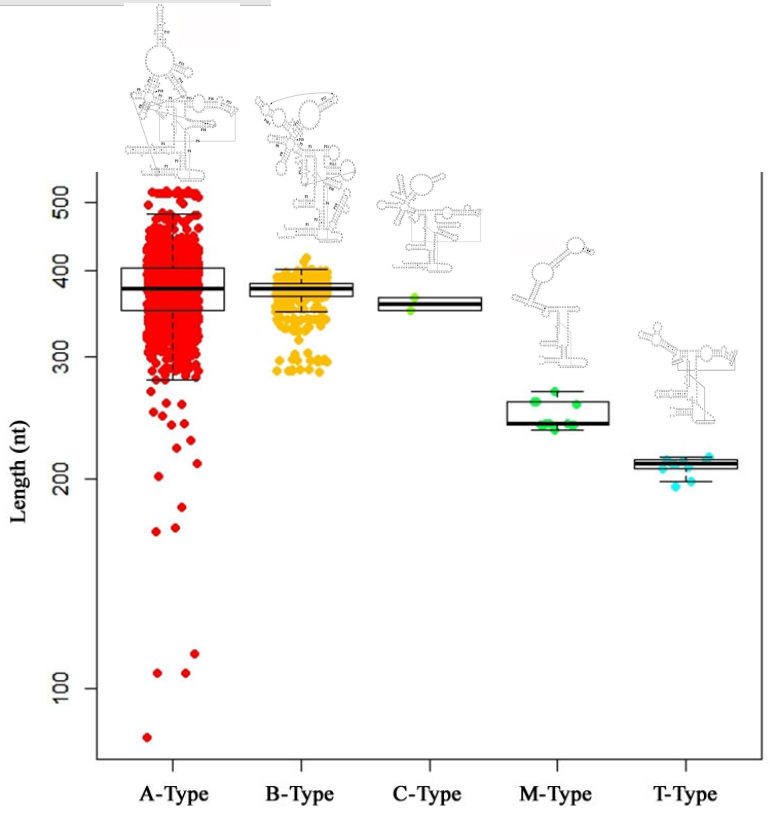
Foundational Genomics Research, PMI SFA

U.S. DEPARTMENT OF ENERGY | Office of Science

Novel Approach: 100x faster identification of all five structural classes of the gene for the non-coding, catalytic RNA, RNase P

Objective	• To create a user-friendly graphical user interface for the rapid identification of RNase P.
New science	• RNase P is an essential, catalytic ncRNA that is ubiquitous in all three kingdoms (Bacteria, Archaea, and Eukaryotes). • This ncRNA is challenging to annotate due to both variable sequence and diverse secondary structure. • The newly developed algorithm can identify RNase P RNA 100x faster than the leading software. • Five distinct RNase P structure types are observed in prokaryotes and the new algorithm is the first to identify all of them, including the rare C-type and T-type RNase Ps. • The software's taxonomic assignment tool facilitates synthetic microbiome studies.
Impact	• This rapid and accurate software tool is enabling the detection of new RNase Ps and facilitating the taxonomic characterization of genomes and microbiomes.



Distribution of RNase P RNA structural classes by type and length. RNase P RNA has a broad diversity of sequence length and structure. A-type RNase P RNAs are the most common structural class. The minimal T-type, C-type, and M-type are uncommon with only 28 organisms identified to date containing one of these structural classes.

P finder: genomic and metagenomic annotation of RNase P RNA gene (rnpB)
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