The nucleotide sequence of the 5S rRNA from *Legionella pneumophila*

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The ribonucleotide sequence of the 5S ribosomal RNA purified from *Legionella pneumophila* strain 62212 was determined enzymatically (1) using the modifications described in (2). The sequence is depicted as folded into the "chair" secondary structure model described by Erdmann et al. (3), which best accommodates base-pairings consistent with previously reported data (4).

In this figure, boxes indicate bases participating in helix formation and circles indicate unpaired bases. Helices are designated by numbers, loops by letters. Evolutionary trees constructed from this and other Gram negative bacterial 5S rRNA sequences indicate that *L. pneumophila* is a member of the Gamma subdivision of the Rhodobacteria. This sequence differs from that of other 5S rRNAs reported for the Gamma subdivision in that helix 2 contains a two base-pair internal loop (indicated by an arrow). Other features, such as (i) a nine base-pair helix 1, (ii) an eight base-pair helix 5, (iii) a three-membered loop e, and (iv) the base sequence of helix 3, are all characteristic of 5S rRNAs from members of the Gamma subdivision of the Rhodobacteria.

Strain 62212 was obtained from A.D. Pearson, Communicable Disease Surveillance Center, London.

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REFERENCES
