Nucleotide sequence of the *rplJL* operon and the deduced primary structure of the encoded L10 and L7/L12 proteins of *Salmonella typhimurium* compared to that of *Escherichia coli*

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Submitted June 21, 1990 EMBL accession no. X53072

Portions of the *S. typhimurium rplJL* operon were isolated by EcoRI digestion from the recombinant pNL1 plasmid (1), cloned on the pUC19 vector (2) and sequenced by the procedure (3). Presented below is the determined nucleotide sequence of *rplJL* and the deduced a.a. sequence of r-proteins L10 and L7/L12 of *S. typhimurium*, as compared to those of *E. coli* (4). Due to the highly conserved structure, L10 protein of *S. typhimurium* is regulatory capable for *rplJL* genes of *E. coli* (5). Only three a.a. (Ser-12, Ala-45 and Ser-109) are different in L7/L12 protein of *S. typhimurium* and *E. coli*. In contrast to the leader sequence of the *rlpJL* mRNA and the L10-binding site (overlined) (6), no alterations were observed in the regions of base pairing necessary for the coupled translation of L10 and L12 cistrons (7).

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                          10        20        30        40        50        60        70        80        90       100
E.coli              GGCCTCCGTCGAAGACCGCAGGAGTTTCGCAAGAAACTTAATCCCCTGCGTAGACGGTGACAGAACGCTAAGATTATTCTTTTATATTCTGGCTTGTTTC
S.typhimurium       ......................C..C........GG.......................................-........C............

       110       120       130       140       150       160       170       180       190       200       210       220
                                                                                   EcoL10  M  A  L  N  L  Q  D  K  Q  A
TGCTCACCGTAATTAAGACGCTCTCTCCGTTTGGAGGAGTGAAGTGAGTTCCAGAGATTTTCT-CTGGCAAACATCCAGGAGCAAAGCTAATGGCTTTAAATCTTCAAGACAAACAAGCG
..........-.............TCT....GA..T...............G..ACA.GAG.T.C.......................................................
                                                                                   StyL10  M  A  L  N  L  Q  D  K  Q  A

       230       240       250       260       270       280       290       300       310       320       330       340
 I  V  A  E  V  S  E  V  A  K  G  A  L  S  A  V  V  A  D  S  R  G  V  T  V  D  K  M  T  E  L  R  K  A  G  R  E  A  G  V
ATTGTTGCTGAAGTCAGCGAAGTAGCCAAAGGCGCGCTGTCTGCAGTAGTTGCGGATTCCCGTGGCGTAACTGTAGATAAAATGACTGAACTGCGTAAAGCAGGTCGCGAAGCTGGCGTA
.......................................................................................................T...........
 I  V  A  E  V  S  E  V  A  K  G  A  L  S  A  V  V  A  D  S  R  G  V  T  V  D  K  M  T  E  L  R  K  A  G  R  E  A  G  V

       350       360       370       380       390       400       410       420       430       440       450       460
 Y  M  R  V  V  R  N  T  L  L  R  R  A  V  E  G  T  P  F  E  C  L  K  D  A  F  V  G  P  T  E  I  A  Y  S  M  E  H  P  G
TACATGCGTGTTGTTCGTAACACCCTGCTGCGCCGTGCTGTTGAAGGTACTCCGTTCGAGTGCCTGAAAGACGCGTTTGTTGGTCCGACCCTGATTGCATACTCTATGGAACACCCGGGC
.................................C.TC............A..................A.............................................
 Y  M  R  V  V  R  N  T  L  L  R  R  v  V  E  G  T  q  F  E  C  L  K  D  t  F  V  G  P  T  E  I  A  Y  S  M  E  H  P  G

