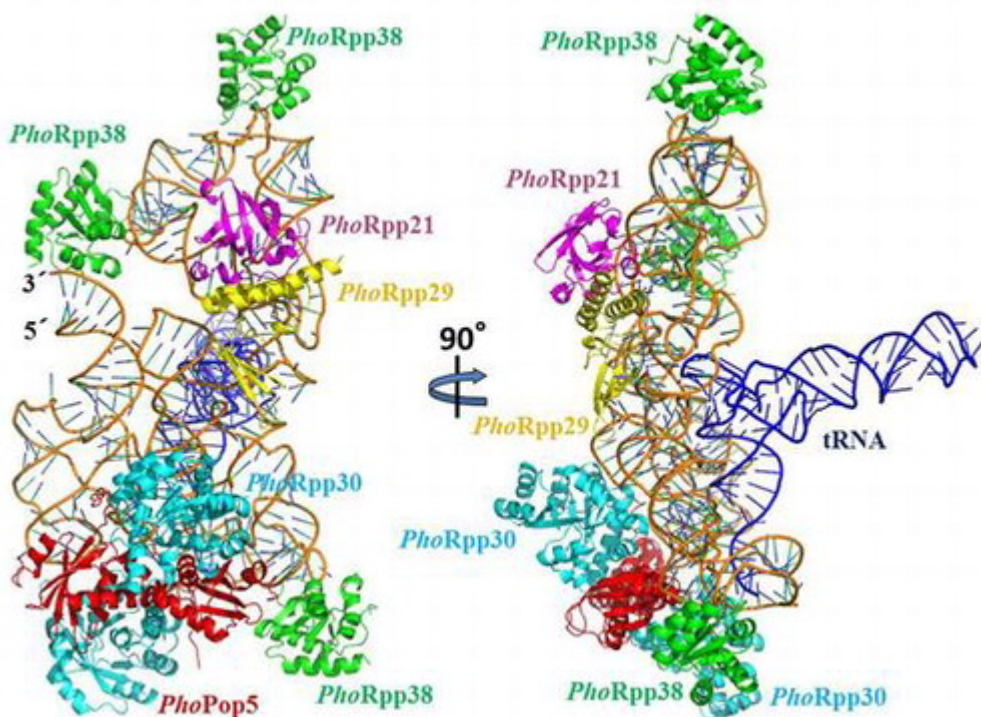


Ribonuclease P (RNase P) is an endoribonuclease that catalyzes the processing of the 5'-leader sequence of precursor tRNA (pre-tRNA) in all phylogenetic domains. We have found that RNase P in the hyperthermophilic archaeon *Pyrococcus horikoshii* OT3 consists of RNase P RNA (*Phop*RNA) and five protein cofactors designated *PhoPop*5, *PhoRpp*21, *PhoRpp*29, *PhoRpp*30, and *PhoRpp*38. Biochemical characterizations over the past 10 years have revealed that *PhoPop*5 and *PhoRpp*30 fold into a heterotetramer and cooperate to activate a catalytic domain (C-domain) in *Phop*RNA, whereas *PhoRpp*21 and *PhoRpp*29 form a heterodimer and function together to activate a specificity domain (S-domain) in *Phop*RNA. *PhoRpp*38 plays a role in elevation of the optimum temperature of RNase P activity, binding to kink-turn (K-turn) motifs in two stem-loops in *Phop*RNA. This review describes the structural and functional information on *P. horikoshii* RNase P, focusing on the structural basis for the *Phop*RNA activation by the five RNase P proteins.



A three-dimensional model of *Pyrococcus horikoshii* RNase P in complex with tRNA on the basis of biochemical and structural data of the *P. horikoshii* RNase P components.