Poster Presentation

MS13.P04

Structure of a canonical RNase YoeB bound to the ribosome

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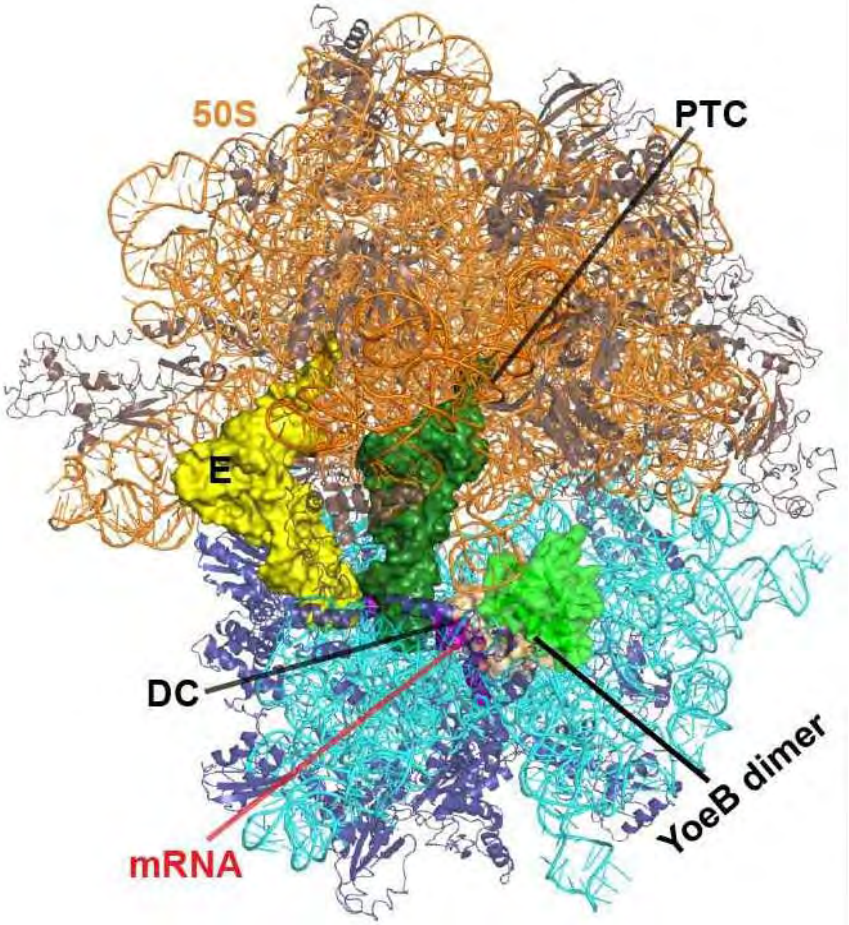
As a typical endoribonuclease, YoeB mediates cellular adaptation in diverse bacteria by degrading mRNAs on its activation. Although the catalytic core of YoeB is thought to be identical to well-studied nucleases, this enzyme specifically targets mRNA substrates that are associated with ribosomes in vivo. However, the molecular mechanism of mRNA recognition and cleavage by YoeB, and the requirement of ribosome for its optimal activity, largely remain elusive. Here, we report the structure of YoeB bound to 70S ribosome in pre-cleavage state, revealing that both the 30S and 50S subunits participate in YoeB binding. The mRNA is recognized by the catalytic core of YoeB, of which the general base/acid (Glu46/His83) are within hydrogen-bonding distance to their reaction atoms, demonstrating an active conformation of YoeB on ribosome. Also, the mRNA orientation involves the universally conserved A1493 and G530 of 16S rRNA. In addition, mass spectrometry data indicated that YoeB cleaves mRNA following the second position at the A-site codon, resulting in a final product with a 3'–phosphate at the newly formed 3' end. Our results demonstrate a classical acid-base catalysis for YoeB-mediated RNA hydrolysis and provide insight into how the ribosome is essential for its specific activity.

[1] *S.Feng, Y.Chen, K.Kamada, H.Wang, K.Tang, M.Wang, Y.Gao, 2013, Nucleic Acid Research, 2013, 41, 9549-9556*



Keywords: Ribosome, RNase