

Nucleotide sequence of the *tuf* gene from *Mycoplasma genitalium*

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A 2.6-kilobase *Hind*III fragment from *Mycoplasma genitalium* (ATCC 33530) was completely sequenced and found to contain an open reading frame coding for a protein of 393 amino acids. The nucleotide sequence is 76% homologous with *tuf* from *M. gallisepticum* (see accompanying paper), while the amino acid sequence shows 81% identity (with conservative replacements) with the EF-Tu of *Escherichia coli tufB* (1). Southern blot hybridization shows that *M. genitalium* contains a single copy of *tuf*. Although the *tuf* gene is followed by sequences which could signal termination of transcription, there is no Shine-Dalgarno (ribosome binding site) sequence nor another open reading frame in the region 5' to *tuf*. Studies showing that sequences upstream of this gene are capable of functioning as a translation initiator in *E. coli* will be published elsewhere.

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          30          60          90          120
TGTITTCACATAAATTAAAGTCCTGAAGATTATAAGCATTATCTCCAGCTTATCTTAAACTTATTAAAAATTAACAACAATAATTTAAACAAATGGCAAGAGAGAAATTTGACCGTTCCAA
(N) A R E K F D R S K
          150          180          210          240
AC CACATGTC CAATGTTGGTACCATTGGTCACATTGCACATGGTAAAACCACTTTAACAGCTGCTATCTGTACAGTTTTAGCAAAGGAGGAAAAATCAGGTCAACCGGTTATGATGAAAT
P R H V K V G T I G H I D H G K T T L T A A I C T V L A K E G K S A A T R Y D E I
          270          300          330          360
TGATAAAGCCCTGAAGAAAAAGCAAGGGAAATCACAAATTAACCTGCACACAGTAGAATATTTCTGACAAACCTGCACTATGCCCATGTTGACTGCTCCCTGGACATGCTGACTACATTA
D K A P E E K A R G I T I N S A H V E Y S S D K R H Y A H V D C P G H A D Y I K
          390          420          450          480
AAATATGATCACAGGTGCTGCACAAATGGATGGAGCTATTCTAGTGTGTTTCAGCACTGATAGTGTGATGCCCAACCCGAGGACACTTACTTGGCCGCAAGTAGGGGTTCCATA
N M I T G A A O M D G A I L V V S A T D S V M P O T R E H I L L A R O V G V P K
          510          540          570          600
AATGGTATTTTTCTCAAAAGTGTGATTTGCTAGTGAAGAGGTACAAGAACTGTTGCTGAAGAAGTACGTGACTGTTAACTCTCTATGGTTTGGTGAAGACACTCTAT
M V V F L N K K D I A S D E R E V O E L V A E E V R D L L T S Y G O E R E V I V G L K P I
          630          660          690          720
TATTTATGCTCAGCTTTAAAGAGCTTGAAGGTGATCCAAAGTGGGABGCTAAGATCCATGATTTGATTAAGCAGTTGATGAATGGATGCTCAACTCCGATCAGTGAAGTAGATAACC
I Y G S A L K A L E G D P R M E A K I H D L I K A V D E M I P T P T R E V D K P
          750          780          810          840
TTTCTTATAGCAATGGAAGTACGACCACTACTGGTAGAGGTACAGTGTGTTACAGGAAGAGTGAAGAAGCTCAAAAGTGAAGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT
F L L A I E D T N I T I G R G T V V T G R V E R G E L K V G O E R E V I V G L K P
          870          900          930          960
AATTAGAAAGCAGTGTACTGGAATGGAATGTTCAAAAAGCACTGATTCAGCAATGGCTGGTGAACAATGCTGGGTATTATTAAGTGGTGGTGAAGTGAAGTGAAGTGAAGTGAAGT
I R K A V V T G I E N F K K E L D S A N A G D N A G V L L R G V E R K E V E R G
          990          1020          1050          1080
TCAAGTTTAGCAAAACCGGCTCTAATTAACCCGACAAAGAAATTTAAAGCTGAGATCTATGCTTTAAGAAAGAAAGAGGTGGTAGACACACTGGTTTTTAAAGCGTTACCGTCTCA
O V L A R P G S I K P N K K F K A E I Y A L K K E E G R N T G F L N G Y R P O
          1110          1140          1170          1200
ATTCTATTTCCGTACCAGTGTGTAATCTGGTTCTATGCTTTAGCTGAAAATACTGAAATGGTTCTACCTGGTGATAATGCTTCTATGCTGTTGAGTTAATTGCTGCTATGCTGTTGTA
F Y F R T T D V T G S I A L A E N T E N V L P G D N A S I T V E L I A P I A C E
          1230          1260          1290          1320
AAAAGGTAGTAACTTCTCAATTCTGGAAGGTGGTAGAAGTGTAGGGGAGGCACTGTAACAGAAGTCTAGAATAGTGAAGTCCGTTTTTGTAGTGTATCTGCTCACTAAGTCTAAAGGAA
K G S K F S I R E G G R T V G A G T V T E V L E *
    
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