Nucleotide sequence of a newly-identified *Escherichia coli* gene, *stpA*, encoding an H-NS-like protein

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An *E. coli* gene, *stpA* (suppression of *td⁻* phenotype), has been identified based on its ability to suppress the mutant phenotype of a plasmid-borne *td⁻* gene from bacteriophage T4. Three suppressor clones were isolated from an *E. coli* *Sau3A* library in pSU20 (1). The clones, which map to 58 min of the *E. coli* chromosome, contain an overlapping DNA segment that imparts the suppression activity (MS, in preparation). DNA sequence analysis of a 978-bp fragment of this segment revealed an ORF that encodes a putative protein of 134 amino acids (Figure 1). Comparative searches (FASTA, TFASTA (2)) showed that the computer-predicted amino acid sequence of *stpA* shares 58% identity with the sequence of *E. coli* *hns*, which encodes H-NS, a DNA-binding protein (3).

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CTGAAATAATCTCGCGCAGGACTGTAAATAGATTAAATTTTGTGGAAATATAATAAGTGA 60
TCGCTTACACTACGCGACGAAATACTTTTTTTGTTTTGGCGTTAAAAGGTTTTCTTTATT 120

ATGTCCGTAATGTTACAAAGTTTAAATAACATTTCGCACCCTCCGTGCGATGGCTCGCGAA 180
M S V M L Q S L N N I R T L R A M A R E
                                     10      20
TTCTCCATTGACGTTCTTGAAGAAATGCTCGAAAAATTCAGGGTTGTCACTAAAGAAAGA 240
F S I D V L E E M L E K F R V V T K E R
                                     30      40
CGTGAAGAAGAAGAACAGCAGCAGCGTGAACCTGGCAGAGCGCCAGGAAAAAATTAGCACC 300
R E E E E Q Q Q R E L A E R Q E K I S T
                                     50      60
TGGCTGGAGCTGATGAAAGCTGACGGAATTAACCCGGAAGAGTTATTGGGTAATAGCTCT 360
W L E L M K A D G I N P E E L L G N S S
                                     70      80
GCTGCTGCACCACGCGCTGGTAAAAACGCCAGCCGCGTCCGGCGAAATATAAATTCACC 420
A A A P R A G K K R Q P R P A K Y K F T
                                     90     100
GATGTTAACGGTGAAACTAAAACCTGGACCGGTACAGGGCCGTACACCGAAGCCAATTGCT 480
D V N G E T K T W T G Q G R T P K P I A
                                     110    120
CAGGCGCTGGCAGAAGGTAAATCTCTCGACGATTTCTGATCTAATTACTGAGGCCGGAT 540
Q A L A E G K S L D D F L I *
                                     130

GTCGCTGCTAGGGCGCGTCCGGCGTCGCTTCTCAAGCTCGTTGGTTCCACGGCATCTTAT 600
CTAACAACCTTGCCATTCCACAAAAACCGCTGATTCTGCAACAGTAACCCGGCACCAA 660
CAAAGCCACTTAATAAGAAGAAACCGCTATTACGGTATAACCCAGTACAACGCCGATTA 720
ATATTAAACCCCGCAGCGATCTGCACCTGGCGCATTAACGGCAAGGGTTGAGATTAT 780
TTACCGCTACTGGCAATCCTGCTTTTTTCCAGCCATCAATCCCATCTTCGAGTAAAAAGA 840
TTTCTGCGGGGGCGGCAATCGCTGCTAATTTATCGGCATTATTACTGGTGCCTTTACCTG 900
CCTGGCAGTGGAATATAATTTGCTCGTGACGTAATTTAGCCGGAAGACCTGACTGTTCCA 960
GCACGGATAATGGAGCCA 978

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Figure 1. Nucleotide sequence of the *stpA* gene. The first ATG is designated as the start codon of the *stpA* gene, although this remains to be experimentally verified.

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