Faculty of Science and Technology
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# Structural basis for the molecular mechanisms of catalytic reaction and substrate recognition by nucleic acid enzymes.

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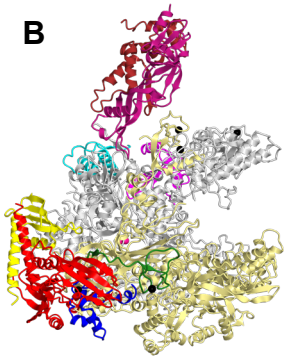
Fig. 1 X-ray structures of nucleic acid enzyme determined.

A

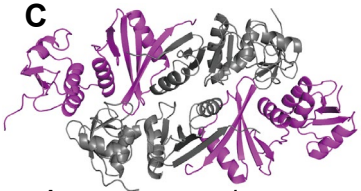
*Sulfolobus solfataricus*
RNA polymerase
*Nature* 451 (2008)

B



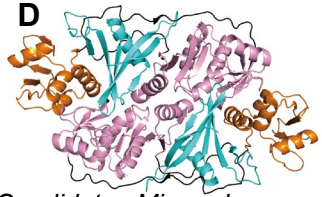
*Thermococcus kodakarensis*
RNA polymerase
*Nature commun* 5 (2014)

C



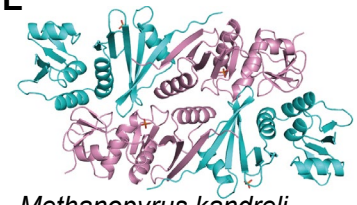
*Aeropyrum pernix*
RNA-splicing endonuclease
*Nucleic Acids Res* 39 (2011)

D



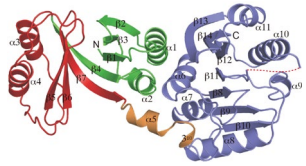
*Candidatus Micrarchaeum acidiphilum*
RNA-splicing endonuclease
*Nucleic Acids Res* 40 (2012)

E



*Methanopyrus kandreli*
RNA-splicing endonuclease
*Nucleic Acids Res* 46 (2018)

F



*Thermococcus kodakarensis*
tRNA methyltransferase Trm11
*Nucleic Acids Res* 44 (2016)

Content:

Our research goal is to reveal the molecular mechanisms of catalytic reaction and substrate recognition of nucleic acid enzymes regarding transcription and post-transcription events. X-ray crystallography is a powerful tool to determine the structures of proteins and nucleic acids (DNA and RNA). Based on the structural information, we perform biochemical studies of the enzymes. These results obtained often provide a novel insight into the substrate specificity of enzymes.

Our favorite model microorganism is Archaea, which is one of three domains of life. There is strikingly similarity of structure and function of enzymes related to transcription and RNA maturation between archaea and eukaryote because the two domains are evolutionally divided from a common ancestor. So far, we have determined the X-ray structures of archaeal enzymes, two RNA polymerases (Fig. 1A and 1B), three RNA-splicing endonucleases (Fig 1C, 1D and 1E) and tRNA methyltransferase Trm11 (Fig. 1F).

Keywords: gene expression, Archaea, X-ray crystallography

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