

# Complete sequence of IS629

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The complete nucleotide sequence of IS629, originally isolated from the *Shigella sonnei* chromosome (1), was determined. IS629 was 1310 base pairs (bp) in length and had 25-bp imperfect inverted repeats at its termini. IS629 contained two large open reading frames named *orfA* and *orfB*: *orfA* (bp position 55 to 381) encodes 108 amino acids; *orfB* (bp position 378 to 1268) encodes 296 amino acids. A possible promoter and the Shine-Dalgarno (SD) sequence were located upstream of the initiation codon ATG for *orfA*. No such sequences were found in the upstream region of *orfB*. The IS629 sequence showed partial homology with those of IS3, IS600 (1), and IS2, and showed almost perfect homology with the IS3411 sequence (2).

## ACKNOWLEDGEMENT

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## REFERENCES

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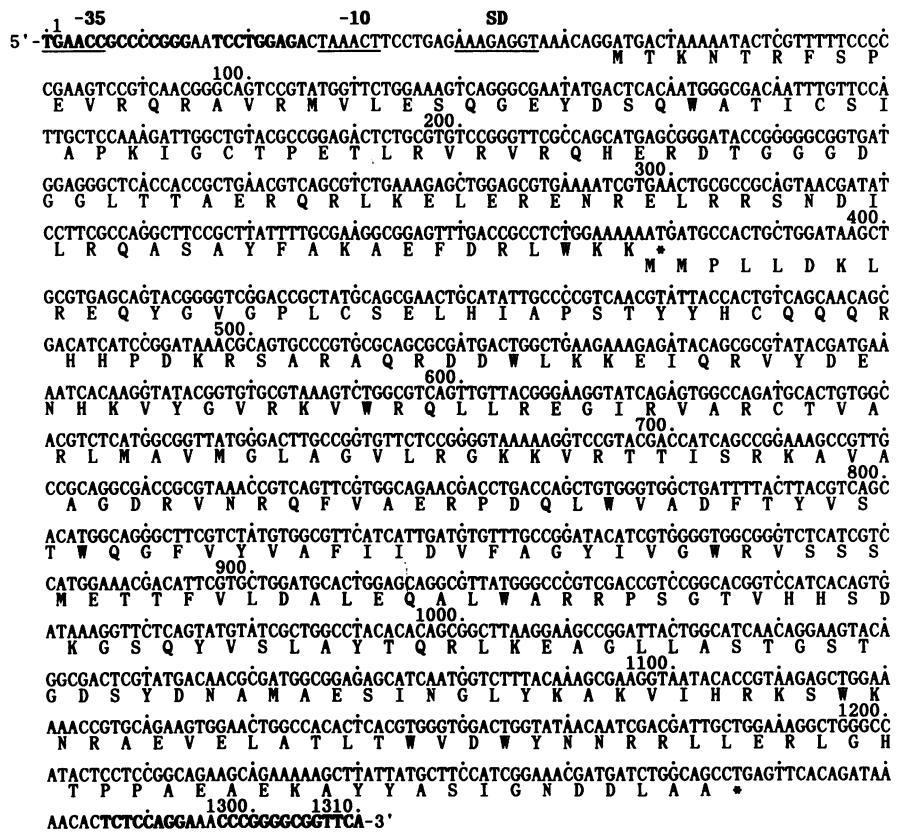


Figure 1. The entire nucleotide sequence of IS629. Terminal inverted repeat sequences are shown by boldface letters. The possible promoter sequence (-10 and -35 regions) and the Shine-Dalgarno sequence (SD) are underlined. Putative amino acid sequences of the two open reading frames (*orfA* and *orfB*) are shown underneath the nucleotide sequence.

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