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A CUGGU/UUGGU-specific MazF homologue from *Methanohalobium evestigatum*Yojiro Ishida¹, Keiko Inouye¹, Ouyang Ming² and Masayori Inouye¹¹Center for Advanced Biotechnology and Medicine, USA²University of Massachusetts, USA

MazF is a sequence-specific endoribonuclease or mRNA interferases, which cleaves RNA at a specific sequence. Since the expression of a specific gene or a group of specific genes can be regulated by MazF, expanding the repertoire of recognition sequences by MazF mRNA interferases is highly desirable for biotechnological and medical applications. Here, we identified a gene for a MazF homologue (MazFme) from *Methanohalobium evestigatum*, an extremely halophilic archaeon. In order to suppress the toxicity of MazFme to the *E. coli* cells, the C-terminal half of the cognate antitoxin MazEme was fused to the N-terminal ends of MazFme. After purification of the MazEme-MazFme fusion protein, MazFme was released from the fusion protein by factor Xa treatment. The free MazFme RNA cleavage specificity was determined by primer extension and synthetic ribonucleotides, revealing that MazFme is a CUGGU/UUGGU-specific endoribonuclease.

Biography

Yojiro Ishida has recently obtained his PhD from Hiroshima University. His mentors are Professor Tadashi Shimamoto, Hiroshima University and Professor Masayori Inouye, Rutgers University. He has developed a new expression system to incorporate a toxic amino acid analogue into a protein to alter the function by using the single-protein production (SPP) system. Furthermore, he developed a residue and stereo specific labeling system for NMR structural studies. Currently, his research focus are: Discovery of new MazF homologues, application of MazF for specific gene regulations, characterization of new Toxin-Antitoxin (TA) systems from *Staphylococcus aureus*, and incorporating ¹⁹F probe into methyl groups of a protein to characterize large molecular weight proteins and membrane proteins using the SPP system in *E. coli*.

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