

# Nucleotide sequence of the 10Sa RNA gene of the $\beta$ -purple eubacterium *Alcaligenes eutrophus*

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In the course of cloning the gene for the RNA component of ribonuclease P (RNase P) from the  $\beta$ -purple eubacterium *Alcaligenes eutrophus*, we have also isolated a clone which contains significant sequence similarity to *Escherichia coli* 10Sa RNA, a 363 nucleotide, stable RNA of unknown function (1, 2, 3). The cloned DNA hybridizes to a ~340 nucleotide RNA in Northern blots of total RNA from *A. eutrophus* and another  $\beta$ -purple eubacterium, *Pseudomonas testosteroni*, but not other organisms tested, including *E. coli* (data not shown). The 10Sa RNA of *A. eutrophus* comigrates in 8M urea polyacrylamide gels with the 341 nucleotide RNase P RNA (also known as 10Sb RNA (1)) (data not shown), as is the case in *E. coli* (1). The *A. eutrophus* 10Sa RNA structural gene (underlined below) is clearly homologous to that of *E. coli*, with overall sequence identity of 51%. Much of the similarity between these sequences is found in the 5' and 3' terminal regions of the genes, whereas the central region shows significantly less similarity. Interestingly, the conservation of primary sequences does not end at the 3' terminus

of the mature *E. coli* 10Sa RNA, but continues for an additional 12 nucleotides into the 3' flanking sequence, which in *E. coli* is removed endonucleolytically from the precursor 10Sa RNA (2, 3).

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1  GTCGACCCGC  GCCAGTGCCT  CTATGTGGGC  GATGACCTGC  GCGACATCCA  GGCCGGCAAC  GGCCGGCATG
71  ATCACCGCAC  AGCCGCCTAT  GCTATTGCGG  CGACGAGCCG  CCGAGACCTG  GGGCGCCGAC  CACCTGATTC
141  GCCACCCGGC  CGAGCTGATC  CCGCTGCTGT  TGCCCGCCGT  GGTCGCCTCA  TTGTGTGCGA  GGGGTATCTG
211  GCCGTTCCGA  ACTCCC CGA  CAGCTGCGTC  CAACCGGTAC  AATCCAGCTT  CCTCACTGGG  CCGACCTGGT
281  TTTCGACGTGG  TTACAAAGCA  GTGAGGCATA  CCGAGGACCC  GTCACCTCGT  TAATCAATGG  AATGCAATAA
351  CTGCTAACGA  CGAACGTTAC  GCACTCGCTT  AATTGCGGCC  GTCCTCGCAC  TGGCTCGCTG  ACGGGCTAGG
421  GTCGCAAGAC  CACGCGAGGT  ATTTACGTCA  GATAAGCTCC  GGAAGGGTCA  CGAAGCCGGG  GACGAAAACC
491  TAGTGACTCG  CCGTCGTAGA  GCGTGTTCGT  CCGATGCGCC  GGTTAAATCA  AATGACAGAA  CTAAGTATGT
561  AGAACTCTCT  GTGGAGGGCT  TACGGACGCG  GGTTCGATTC  CCGCCGGCTC  CACCAGTATT  CAGTCCGATG
631  CAGCACCTGC  AG

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