Sequence of the ribonuclease P RNA gene from the cyanobacterium *Anacystis nidulans*

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The gene encoding the RNA component of ribonuclease P (RNase P) from the cyanobacterium *Anacystis nidulans* (*Synechococcus* PCC 6301) was cloned during the course of a continuing phylogenetic study of this catalytic RNA. The gene was identified by Southern analysis of genomic digests using an oligonucleotide probe containing the most highly conserved sequence in known eubacterial RNase P RNAs (5'-GAAAGTCCIIGCT-3'; I = inosine) (1). T7 RNA polymerase rolling-circle transcripts generated from the 'sense' strand of the clone have RNase P enzymatic activity *in vitro* (data not shown) (2), proving that the gene encodes a functional RNase P RNA. The nucleotide sequence of the *A. nidulans* RNase P RNA gene was determined. The secondary structure of the RNA, based on phylogenetic comparisons, is shown (Figure). This is the first available RNase P RNA sequence from the cyanobacterial lineage of the eubacteria.

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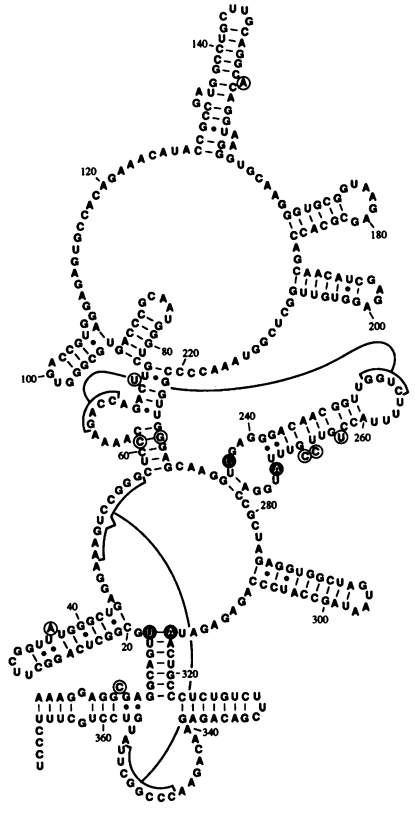

Figure. Secondary structure of *A. nidulans* RNase P RNA. Watson–Crick pairs are shown with lines (–), non-Watson–Crick pairs with filled circles (●). Lines and brackets indicate long-range pairings in the secondary structure. Variation in bases in the *A. nidulans* RNase P RNA which otherwise are completely conserved among eubacteria are indicated by filled circles; nucleotides which have no counterpart in other known eubacterial RNase P RNAs are circled. The locations of the 5' and 3' ends of the RNA have not been determined experimentally, but are based on the established mature ends of the *E. coli* RNase P RNA (3).

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