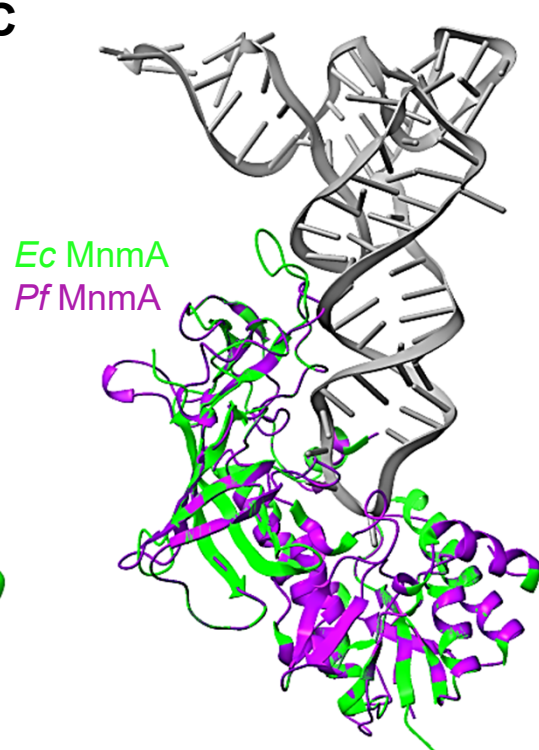


A**B****C****D**

Root mean square deviation (RMSD, Å) values for structural alignments of *Ec* MnmA (PDB id: 2DER) with MnmA homology models

Sy MnmA	Bs MnmA	At MnmA	Sc Mtu1	<i>Pf</i> MnmA	Bm MnmA	Ta MnmA	Tg MnmA	Et MnmA
0.181	0.924	0.219	0.153	0.264	0.170	0.200	0.153	0.943

E