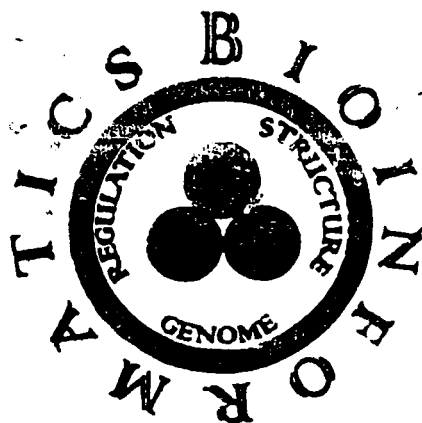


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## CONSERVED RNA STRUCTURES REGULATE INITIATION OF TRANSLATION OF *ESCHERICHIA COLI* AND *HAEMOPHILUS INFLUENZAE* RIBOSOMAL PROTEIN OPERONS

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**Keywords:** *gamma-proteobacterium*, *ribosomal protein*, *operon*, *RNA secondary structure*

Operons of ribosomal proteins of *E.coli* are a well known example of autoregulation of transcription initiation based on RNA secondary structures. These structures are conserved in other enterobacteria. In this study we analyzed operons of ribosomal proteins in the completely sequenced of a more distantly related *H.influenzae*.

We have identified operons of ribosomal proteins in *H.influenzae* using published annotations and GOLDIE 2.0 software for identification of conserved gene strings and then analyzed secondary structures of RNA. We have found conserved RNA structures in three operons.

Operon alpha is controlled by binding of S4 to a pseudoknot structure at start of gene *rpsM* encoding protein S13. The structure involving high order interactions is identical in *E.coli* and *H.influenzae*, whereas the other regions share structural, but not sequence similarity.

Operon S15 consists of a single gene *rpsQ* encoding S15. This operon is autoregulated by formation of alternative structures: either a pair of hairpins or a pseudoknot. It is interesting to note that only part of the extensive secondary structure found in *E.coli* is conserved in *H.influenzae*, but it is exactly the domain experimentally proven to be recognized by S15.

Operon *spc* is controlled by binding of S8 at the start of gene *rplE* encoding L5. The binding site is a hairpin resembling the S8 binding site in 16S rRNA. In fact, there two different structures can be formed both in *E.coli* and *H.influenzae*, both of which are corroborated by complementary substitutions. Thus it is plausible that some sort of alternative structure formation is involved in translation regulation of this operon.

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