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Structural Diversity in Homologous Catalytic RNAs. Andrey S. Krasilnikov*, Tao Pan[†], Alfonso Mondragón*, *Dept. of Biochemistry, Molecular Biology & Cell Biology, Northwestern Univ., Evanston, IL 60208, [†]Dept. of Biochemistry and Molecular Biology, Univ. of Chicago, Chicago, IL 60637.

RNase P is one of only two ribozymes conserved in all three kingdoms of life and it is required in the 5' maturation of all tRNAs. Bacterial RNase P can be sub-divided into two major types (A, B) based on their sequence characteristics. The bacterial RNase P RNA component consists of between 350-450 nucleotides, while the protein component is a small, basic protein. Eubacterial P RNAs consist of two domains: a specificity domain or S-domain and a catalytic domain or C-domain. Previously, we have solved the structure of the *B. subtilis* S-domain and the structure revealed the general features of this domain, the interactions that help maintain the overall fold of the molecule, and a large non-helical, but well-structured module that is conserved in all RNase P's. In order to extend our understanding of bacterial RNase P to other types, we have solved the 2.9Å X-ray structure of the S-domain of an A-type bacterial RNase P. The new structure shows that the binding site in both bacterial types is very similar, but the overall structure shows significant differences. Comparison of the structures helps understand the role of several conserved and non-conserved regions. Additionally, the structures of the S-domain of an A- and B-type bacterial RNase P are the first examples of two large RNA structures with identical function but with a significantly different fold. The comparison provides important clues on the general architecture of large RNA molecules.