       470       480       490       500       510       520       530       540       550       560       570       580
 A  A  A  R  L  F  K  E  F  A  K  A  N  A  K  F  G  V  K  A  A  A  F  E  G  E  L  I  P  A  S  Q  I  D  R  L  A  T  L  P
GCTGCTGCTCGTCTGTTCAAAGAGTTCGCGAAAGCGAATGCAAAATTTGAGGTCAAAGCCGCTGCCTTTGAAGGTGAGCTGATCCCGGCGTCTCAGATCGACCGCCTGGCAACTCTGCCG
.......................................................T..A.............................................................
 A  A  A  R  L  F  K  E  F  A  K  A  N  A  K  F  G  V  K  A  A  A  F  E  G  E  L  I  P  A  S  Q  I  D  R  L  A  T  L  P

       590       600       610       620       630       640       650       660       670       680       690       700
 T  Y  E  E  A  I  A  R  L  M  A  T  M  K  E  A  S  A  G  K  L  V  R  T  L  A  A  V  R  D  A  K  E  A  A ***
ACCTACGAAGAAGCAATTGCACGCCTGATGGCAACCATGAAAGAAGCTTCGGCTGGCAAACTGGTTCGTACTCTGGCTGCTGTACGCGATGCGAAAGAAGCTGCTTAATCGCAGTTATCT
.......................................................C..A.................A...........G...........G...
 T  Y  E  E  A  I  A  R  L  M  A  T  M  K  E  A  S  A  G  K  L  V  R  T  L  A  A  V  R  D  A  K  E  A  A ***

       710       720       730       740       750       760       770       780       790       800       810       820
                                                EcoL7/12  M  S  I  T  K  D  Q  I  I  E  A  V  A  A  M  S  V  M  D  V  V  E
TTTTAACGCATTCGCTTACGTATAAACTTATTCTGATATTCAGGAACAATTTAAATGTCTATCACTAAAGATCAAATCATTGAAGCAGTTGCAGCTATGTCTGTAATGGACGTTGTAGAA
..A.C.A.....T.......................................................................AT.C........C...................
                                                StyL7/12  M  S  I  T  K  D  Q  I  I  E  A  V  s  A  M  S  V  M  D  V  V  E

       830       840       850       860       870       880       890       900       910       920       930       940
 L  I  S  A  M  E  E  K  F  G  V  S  A  A  A  A  V  A  V  A  A  G  P  V  E  A  A  E  E  K  T  E  F  D  V  I  L  K  A  A
CTGATCTCTGCAATGGAAGAAAAATTCGGTGTTTCCGCTGCTGCTGCTGTAGCTGTAGCTGCTGGCCCGGTTGAAGCTGCTGAAGAAAAAACTGAATTCGACGTAATTCTGAAAGCTGCT
.....T.................................................C.....................................................................
 L  I  S  A  M  E  E  K  F  G  V  S  A  A  A  A  V  A  V  A  A  G  P  a  E  A  A  E  E  K  T  E  F  D  V  I  L  K  A  A

       950       960       970       980       990      1000      1010      1020      1030      1040      1050      1060
 G  A  N  K  V  A  V  I  K  A  V  R  G  A  T  G  L  G  L  K  E  A  K  D  L  V  E  S  A  P  A  A  L  K  E  G  V  S  K  D
GGCGCTAACAAAGTTGCTGTTATCAAAGCAGTACGTGGCGCAACTGGCCTGGGTCTGAAAGAAGCTAAAGACTTGGTAGAATCTGCACCGGCTGCTCTGAAAGAAGGCGTGAGCAAAGAC
.......................................................C............T.....C.......................T
 G  A  N  K  V  A  V  I  K  A  V  R  G  A  T  G  L  G  L  K  E  A  K  D  L  V  E  S  A  P  A  A  L  K  E  G  V  S  K  D

      1070      1080      1090      1100      1110      1120      1130
 D  A  E  A  L  K  K  A  L  E  E  A  G  A  E  V  E  V  K ***
GACGCAGAAGCACTGAAAAAAGCTCTGGAAGAAGCTGGCGCTGAAGTTGAAGTTAAATAAGCCAACCCTTCC
.....T..............T.....................................
 D  A  E  A  L  K  K  s  L  E  E  A  G  A  E  V  E  V  K ***
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